

Table 488

	PLACE1009477	13.59	11.11	12.81	10.3	9.83	6.89	8.75	11.15	10.89						
	PLACE1009493	5.63	4.68	4.85	3.04	3.33	2.25	3.06	2.29	1.49	**	**	-	-	-	-
5	PLACE1009502	11.43	9.82	8.39	5.92	5.81	5.8	4.63	7.61	3.19	*	*	-	-	-	-
	PLACE1009524	7.56	7.26	7.63	1.87	3.86	2.97	2.66	3.37	2.46	**	*	-	-	-	-
	PLACE1009527	18.34	12.36	9.71	6.88	11.49	9.95	6.88	5.14	3.52	*	*	-	-	-	-
	PLACE1009531	25.38	45.76	31.03	26.02	25.63	22.82	19.07	17.64	15.03						
	PLACE1009535	12.3	11.08	8.3	3.83	6.2	5.84	3.36	3.71	4.06	*	**	-	-	-	-
	PLACE1009539	8.83	10.23	7.02	4.34	7.56	5.81	5.39	6.61	6.43						
10	PLACE1009540	37.43	26.63	27.99	14.5	25.74	28.63	21	11.9	8.26	*	*	-	-	-	-
	PLACE1009542	12	5.45	5.7	3.62	4.51	6	3.18	3.59	2.67						
	PLACE1009546	12.67	10.42	6.26	3.72	5.36	5.98	4.35	10.8	3.66						
	PLACE1009556	7.91	6.37	6.72	5.1	4.62	3.16	3.16	2.46	2.95	*	**	-	-	-	-
	PLACE1009559	11.99	15.44	10.67	4.76	13.77	8.59	5.94	5.33	6.24	**	*	-	-	-	-
	PLACE1009571	7.82	9.37	5.59	3.8	7.13	3.69	5.84	2.83	4.48						
15	PLACE1009573	22.09	15.96	12.31	9.76	17.27	9.7	8.26	8.91	7.87	*	*	-	-	-	-
	PLACE1009576	13.53	9.49	9.65	4.21	6.31	4.13	5.49	5.78	4.15	*	*	-	-	-	-
	PLACE1009580	9.86	9.33	7.56	5.13	7.69	4.5	8.75	3.59	4.85						
	PLACE1009581	12.95	12.1	8.15	7.19	5.84	4.99	3.45	2.48	3.53	*	**	-	-	-	-
	PLACE1009587	13.3	7.18	8.26	7.06	6.26	5.41	3.85	4.9	4.28						
20	PLACE1009593	18.08	14.97	12.54	14.73	10.76	9.75	5.8	5.66	6.75	**	*	-	-	-	-
	PLACE1009595	24.28	22.3	15.19	12.22	14.76	12.77	19.19	14	13.81						
	PLACE1009596	8.31	5.39	3.71	3.49	5.52	2.24	4.95	2.48	3.3						
	PLACE1009600	19.52	17.07	12.01	6.59	8.79	3.99	8.49	7.24	8.2	*	*	-	-	-	-
	PLACE1009604	19.98	10.38	8.96	4.18	6.3	6.58	3.83	5.54	4.55						
	PLACE1009607	17.2	18	14.19	8.35	9.63	7.58	19.54	17.62	14.33	**	*	-	-	-	-
	PLACE1009613	8.31	8.44	6.06	5.1	6.18	4.22	4.39	2.55	3.96	*	*	-	-	-	-
25	PLACE1009621	18.02	17.88	15.95	7.12	14.76	8.85	8.46	6.45	12.83	*	*	-	-	-	-
	PLACE1009622	16.93	9.51	8.44	5	5.84	4.48	4.96	3.18	4.98						
	PLACE1009624	23.04	19.02	15.23	8.31	9.71	5.05	7.94	5.67	7.85	**	*	-	-	-	-
	PLACE1009637	8.56	7.93	7.75	3.81	7.55	4.55	3.93	3.27	4.29	*	**	-	-	-	-
	PLACE1009639	14.9	6.92	3.57	7.62	5.31	8.34	6.06	5.69	7.84						
30	PLACE1009654	23.03	16.88	13.87	7.6	11.88	8.66	7.4	8.08	10.22	*	*	-	-	-	-
	PLACE1009659	17.62	16.71	15.38	8.59	15.54	12.83	6.78	8.01	7.95	**	*	-	-	-	-
	PLACE1009665	13.55	12.11	8.08	5.71	10.66	10.87	8.53	10.59	6.01						
	PLACE1009669	10.91	11.58	11.44	5.71	8.38	5.23	8.32	8.02	8.98	**	**	-	-	-	-
	PLACE1009670	10	4.03	5.32	3.93	4.76	8.45	5.57	4.18	5.29						
	PLACE1009706	13.41	10.39	7.63	11.97	12.63	1.57	6.84	3.75	9.58						
35	PLACE1009721	15.79	10.82	9.31	5.16	6.52	4.42	9.11	3.24	6.91	*	*	-	-	-	-
	PLACE1009731	5.6	6.57	11.06	5.5	8.58	5.78	5.45	4.8	9.13						
	PLACE1009735	9.43	10.36	12.52	8.67	8.77	6.91	8.15	10.58	12.7						
	PLACE1009737	8.38	8.02	10.98	5.74	17.02	9.89	4.98	11.47	4.66						
	PLACE1009741	8.67	7.59	11.34	6.59	7.8	4.16	2.63	4.89	4.5	*	*	-	-	-	-
40	PLACE1009752	9.51	12.78	18.39	7.46	12.57	11.15	4.36	9.17	6.85						
	PLACE1009763	16.81	19.39	15.73	12.5	15.24	13.69	4.1	8.02	6.41	**	*	-	-	-	-
	PLACE1009766	7.54	8.76	7.16	6.98	11.81	6.16	9.17	7.21	6.61						
	PLACE1009772	12.62	18.28	13.46	16.58	26.84	15.97	7.94	11.57	13.51						
	PLACE1009782	7.96	6.95	7.99	4.24	6.2	9.33	6.26	4.41	4.35	*	*	-	-	-	-
	PLACE1009794	8.71	9.98	15.31	6.91	7.94	5.64	5.81	8.68	9.35						
45	PLACE1009798	15.7	11.58	19.23	8.55	9.28	7.81	5.76	14.83	6.68	*	*	-	-	-	-
	PLACE1009845	5.69	8.07	10.29	5.79	6.81	9.4	3.27	3.21	4.35	*	*	-	-	-	-
	PLACE1009849	4.29	6.11	7.54	5.25	6.21	5.82	3.81	4.56	5.57						
	PLACE1009857	5.97	7.92	9.09	4.47	4.42	3.88	4.36	2.37	3.86	*	*	-	-	-	-
	PLACE1009861	21.52	19.65	20.31	10.08	12.87	8.67	13.97	16.84	16.82	**	*	-	-	-	-
	PLACE1009872	225.97	496.72	352.07	405.22	548.08	335.22	583.26	839.73	801.36	*	*	-	-	-	-
	PLACE1009877	93.23	95.23	121.84	37.51	29.99	31.46	33.83	34.28	50.76	**	*	-	-	-	-
50	PLACE1009879	8.31	6.4	8.23	4.6	3.94	4.45	5.4	6.04	6.14	*	*	-	-	-	-
	PLACE1009886	6.21	5.71	6.04	3.1	4.43	3.64	3.76	3.74	3.91	**	*	-	-	-	-
	PLACE1009888	16.61	15.12	18.96	7.12	11.3	10.4	7.67	15.82	6.68	*	*	-	-	-	-
	PLACE1009908	10.69	13.22	16.94	7.9	15.1	13.2	5.89	21.59	11.16						
	PLACE1009919	18.85	20.8	15.18	25.14	44.25	16.53	6.38	10.08	11.16						
	PLACE1009921	12.5	11.43	13.89	6.9	11.45	10.84	6.74	7.53	6.61	**	*	-	-	-	-
55	PLACE1009923	37.38	53.14	35.03	28.71	69.72	45.4	23.4	36.13	28.69						
	PLACE1009924	26.03	16.67	21.48	6.94	14.99	12.69	29.73	40.32	10.31						
	PLACE1009925	10.23	25.64	14.3	6.85	14.35	14.92	6.32	35.83	7.94						

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	PLACE1009931	29.02	24.07	26.54	12.24	15.5	14.51	9.57	9.79	10.08	**	**	-	-
	PLACE1009935	8.86	7.44	9.7	2.78	11.02	5.42	14.95	3.43	6.35	*	*	-	-
5	PLACE1009947	6.29	6.77	9.33	4.25	4.43	3.14	2.04	2.93	4.01	*	*	-	-
	PLACE1009961	7.86	10.21	16.93	5.24	6.64	4.49	4.58	6.45	5	*	*	-	-
	PLACE1009971	7.79	7.18	10.26	3.38	7.18	3.34	3.67	4.69	3.08	*	*	-	-
	PLACE1009982	20.35	18.31	15.25	6.6	11.54	11.1	7.87	5.59	13.47	*	*	-	-
	PLACE1009992	12.32	8.01	11.62	6.39	8	6.72	5.24	5.76	6.38	*	*	-	-
10	PLACE1009995	21.27	22.11	27.33	13.99	19.4	11.61	8.12	16.7	12.66	*	*	-	-
	PLACE1009997	23.76	8.03	15.66	6.79	12.9	5.63	10.63	9.44	8.19	*	*	-	-
	PLACE1010002	14.56	6.35	12.19	4.66	8.08	5.35	5.32	14.28	7.75	*	*	-	-
	PLACE1010011	15.51	14.11	17.86	6.19	7.34	6.29	9.9	6.46	10.43	**	*	-	-
	PLACE1010013	6.16	5.13	12.68	2.37	2.99	1.56	3.53	4.24	2.98	*	*	-	-
	PLACE1010021	15.95	20.29	19.12	7.11	14.51	9.31	5.22	8.04	6.15	*	**	-	-
	PLACE1010023	27.49	31.11	21.32	17.41	29.7	20.44	16.49	7.28	6.33	*	*	-	-
15	PLACE1010031	20.87	15.58	32.54	10.16	16.34	7.15	9.85	8.36	10.28	*	*	-	-
	PLACE1010039	20.5	6.62	10.22	3.99	6.51	3.25	2.91	6.23	3.6	*	*	-	-
	PLACE1010045	11.17	9.8	13.16	5.75	8.43	6.1	5.11	5.8	5.51	*	**	-	-
	PLACE1010053	7.04	5.22	9.04	6.47	4.19	2.39	2.32	2.12	1.16	*	*	-	-
	PLACE1010060	18.9	18.89	15.21	7.4	8.59	8.37	12.03	13.21	10.77	**	*	-	-
	PLACE1010069	10.06	6.9	13.66	5.33	6.93	4.79	2.86	4.42	3.79	*	*	-	-
20	PLACE1010070	8.15	7.09	9.72	2.34	9.93	4.09	3.65	3.87	2.87	**	*	-	-
	PLACE1010074	63.56	56.74	39.11	24.21	42.72	26.72	25.32	15.29	17.22	*	*	-	-
	PLACE1010076	60.58	44.35	55.45	21.22	23.2	19.4	13.41	12.75	17.59	**	*	-	-
	PLACE1010078	13.76	11.23	14.35	6.69	10.2	8.63	4.38	4.87	4.45	*	**	-	-
	PLACE1010081	27.34	19.16	21.57	12.55	15.05	11.39	11.73	7.47	11.77	*	*	-	-
	PLACE1010083	7.1	7.48	5.64	1.97	2.64	2.62	1.69	2.61	1.96	**	**	-	-
25	PLACE1010089	11.95	9.65	9.57	5.5	5.81	4.38	4.84	2.48	4.43	**	**	-	-
	PLACE1010096	14.85	29.75	16.35	5.81	14.35	9.63	7.28	8.67	5.49	*	*	-	-
	PLACE1010102	22.29	34.08	23.15	9.26	16.03	13.51	7.63	9.06	7.61	*	**	-	-
	PLACE1010105	18.16	20.35	15.99	6.52	12.73	7.6	4.02	4.82	4.1	*	**	-	-
	PLACE1010106	19.44	22.57	15.73	8.29	8.94	12.84	10.96	10.43	10.44	*	*	-	-
30	PLACE1010130	6.62	6.56	4.7	3.25	3.39	2.18	3.26	3.47	3.87	*	*	-	-
	PLACE1010132	20.18	25.39	20.56	20.18	19.1	12.29	12.71	11.47	12.5	**	*	-	-
	PLACE1010134	10.35	11.42	9.68	6.05	6.05	5.55	6.72	4.12	2.88	**	*	-	-
	PLACE1010139	74.68	88.11	79.85	37.26	51.16	43.94	15.68	26.17	18.6	**	*	-	-
	PLACE1010148	10.48	7.43	9.71	13.14	7.54	4.86	3.27	4.13	7.63	**	*	-	-
	PLACE1010155	9.79	7.58	7.63	3.3	5.89	2.96	2.11	2.26	2.53	*	*	-	-
	PLACE1010156	32.59	25.06	24.61	14.7	18.09	11.09	7.29	10.58	14.48	*	**	-	-
35	PLACE1010161	8.48	13.16	10.69	5.15	8.21	6.03	4.47	3.31	5.46	*	*	-	-
	PLACE1010181	8.66	8.08	6.51	2.62	6.54	5.02	3.74	4.12	2.93	**	*	-	-
	PLACE1010194	8.57	7.46	6.67	3.93	4.98	3.84	2.86	2.08	2.37	**	*	-	-
	PLACE1010202	8.39	6.76	12.45	8.31	10.9	5.79	3.56	3.42	2.04	*	*	-	-
	PLACE1010231	12.97	10.31	14.49	7.96	15.61	7.14	8.93	9.42	8.37	*	*	-	-
40	PLACE1010235	12.62	15	11.24	4.59	11.54	4.53	6.11	5.14	4.76	**	*	-	-
	PLACE1010237	5.04	3.77	4.4	2.18	2.37	2.25	2.72	0.64	1.32	**	*	-	-
	PLACE1010251	9.46	4.47	6.29	5.09	4.79	10.14	3.78	5.92	3.88	*	*	-	-
	PLACE1010261	8.26	6.41	4.7	3.42	2.86	2.61	4.52	5.73	4.64	*	*	-	-
	PLACE1010270	7.53	8.07	6.36	3.29	6.44	3.19	3.88	4.95	3.8	**	*	-	-
	PLACE1010273	8.97	10.55	5.7	2.72	5.68	3.04	2.78	2.04	3.83	*	*	-	-
45	PLACE1010274	20.97	18.72	29.56	10.88	16.29	14.38	6.73	5.73	6.16	**	*	-	-
	PLACE1010277	15.29	14.99	14.3	8.87	13.93	8.53	11.24	4.25	6.68	*	*	-	-
	PLACE1010293	16.94	20.61	17.07	9.41	11.63	8.24	17.5	8.1	13.23	**	*	-	-
	PLACE1010297	38.08	33.94	34.95	17.91	31.69	15.63	31.8	20.1	25.32	*	*	-	-
	PLACE1010300	21.55	15.58	11.87	9.15	8.78	7.88	3.82	5.36	5.08	*	*	-	-
	PLACE1010310	323.02	293.14	231.29	170.36	221.96	136.69	214.56	235.35	207.22	*	*	-	-
50	PLACE1010321	10.7	10.58	7.81	4.96	7.93	6.91	5.6	6.6	6.56	*	*	-	-
	PLACE1010324	6.25	5.69	6.54	2.88	4.51	2.6	4.43	3.34	2.72	*	**	-	-
	PLACE1010329	14.25	11.37	11.93	5.93	10.64	4.89	9.64	9.84	9.32	*	*	-	-
	PLACE1010330	12.28	14.21	10.49	11.84	10.18	7.63	12	7.94	17.86	*	*	-	-
	PLACE1010335	27.7	52.66	38.23	18.39	9.7	13.5	16.61	15.38	28.61	*	*	-	-
	PLACE1010341	6.44	4.91	4.72	2	3.7	1.35	4.14	2.93	4.21	*	*	-	-
55	PLACE1010342	2.35	2.93	2.85	2.16	1.61	1.84	1.14	1.19	0.83	*	**	-	-
	PLACE1010346	10.42	6.88	7.23	4.08	5.74	2.77	5.84	6.92	5.88	*	*	-	-
	PLACE1010362	13.25	8.57	9.24	6.56	7.06	3.39	11.5	13.76	14.05	*	*	-	-

Table 490

	PLACE1010364	11.29	7.43	7.22	2.26	3.51	2.16	4.95	3.65	4.16	*	*	-	-
	PLACE1010368	10.78	8.61	7.03	3.98	8.56	5.19	7.58	7.15	5.73	*	*	-	-
5	PLACE1010373	30.2	26.81	24.17	14.82	22.58	10.46	24.63	20.09	20.87	*	*	-	-
	PLACE1010383	18.56	18.15	16.04	10	15.54	3.52	27.13	12.41	12.03	*	*	-	-
	PLACE1010385	2.48	1.73	1.18	0.83	2.33	0.49	2.65	1.19	2.06	*	*	-	-
	PLACE1010389	8.48	7.51	8.42	3.75	4.47	5.47	3.96	4.51	2.91	**	**	-	-
	PLACE1010401	3.24	0.96	4.6	2.29	2.49	1.63	2.81	2.31	1.6	*	*	-	-
10	PLACE1010410	22.91	15.39	21.28	8.31	20.95	12.79	12.79	10.9	11.3	*	*	-	-
	PLACE1010418	18.78	19.01	17.17	5.75	13.45	6.67	11.25	18.37	11.11	*	*	-	-
	PLACE1010425	10.58	10.75	18.36	4.2	4.88	3.19	8.87	11.17	8.75	*	*	-	-
	PLACE1010443	12.48	14.66	16.77	5.6	14.99	6.09	8.79	8.23	11.76	*	*	-	-
	PLACE1010445	36.17	45.7	37.43	17.58	20.28	18.29	39.23	32.46	41.56	**	**	-	-
	PLACE1010481	60.4	46.95	65.37	22.92	26.42	21.44	27.71	30.53	27.4	**	**	-	-
15	PLACE1010482	127.4	82.31	84.53	104.64	120.51	109.85	62.48	50.87	49.97	*	*	-	-
	PLACE1010491	71.28	72.3	73.41	43.51	47.95	35.09	68.63	86.51	74.84	*	*	-	-
	PLACE1010492	20.32	20.74	19.72	20.62	27.04	23.27	9.07	12.55	10.15	**	**	-	-
	PLACE1010509	11.2	13.07	17.83	8.18	12.58	8.24	5.79	8.34	7.68	*	*	-	-
	PLACE1010518	9.76	12.31	18.67	8.17	8.57	7.5	8.04	6.33	6.73	*	*	-	-
	PLACE1010522	8.32	9.35	9.63	6.71	11.42	6.63	6.37	5.88	7.65	*	*	-	-
20	PLACE1010529	13.09	22.15	14.64	11.31	17.05	8.58	7.61	9.45	9.29	**	**	-	-
	PLACE1010547	36.79	34.33	38.34	12.39	16.81	11.19	21.21	24.3	23.05	**	**	-	-
	PLACE1010560	10.15	9.34	9.56	6.09	4.54	5.89	6.02	5.35	6.13	**	**	-	-
	PLACE1010562	4.79	4.39	12.01	8.8	8.65	6.38	5.41	7.48	4.4	*	*	-	-
	PLACE1010579	74.54	67.98	59.08	46.33	48.92	48.24	56.27	84.49	60.31	*	*	-	-
	PLACE1010580	38.79	45.7	46.75	22.24	30	17.17	31.95	38.27	36.2	*	*	-	-
25	PLACE1010599	29.35	25.54	32.71	12.61	15.12	14.18	19.83	24.34	23.16	**	**	-	-
	PLACE1010606	31.76	30.37	40.62	15.46	18.15	14.23	22.77	25.83	28.81	*	*	-	-
	PLACE1010616	16.39	26.11	18.04	12.85	17.78	7.33	34.49	3.67	4.92	**	**	-	-
	PLACE1010622	9.08	4.75	12.08	2.52	4.28	2.63	11.54	11.12	6.28	*	*	-	-
	PLACE1010624	292.79	228.16	204.46	212.8	278.88	210.51	168.11	171.99	155.01	*	*	-	-
	PLACE1010628	48.66	44.83	51.05	27.25	26.82	37.41	15.79	19.04	21	*	*	-	-
30	PLACE1010629	19.03	17.43	20.71	12.12	16.38	15.36	14.93	10.66	11.67	*	*	-	-
	PLACE1010630	15.62	16.61	29.46	8.82	19.7	10.88	11.96	14.1	11.42	*	*	-	-
	PLACE1010631	22.99	34.46	25.54	20.07	21.82	17.69	19.23	10.89	16.98	*	*	-	-
	PLACE1010651	8	10.03	11.34	5.4	9.54	5.75	4.35	5.43	5.06	**	**	-	-
	PLACE1010661	13.76	16.34	32.78	7.67	13.64	27.31	6.28	10.55	7.26	*	*	-	-
	PLACE1010662	28.68	22.75	30.53	8.67	12.27	9.85	25.45	28.04	24.56	*	*	-	-
35	PLACE1010668	37.33	37.7	40.55	22.62	25.66	20.72	36.78	44.21	37.46	**	**	-	-
	PLACE1010702	12.3	8.26	13.51	6.5	7.73	5.49	8.16	17.08	6.46	*	*	-	-
	PLACE1010709	70.65	75.49	68.95	55.09	47.9	57.04	50.07	52.69	55.39	**	**	-	-
	PLACE1010713	60.41	68.48	77.71	36.46	48.82	48.26	28.63	32.14	23.64	**	**	-	-
	PLACE1010714	14.85	12.78	15.24	4.19	7.98	4.28	3.33	8.97	5.69	**	**	-	-
	PLACE1010716	10.07	15.73	17.8	4.88	22.94	9.1	5.99	13.73	3.7	*	*	-	-
40	PLACE1010717	16.27	25.02	15.64	13.63	18.64	10.49	10.76	15.16	3.55	*	*	-	-
	PLACE1010720	27.49	32.65	34.2	14.65	18.34	8.25	20.45	22.85	22.74	**	**	-	-
	PLACE1010739	32.05	33.62	24.71	15.33	21.42	15.16	17.5	28.68	18.95	*	*	-	-
	PLACE1010743	44.76	28.81	34.77	15.52	24.11	19.41	14.02	9.67	5.8	*	*	-	-
	PLACE1010752	26.13	19.45	22.02	11.29	9.49	11.37	16.27	24.35	13.97	**	**	-	-
	PLACE1010761	15.13	12.05	32.55	15.98	9.45	8.78	11.14	13.99	12.89	*	*	-	-
45	PLACE1010771	28.91	75.96	37.99	25.83	90.51	39.2	31.02	18.86	25.47	**	**	-	-
	PLACE1010784	98.45	116.91	93.11	48.56	63.14	52.26	30.32	31.37	33.38	**	**	-	-
	PLACE1010786	16.19	15.53	16.87	8.23	15.52	9.85	7	6.49	9.87	**	**	-	-
	PLACE1010789	46.25	33.26	40.6	14.8	19.17	10.09	44.64	47.22	35.88	**	**	-	-
	PLACE1010800	13.97	9.78	14.67	8.91	6.6	5.82	4.05	5.43	4.76	*	*	-	-
50	PLACE1010802	13.35	16.74	27.18	16.21	23.96	4.91	12.32	5.78	37.85	*	*	-	-
	PLACE1010811	26.9	21.58	31.28	13.09	18.01	12.69	11.33	11.86	10.25	*	*	-	-
	PLACE1010813	10.21	6.96	9.67	4.84	4.38	4.87	3.92	2.83	2.64	*	*	-	-
	PLACE1010827	10.79	10.81	12.05	5.43	7.46	5.87	6.65	5.02	3.76	**	**	-	-
	PLACE1010833	9.18	9.98	8.82	3.14	6.94	3.42	1.97	2.07	1.97	*	*	-	-
	PLACE1010839	24.14	30.08	20.18	11.7	20	12.82	16.21	11.13	15.42	*	*	-	-
55	PLACE1010858	15.47	10.08	17.88	6.16	6.58	4.26	11.23	8.32	12.26	*	*	-	-
	PLACE1010857	32.67	31.48	18.71	21.99	18.34	15.41	16.23	15.82	15.61	*	*	-	-
	PLACE1010870	5.83	4.92	4.28	3.87	3.55	2.92	2.91	2.04	1.94	*	*	-	-
	PLACE1010877	26.07	20.6	20.89	14.13	8.42	9.71	13.42	12.71	7.25	**	**	-	-

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	PLACE1010882	17.06	13.54	8.42	6.17	5.69	5.82	7.13	5.03	5.37	*	-	-
	PLACE1010891	27.43	30.32	21.15	13.46	14.41	7.46	15.36	15.07	24.71	*	-	-
5	PLACE1010896	13.62	18.23	16.16	6.92	8.03	5.78	3.54	4.62	4.06	**	**	-
	PLACE1010900	66.6	75.65	67.52	55.68	59.03	45.47	67.12	53.92	39.14	*	-	-
	PLACE1010916	104.52	71.53	76.5	35.13	35.16	33.1	29.84	23.73	27.17	**	**	-
	PLACE1010917	14.21	14.67	11.27	7.82	5.59	7.41	7.69	7.06	8.76	**	**	-
	PLACE1010924	5.86	2.7	4.51	2.89	4.47	3.08	2.47	3.1	1.31	*	-	-
	PLACE1010925	4.94	4.55	4.99	1.88	2.53	1.67	3.09	1.69	1.78	**	**	-
10	PLACE1010926	13.94	11.16	11.63	5.87	7.64	6.22	5.6	4.23	4.99	**	**	-
	PLACE1010942	207.77	196.21	175.46	147.15	130.24	102.36	197.42	120.16	123.73	*	-	-
	PLACE1010943	31.5	25.2	22.98	12.49	22.16	9	15.12	16.22	13.62	*	-	-
	PLACE1010944	63.2	92.75	68.43	51.82	78.63	47.87	87	58.47	73.16	*	-	-
	PLACE1010947	33.76	22.26	22.3	12.84	13.89	8.22	22.66	11.99	13.89	*	-	-
15	PLACE1010954	10.33	11.3	11.05	5.3	5.81	5.51	5.34	5.12	4.22	**	**	-
	PLACE1010960	15.62	30.44	20.31	7.94	8.25	7.04	11.37	9.05	8.5	*	-	-
	PLACE1010965	13.17	14.34	9.79	7.54	4.78	3.78	4.15	4.73	5.18	*	**	-
	PLACE1010968	18.41	14.95	14.27	6.84	9.6	5.59	12.62	6.34	9.37	**	*	-
	PLACE1010978	57.65	54.74	36.05	40.68	34.09	13.7	16.85	10.36	20.32	*	-	-
	PLACE1010982	21.44	26.06	15.9	7.42	6.54	11.09	10.66	7.85	9.32	*	-	-
20	PLACE1010990	327.98	344.55	256.15	258.07	367.78	240.66	208.45	171.08	173.44	*	-	-
	PLACE1011017	100.16	59.4	54.99	23.72	27.4	15.8	91.94	75.46	99.74	*	-	-
	PLACE1011019	13.37	8.64	6.46	8.37	6.37	4.79	6.61	7.41	7.81	*	-	-
	PLACE1011026	17.67	16.91	13.69	8.74	11.48	8.93	15.71	13.37	15.94	*	-	-
	PLACE1011032	5.5	8.88	7.51	2.84	5.75	2.99	4.5	3.38	3.21	*	-	-
	PLACE1011041	11.32	11.72	11.41	4.79	6.17	4.9	2.74	0	1.85	**	**	-
25	PLACE1011045	30.68	27.07	24.09	20.73	22.77	14.24	25.68	22.96	30.06	*	-	-
	PLACE1011046	10.75	10.03	9.15	3.68	6.42	4.38	4.21	3.5	2.56	**	**	-
	PLACE1011054	23.11	26.67	18.54	13.24	17.45	11.68	27.3	21.77	27.93	*	-	-
	PLACE1011056	5.67	3.31	3.16	3.73	4.11	8.46	6.33	3.05	6.91	*	-	-
	PLACE1011057	10.04	10.53	7.99	8.15	6.14	3.72	11.95	6.55	7.6	*	-	-
	PLACE1011059	19.4	17.96	11.33	7.08	9.45	9.52	6.53	6.86	9.19	*	-	-
30	PLACE1011065	9.28	7.31	5.97	5.75	7.03	4.1	2.13	5.18	0.49	*	-	-
	PLACE1011087	26.84	40.15	33.04	57.32	27.48	16.29	127.9	19.42	37.4	*	-	-
	PLACE1011090	10.52	7.52	6.48	3.01	5.18	3.1	6.04	4.61	6.16	*	-	-
	PLACE1011109	43.09	16.58	13.76	6.5	19.94	4.84	12.2	7.21	12.97	*	-	-
	PLACE1011114	17.98	24.04	19.89	13.12	19.15	8.13	12.09	13.25	14.96	*	-	-
35	PLACE1011116	30.03	28.53	37.37	10.98	8.87	7	8.26	10.18	5.99	**	-	-
	PLACE1011122	5.9	6.6	5.93	4.16	4.82	3.11	3.97	4.69	2.89	*	-	-
	PLACE1011133	6.47	4.35	6.51	3.81	3.93	3.81	2.72	5.4	2.91	*	-	-
	PLACE1011134	5.48	5.99	6.34	4.28	4.27	3.64	3.72	3.86	3.76	**	**	-
	PLACE1011143	4.76	9.67	5.59	2.21	5.45	3.27	2.93	3.83	4.13	*	-	-
	PLACE1011146	10.48	13.56	12.48	9.3	11.11	4.11	4.38	6.69	4.48	**	-	-
40	PLACE1011160	7.71	9.99	6.71	4.98	7.77	3.25	6.45	4.47	3.78	*	-	-
	PLACE1011169	21.99	27.95	32.58	8.87	19.75	11.83	12.6	15.59	9.42	*	-	-
	PLACE1011181	5.25	3.37	6	2.06	4.49	2.29	2.61	4.09	3.85	*	-	-
	PLACE1011185	60.3	36.78	36.17	37.68	34.15	24.31	17.32	33.87	29.05	*	-	-
	PLACE1011186	25.07	30.45	27.42	12.69	20.01	15.83	19.93	27.9	21.4	*	-	-
	PLACE1011203	10.27	18.2	13.6	9.36	12.5	6.83	8.02	13.49	10.02	*	-	-
45	PLACE1011214	7.39	9.12	10.92	5.57	5.78	3.95	1.49	2.02	3.84	*	**	-
	PLACE1011219	7.03	5.86	7.27	8.39	4.52	4.58	9.07	4.64	3.23	*	-	-
	PLACE1011221	10.63	11.42	9.42	5.44	10.51	4.92	4.92	5.52	6.28	**	-	-
	PLACE1011229	13.76	13.72	12.78	9.23	7.48	4.86	6.43	7.1	4.99	**	**	-
	PLACE1011231	34.58	28.7	50.02	23.03	24.8	13.82	19.12	24.97	26.97	*	-	-
	PLACE1011236	13.02	10.94	13.96	5.99	7.59	5.06	4.42	6.98	4.82	**	**	-
50	PLACE1011247	571.8	409.73	639.71	528.63	738.01	566.23	553.23	542.58	267.58	*	-	-
	PLACE1011263	4.49	7.26	9.65	4.09	5.29	4.39	2.77	4.83	3.37	*	-	-
	PLACE1011273	9.77	15.11	15.29	8	7.81	4.87	6.04	5.28	3.97	*	-	-
	PLACE1011278	21.08	26.71	20.88	9.67	19.17	11.18	9.31	5.1	7.74	*	-	-
	PLACE1011289	8.76	9.56	9.49	5.47	7.47	4.38	4.05	4.14	4.61	*	**	-
	PLACE1011291	3.27	1.73	2.37	1.38	1.37	0.09	2.52	4.22	1.75	*	-	-
	PLACE1011296	15.1	14.79	20.48	7.86	6.09	7.28	12.72	18.07	15.96	**	-	-
55	PLACE1011310	49.57	40.91	47.27	26.08	24.65	29.43	26.25	31.46	34.3	**	*	-
	PLACE1011311	12.85	11.18	13.64	5.84	6.4	7.88	4.02	7.29	3.99	**	**	-
	PLACE1011321	316.11	225.18	251.29	230.23	241.81	208.08	340.56	284.43	231.07	*	-	-

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	PLACE1011325	67.49	68.67	34.36	32.79	55.55	25.52	26.06	16.66	23.25	*	-
	PLACE1011332	37.6	32.99	20.69	24.89	22.84	17.06	26.8	25.39	39.36	*	-
	PLACE1011340	6.86	4.22	8.9	7.42	3.33	10.93	4.69	1.22	1.76	*	-
5	PLACE1011353	13.06	9.45	9.31	4.05	5.07	3.21	9.83	8.83	10.17	**	-
	PLACE1011360	7.09	6.29	7.09	5.01	4.64	2.08	4.25	9.92	6.13	*	-
	PLACE1011364	36.2	48	46.69	18.82	32.17	16.48	29.78	23.08	23.29	*	-
	PLACE1011365	56.47	40.06	43.45	30.4	25.78	22.53	35.29	36.44	44.51	*	-
	PLACE1011371	8.03	11.85	15.3	3.37	4.12	1.15	3.67	7.88	4.18	*	-
10	PLACE1011375	7.04	6.27	10.93	2.06	3.1	2.3	1.72	3.77	5.21	*	-
	PLACE1011386	164.83	196.07	182.53	143.65	164.65	123.82	185.62	179.87	160.52	*	-
	PLACE1011399	13.53	14.93	12.77	5.31	8.23	5.03	14.49	12.53	13.08	*	-
	PLACE1011406	24.35	18.36	25.14	17.24	17.93	13.01	14.05	16.63	13.24	*	-
	PLACE1011407	11.96	8.15	11.8	4.39	4.52	4.88	4.7	7.06	4.99	**	*
	PLACE1011419	45.6	33.74	47.01	28.72	27.55	25.25	33.12	24.14	29.66	*	-
15	PLACE1011433	12.4	6.05	13.11	5.89	9.23	4.52	4.03	6.39	4.28	*	-
	PLACE1011440	22.91	21.43	16.68	17.18	6.65	6.34	4.22	2.79	3.13	**	-
	PLACE1011452	21.99	27.18	21.9	7.47	5.58	8.33	1.98	2.55	3.76	**	-
	PLACE1011465	8.59	10.4	8.63	4.43	3.74	3.61	3.27	3.42	2.9	**	-
	PLACE1011472	12.35	11.03	8.39	5.76	5.63	4.74	4.12	4.06	4.53	*	-
	PLACE1011477	6.89	4.15	8.42	3.82	3.1	2.49	5.68	5.36	7.03	*	-
20	PLACE1011478	147.8	127.45	151.17	98.43	129.14	92.91	97.94	88.28	67.65	**	-
	PLACE1011492	8.86	4.94	8.71	5.63	3.6	3.44	7.78	6.26	3.91	*	-
	PLACE1011498	11.86	13.27	11.87	6.42	7.11	5.44	7.49	6.76	6.34	**	-
	PLACE1011501	5.51	5	4.76	1.97	2.88	1.92	1.53	1.09	0.63	**	-
	PLACE1011503	8.36	7.18	8.72	3.16	3.42	2.41	3.54	1.96	1.63	**	-
	PLACE1011509	6.79	8.76	6.8	2.67	3.22	3.57	3.54	1.66	2.46	**	-
25	PLACE1011514	39.36	42.6	35.59	29.05	24.04	21.59	28.05	21.32	28.44	**	-
	PLACE1011516	2.25	2.2	3.02	1.65	1.39	0.92	2.22	1.19	1.28	*	-
	PLACE1011520	56.28	54.22	44.97	60.14	59.13	46.66	37.37	33.63	31.08	*	-
	PLACE1011538	3.92	2.67	3.99	1.41	2.25	0.89	1.63	0.52	1.52	*	-
	PLACE1011555	5.04	5.36	4.18	1.71	1.41	2.12	2.42	1.56	2.13	**	-
	PLACE1011561	40.83	32.97	31.05	28.42	20.97	80.97	15.06	18.06	18.45	**	-
30	PLACE1011563	10.59	8.43	6.69	4.39	3.31	1.28	2.74	2.46	2.05	*	-
	PLACE1011567	8.99	5.72	8.85	4.85	2.48	0.94	3.39	1.71	1.08	*	-
	PLACE1011569	17.38	15.57	12.39	8.98	14.17	5.41	4.61	3.24	6.59	**	-
	PLACE1011576	9.4	4.88	4.15	2.79	3.81	3.52	4.89	6.65	7.51	*	-
	PLACE1011586	11.29	10.02	9.62	6.88	3.58	5.48	4.18	5.75	5.57	**	-
	PLACE1011635	30.93	17.84	23.55	13.98	14.55	6.78	13.1	10.06	12.62	*	-
35	PLACE1011641	17.21	13.31	15.5	11.83	10.3	8.13	12.16	8.31	8.02	*	-
	PLACE1011642	14.04	9.07	8.81	4.73	8.8	2.98	2.08	3.09	1.68	**	-
	PLACE1011643	21.88	15.91	14.62	9.69	7.73	4.5	12.37	9.92	7.66	*	-
	PLACE1011646	50.88	55.98	42.92	29.54	24.58	20.05	12.83	13.88	9.31	**	-
	PLACE1011649	101.51	209.33	140.08	111.98	127.38	61.19	33.86	36.5	31.67	*	-
40	PLACE1011650	21.23	16.3	17.27	6.34	7.58	5.35	13.14	9.77	13.14	**	-
	PLACE1011661	38.54	29.6	21.98	17.54	11.85	16.02	29.9	27.07	30.09	*	-
	PLACE1011664	4693.7	3704.8	3103.3	1925.9	2495.7	2690.1	3081.7	3779.5	2474.5	*	-
	PLACE1011672	14.58	19.19	17.05	4.82	11.54	6.52	8.71	6.37	8.66	*	-
	PLACE1011675	27.27	28.5	23.64	11.76	7.61	13.02	10.47	6.83	11.83	**	-
	PLACE1011682	31.95	30.83	21.79	24.47	12.69	9.16	19.26	16.69	17.56	*	-
45	PLACE1011708	240.54	265.47	223.19	186.79	250.35	199.96	147.11	130.97	144.28	*	-
	PLACE1011719	2115.1	1324.5	1826.8	1953.8	1265.9	1000.2	1428.6	860.26	1269.9	*	-
	PLACE1011725	14.63	11.44	8.67	4.74	6.3	2.04	9.22	9.94	8.53	*	-
	PLACE1011729	17.92	12.45	10.92	5.48	6.85	3.57	9.59	6.92	10.12	*	-
	PLACE1011741	19.11	16.45	8.97	6.48	6.39	4.13	6.03	4.62	6.01	*	-
	PLACE1011749	198.63	245.38	186.1	98.37	139.73	93.5	146.64	106.95	169.56	*	-
50	PLACE1011757	55.97	64.31	51.13	22.6	27.43	20.99	59.9	47.96	65.48	**	-
	PLACE1011762	112.55	118.61	84.99	66.65	83.7	57.21	113.37	92.71	109.2	*	-
	PLACE1011778	14.17	14.57	14.58	9.09	8.23	7.54	9.58	8.34	17.29	**	-
	PLACE1011783	34.3	38.67	23.05	14.78	12.16	17.09	15.47	21.92	20.45	*	-
	PLACE1011795	26.86	17.86	14.49	8.41	7.89	4.41	13.16	9.37	14.56	*	-
	PLACE1011810	6.46	2.52	3.35	2.53	2.07	0.8	3.19	3.06	3.38	*	-
55	PLACE1011824	86.62	55.93	50.79	29.92	21.66	12.01	21.62	24.56	19.64	*	-
	PLACE1011825	47.11	53.31	45.03	28.52	34.47	24.16	61.42	44.87	47	**	-
	PLACE1011835	12.82	11.42	11.32	5.55	7.84	4.84	7.39	9.98	8.67	**	-

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	PLACE1011836	18.92	14.13	10.67	5.56	9.72	5.44	13.34	9.9	14.01			
	PLACE1011847	18.99	15.08	12.62	9.39	11.06	5.84	18.15	10.26	13.1	*	-	
	PLACE1011855	44.67	41.99	25.3	17.11	33.33	14.76	56.6	42.68	40.57	*	-	
5	PLACE1011858	17.26	16.38	17.11	5.33	7.08	6.53	8.22	8.74	5.1	**	**	-
	PLACE1011874	23.12	12.72	25.71	16.84	19.22	7.85	10.17	8.71	12.51	*	-	
	PLACE1011875	10.68	9.98	11.17	5.18	10.63	6.67	7.18	6.04	4.93	**	-	
	PLACE1011877	4.39	5.14	4.95	3.7	5.52	3.78	2.59	4.05	4.24	*	-	
	PLACE1011891	21.71	17.57	18.99	7.39	14.47	8.67	8.21	9.5	7.86	*	**	-
10	PLACE1011896	15.35	16.64	24.3	10.41	10.14	12.14	5.01	8.13	7.98	*	-	
	PLACE1011920	16.12	14.42	15.9	7.68	8.85	7.76	6.46	2.46	3.24	**	-	
	PLACE1011922	9.14	7.55	8.03	4.49	8.39	4.08	7.97	6.15	5.33	*	-	
	PLACE1011923	166.86	139.43	146.9	104.2	117.42	86.95	136.93	140	124.61	*	-	
	PLACE1011937	11.45	9.18	10.8	8.58	6.75	5.1	5.71	6.29	5.46	*	**	-
	PLACE1011939	20.33	21.55	26.93	12.79	15.19	13.44	14.58	11.31	12.67	*	-	
15	PLACE1011940	46.38	48.76	46.73	35.11	34.53	31.67	43.31	41.44	39.86	**	**	-
	PLACE1011962	58.59	70.73	80.18	30.15	38.09	28.84	47.96	47.68	42.57	*	-	
	PLACE1011964	53.78	49.36	46.95	41.43	47.33	36.34	22.23	20.62	20.74	*	-	
	PLACE1011978	50.21	52.86	64.71	38.6	31.39	22.36	22.46	20.19	18.12	**	-	
	PLACE1011980	13.57	18.54	10.96	9.65	15.28	6.53	4.68	9.99	8.31	*	-	
	PLACE1011981	46.23	28.89	45.44	16.98	15.61	9.98	14.66	11.01	11.18	*	**	-
20	PLACE1011982	116.69	99.4	123.56	57.42	68.6	45.01	97.45	90.55	115.07	**	-	
	PLACE1011995	8.31	11.27	12.33	5	7.29	7.22	6.27	8.29	4.87	*	-	
	PLACE1012023	36.36	36.13	39.16	21.46	26.03	23.3	20.6	21.06	24.79	**	-	
	PLACE1012026	72.96	80.46	66.75	52.71	40.29	50.42	21.72	33.87	25.71	**	-	
	PLACE1012031	6.69	7.34	9.86	2.73	6.11	3.89	3.41	3.11	3.97	*	-	
	PLACE20000003	144.75	222.75	62.64	74.47	133.88	40.79	39.01	32.21	30.64	*	-	
25	PLACE20000005	20.72	25.78	18.16	9.79	22.43	11.52	5.79	8.65	14.3	*	-	
	PLACE20000006	74.92	51.78	61.3	27.4	24.75	21.12	50.02	43.94	72.77	**	-	
	PLACE20000007	11.31	11.29	12.93	6.68	7.02	5.2	5.63	10.02	7	**	-	
	PLACE20000011	20.07	19.36	23.84	14.92	4.58	15.77	9.39	11.52	19.43	*	-	
	PLACE20000014	10.47	6.72	12.3	4.76	6.02	3.48	3.63	6.9	4.73	*	-	
30	PLACE20000015	63.77	83.22	43.62	34.06	43.14	43.39	19.29	26.64	36.8	*	-	
	PLACE20000017	64.44	66.07	78.07	40.68	48.09	29.95	59.7	61.53	44.91	*	-	
	PLACE20000021	131	136.36	142.32	116.28	142.66	101.82	89.75	68.71	86.35	**	-	
	PLACE20000022	6.52	6.75	7.52	3.85	5.14	3.55	4.53	1.84	5.72	*	-	
	PLACE20000030	277.18	275.48	252.39	182.81	167.16	156.31	125.23	96.07	135.65	**	-	
	PLACE20000032	8.03	6.4	8.6	4.38	5.33	2.81	4.32	15.18	4.01	*	-	
35	PLACE20000033	19.24	16.61	20.22	9.43	14.03	10.83	8.93	12.91	10.87	**	-	
	PLACE20000034	212.75	182.06	146.24	219.9	195.86	170.13	146.86	112.34	125.26	*	-	
	PLACE20000035	8.9	10.84	13.51	4.94	3.89	4.8	3.72	4.38	6.52	**	-	
	PLACE20000043	13.64	20.44	15.11	6.28	13.12	6.04	6.05	7.64	6.22	*	-	
	PLACE20000044	7.28	9.48	9.44	3.48	5.71	4.79	4.48	4.25	4.59	*	**	-
	PLACE20000047	17.41	19.39	12.83	6.83	12.83	7.05	7.81	8.54	5.78	*	-	
40	PLACE20000050	18.34	17.87	22.05	7.34	8.98	7.31	7.51	8.31	7.94	**	-	
	PLACE20000051	53.75	61.97	78.23	34.92	41.03	37.86	22.68	14.04	20.77	**	-	
	PLACE20000062	44.19	44.8	62.08	41.54	45.17	33.58	38.88	38.06	40.24	*	-	
	PLACE20000072	216.69	181.79	181.98	200.73	185.27	186.23	111.76	113.44	105.53	**	-	
	PLACE20000073	8.16	10.75	9.27	3.77	4.89	3.62	4.56	4.79	3.59	**	-	
	PLACE20000097	120.94	128.07	120.9	148.48	131.74	105.73	90.14	87.25	86.79	**	-	
45	PLACE20001000	13.48	14.19	15.99	6.02	8.77	5.66	4.8	3.51	6.24	**	-	
	PLACE20001003	355.83	328.95	197.42	251.22	436.52	235.01	231.23	336.03	237.95	*	-	
	PLACE20001006	32.23	23.41	23.14	14.46	6.17	13.03	9.13	10.5	5.27	*	-	
	PLACE20001011	152.37	157.38	125.3	88.6	105.91	83.66	90.52	44.23	69.19	*	**	-
	PLACE20001015	27.01	16.97	16.32	19.6	21.67	16.26	13.74	11.32	11.83	*	-	
	PLACE20001018	229.23	214.41	143.27	124.01	152.19	92.15	153.7	62.85	67.07	*	-	
50	PLACE2000124	7.33	5.71	5.57	2.12	1.78	1.55	2.01	1.55	1.09	**	-	
	PLACE2000132	18.07	19.01	19.11	15.64	11.16	12.49	9.7	6.52	8.48	*	**	-
	PLACE2000136	33.6	40.68	24.33	13.95	42.68	22.54	9.98	17.8	18.28	*	-	
	PLACE2000137	6.87	5.34	6.91	1.61	2.95	2.09	1.24	1.8	2.36	*	-	
	PLACE2000140	11.37	11.51	12.2	8.07	9.45	9.49	11.48	11.25	10.8	*	-	
	PLACE2000147	10.22	7.24	9.46	6.01	5.85	4.51	7.52	7.6	9.27	*	-	
55	PLACE2000159	17.95	21.42	13.85	5.51	9.57	6.43	4.84	5.27	2.27	*	-	
	PLACE2000164	8.53	12.11	9.44	3.18	4.26	4.12	4.98	9.97	2.13	**	-	
	PLACE2000170	38.84	46.93	33	28	28.56	22.27	30.03	23.36	30.82	*	-	

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	PLACE2000172	9.55	12.02	10.86	4.88	5.87	3.32	4.01	4.8	6.2	**	-	-
	PLACE2000173	16.63	20.86	19.04	9.66	11.13	9.7	6.74	6.23	3.14	**	-	-
5	PLACE2000174	6.73	7.76	6.4	3.37	4.73	2.4	3.08	3.26	1.62	*	-	-
	PLACE2000176	47.07	39.92	36.01	26.8	32.78	24.97	24.68	26.79	25.41	*	-	-
	PLACE2000187	11.49	9.44	7.22	4.28	4.58	4.45	2.47	4.64	3.94	*	-	-
	PLACE2000216	15.24	13.28	16.1	7.83	10.53	7.67	11.12	11.23	10.67	**	-	-
	PLACE2000219	43.32	28.21	37.3	18.17	6.67	13.94	7.68	7.79	6.4	*	-	-
	PLACE2000221	9.58	7.64	7.46	2.22	3.99	1.24	4.08	2.43	3.07	**	-	-
10	PLACE2000223	16.67	12.34	12.95	4.95	6.75	4.32	4.43	2.01	2.87	**	-	-
	PLACE2000231	8.48	8.65	7.01	3.78	5.92	4.27	4.19	2.32	3.59	*	-	-
	PLACE2000235	7.02	5.03	3.66	1.54	5.33	1.9	4.43	3.57	3.78	*	-	-
	PLACE2000246	21.31	17.8	13.21	7.9	13.4	6.47	11.52	9.6	10.91	*	-	-
	PLACE2000264	41.11	43.3	30.68	20.28	22.27	18.14	15.54	15.85	15.69	*	-	-
	PLACE2000274	6.8	7.42	7.36	4.35	3.04	1.89	3.84	3.12	4.31	**	-	-
15	PLACE2000287	32.11	30.76	24.99	20.39	25.61	21.53	17.96	15.3	19.45	**	-	-
	PLACE2000296	42.94	34.88	35.63	23.36	22.17	20.37	32.02	14.36	29.35	*	-	-
	PLACE2000302	252.74	304.77	237.45	265.35	267.99	217.29	124.09	112.58	106.48	**	-	-
	PLACE2000305	21.47	23.58	17.69	16.14	17.23	16.65	22.14	18.21	22.01	*	-	-
	PLACE2000317	37.2	38.12	23.24	20.01	28.38	14.37	31.05	33.16	31.64	*	-	-
20	PLACE2000324	18.44	17.84	10.35	6.13	8.75	4.98	3.24	8.74	3.2	*	-	-
	PLACE2000334	21.38	17.6	11.43	10.36	9.7	9.37	7.54	6.15	9.1	*	-	-
	PLACE2000335	71.59	66.59	54.82	51.15	35.99	40.86	33.77	36.69	29.67	*	-	-
	PLACE2000340	20.62	28.95	19	17.88	23.88	12.85	16.23	14.73	16.82	*	-	-
	PLACE2000341	14.8	11.92	10.45	5.66	5.34	5.33	5.38	5.46	7.66	**	-	-
	PLACE2000342	23.53	21.95	21.97	16.28	11.86	11.51	22.81	14.69	23.12	**	-	-
	PLACE2000347	9.57	9.26	10.05	4.16	2.94	3.3	5.78	3.54	5.48	**	-	-
25	PLACE2000357	112.17	70.59	69.73	83.45	100.62	78.25	23	68.79	48.54	*	-	-
	PLACE2000358	57.37	32.53	34.74	25.22	20.69	15.46	44.93	47.18	42.01	*	-	-
	PLACE2000359	66.39	48.68	57.2	40.91	54.54	32.45	1.96	27.1	55	*	-	-
	PLACE2000368	24.09	23.36	19.56	12.65	12.71	9.05	11.75	9.72	10.83	**	-	-
	PLACE2000371	12.17	9.37	8.13	5.98	7.76	4.49	7.64	10.97	6.2	*	-	-
30	PLACE2000373	8.3	7.58	8.83	4.52	6.25	4.81	3.89	1.17	2.44	**	-	-
	PLACE2000374	20.82	21.57	18.21	16.3	16.71	14.02	11.71	11.44	14.19	*	-	-
	PLACE2000379	109.97	110.55	125.02	99.68	141.5	83.14	84.64	65.75	71.64	**	-	-
	PLACE2000386	27.43	27.19	20.99	10.83	12.4	11.22	15.3	17.99	10.26	*	-	-
	PLACE2000388	250.97	170.64	209.4	172.85	236.63	173.11	130.31	109.84	93.57	*	-	-
	PLACE2000392	241.74	206.31	271.34	159.33	198.67	145.83	119.57	115.9	95.8	*	-	-
35	PLACE2000394	10.8	10.42	13.61	8.59	15.25	7.68	5.68	9.12	6.51	*	-	-
	PLACE2000398	16.83	19.82	17.04	9.21	12.98	10.99	7.5	15.14	8.57	**	-	-
	PLACE2000399	30.6	27.17	17.03	25.63	27.41	28.06	9.08	19.74	20.17	*	-	-
	PLACE2000402	5.25	8.04	8.31	4.2	9.81	3.39	4.84	3.89	6.41	*	-	-
	PLACE2000404	24.79	49.52	29.14	49.74	21.66	25.22	16.23	19.06	8.51	*	-	-
40	PLACE2000411	5.67	8.96	6.76	7.21	11.84	6.13	5.19	4.54	7.08	*	-	-
	PLACE2000418	10.3	8.94	9.67	6.1	3.09	4.67	4.68	5.3	4.11	**	-	-
	PLACE2000419	96.71	94.48	148.23	58.48	57.97	27.06	44.37	46.85	45.47	*	-	-
	PLACE2000425	9.83	11.3	13.49	7.49	11.26	6.24	5.84	7.49	5.62	*	-	-
	PLACE2000427	15.21	22.92	21.67	15.7	21.56	15.92	5.61	6.9	4.76	**	-	-
	PLACE2000433	25.58	27.32	26.12	13.97	18.4	14.15	21.62	27.64	18.08	**	-	-
45	PLACE2000435	16.36	18.11	21.19	9.69	13.76	7.6	8.43	10.79	12.73	*	-	-
	PLACE2000438	35.17	36.25	36.72	24.14	34.38	15.98	38.19	37.23	25.32	*	-	-
	PLACE2000450	24.38	41.59	23.11	16.35	37.33	18.21	23.47	16.65	30.25	*	-	-
	PLACE2000455	51.05	47.04	53.6	30.31	36.57	21.71	39.12	34.02	35.42	*	-	-
	PLACE2000458	13.07	11.58	13.21	6.82	7.75	7.03	6.6	8.78	5.76	**	-	-
	PLACE2000464	9.95	10.55	11.94	7.59	6.37	5.51	7.66	8.47	7.16	*	-	-
	PLACE2000465	182.2	189.36	208.18	166.02	148.04	156.91	139.29	234.97	151.61	*	-	-
50	PLACE2000473	23.66	24.51	24.43	18.65	18.15	16.44	24.18	30.07	29.1	**	-	-
	PLACE2000477	14.25	12.47	18.55	9.69	12.47	6.23	10.6	9.09	9.9	*	-	-
	PLACE3000004	49.49	41.47	56.9	42.63	53.35	39.93	39.48	28.43	32.45	*	-	-
	PLACE3000009	30.13	36.74	28.18	19.79	35.05	20.31	13.54	15.44	20.29	**	-	-
	PLACE3000020	27.99	24.44	23.74	13.45	15.84	8.65	14.29	14.44	13.63	**	-	-
	PLACE3000029	13.95	12.7	16.35	6.3	9.27	7.3	4.88	16.59	5.52	**	-	-
55	PLACE3000038	6.52	4.32	7.69	5.63	3.97	4.12	2.68	6.85	6.16	*	-	-
	PLACE3000052	8.21	5.21	10.48	3.93	4.29	4.15	2.75	5.07	2.29	*	-	-
	PLACE3000059	7.39	8.1	10.8	4	5.08	2.55	2.83	4.28	4.31	*	-	-

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PLACE30000057	49.68	40.52	57.37	38.78	41.13	26.15	39.8	46.08	41.69	**	*
PLACE30000069	22.6	20.15	23	9.32	14.75	10.81	1.9	9.3	14.21	*	*
PLACE30000070	28.36	29.24	22.17	14.93	25.34	18.73	8.92	18.55	15.16	*	*
PLACE30001003	7.35	7.9	9.44	5.25	4.6	6.3	4.2	4.32	5.29	*	*
PLACE30001019	35.89	28	31.30	15.16	14.79	15.09	25.05	30.71	30.91	**	*
PLACE30001021	42.11	31.92	37.82	38.13	38.16	27.02	30.65	23.15	27.55	**	*
PLACE30001074	419.8	380.05	314.65	379.74	412.05	282.09	411.56	374.59	344.25	*	*
PLACE30001335	20.62	25.67	26.77	15.03	9.34	8.12	18.24	11.89	14.16	**	*
PLACE30001336	7.68	8.11	13.15	7.22	3.68	4.18	4.52	3.19	1.88	*	*
PLACE30001342	24.15	23.16	11.04	24.59	15.08	9.37	6.94	11.76	11.56	**	*
PLACE30001445	16.45	15.13	16.32	12.04	26.52	9.83	8.46	9.12	7.66	*	*
PLACE30001447	109.42	62.46	138.49	40.47	87.42	32.89	57.71	63.5	68.14	*	*
PLACE30001448	66.44	59.97	67.42	62.74	65.96	38.34	37.63	28.14	36.79	**	*
PLACE30001514	10.3	11.14	12.88	7.95	8.64	6.56	7.31	6.3	7.34	*	*
PLACE30001525	54.28	50.77	22.77	23.99	28.34	24.77	10.12	11.93	8.57	**	*
PLACE30001566	8.77	6.56	8.44	2.67	5.38	4.07	2.62	2.16	2.62	**	*
PLACE30001577	38.44	50.52	36.49	23.64	29.36	25.04	21.36	24.91	20.01	*	*
PLACE30001581	10.22	9.95	10.13	4.45	4.83	3.36	2.93	2.25	3.02	**	*
PLACE30001589	19.92	23.65	15.93	8.71	11.77	10.32	5.77	7.29	4.57	**	*
PLACE30001609	16.6	6.89	7.95	4.88	4.57	2.21	2.88	2.72	3.49	*	*
PLACE30001618	12.63	9.87	10.46	6.14	6.69	4.33	5.58	7.04	4.77	**	*
PLACE30001944	1627	2636	2193.4	1710	2606	2399	3320	2826.5	2357	*	*
PLACE30001977	7.18	4.55	3.38	2.14	1.71	1.66	2.79	2.24	2.57	*	*
PLACE30001998	19.46	15.17	17.17	4.98	8.73	7.24	6.73	5.87	6.07	**	*
PLACE30002005	12.53	16.93	18.84	5.91	6.83	4.67	7.22	6.07	4.15	**	*
PLACE30002007	7.97	6.69	7.83	2.48	4.45	2.85	2.71	2.19	2.08	**	*
PLACE30002008	5.49	5.5	6.02	1.68	6.49	2.2	2.64	3.52	2.46	**	*
PLACE30002023	40.02	27.48	31.62	27.29	30.91	23.89	26.59	30.58	23.2	*	*
PLACE30002025	20.76	15.1	17.45	10.19	8.64	8.25	15.48	14.18	17.02	**	*
PLACE30002018	13.39	10.52	10.44	6.03	3.81	2.29	4.65	4.57	4.60	**	*
PLACE30002201	61.41	56.02	42.84	39.7	37	28.53	36.05	41.5	44.54	*	*
PLACE30002221	12.37	9.42	8.54	5.7	3.63	2.33	5.19	3.54	2.87	**	*
PLACE30002225	180.89	144.07	131.66	176.14	175.29	127.1	77.77	64.65	86.2	**	*
PLACE30002226	20.28	21.59	18.74	7.11	11.09	8.3	4.85	2.23	7.19	**	*
PLACE30002301	17.46	18.98	14.94	9.27	14.11	10.52	4.65	3.25	5.88	**	*
PLACE30002317	17.8	13.66	8.55	6.08	2.29	4.95	6.33	9.35	7.91	*	*
PLACE30002325	9.61	7.55	8.28	4.48	5.65	4.02	5.72	2.93	4.77	**	*
PLACE30002342	58.11	21.74	48.85	17.82	13.76	17.4	11.61	12.09	11.25	*	*
PLACE30002444	18.63	13.16	20	8.5	7.54	7.64	10.16	10.96	16.61	*	*
PLACE30002553	56.99	47.97	42.85	32.37	25.93	24.8	32.98	24.76	32.96	*	*
PLACE30002554	27.82	25.4	19.01	15.47	10.42	14.64	15.57	11.42	13.74	*	*
PLACE30002727	14.58	20.8	8.128	5.71	8.52	5.71	8.32	6.43	8.38	*	*
PLACE3000276	13.09	13.68	8.83	2.78	7.9	3.42	3.8	2.8	3.1	**	*
PLACE30003004	37.31	39.14	39.5	28.72	17.9	18.26	33.17	28.5	40.23	*	*
PLACE30003009	12.29	9.64	9.42	6.2	5.6	4.27	5.42	4.79	6.47	**	*
PLACE30003010	51.34	49.06	45.31	11.5	35.47	14.78	19.66	9.79	16.36	*	*
PLACE30003020	24.3	28.51	33.32	14.31	20.51	12.27	15.7	15.03	15.45	**	*
PLACE300030322	43.24	35.12	23.63	31.55	31.68	23.75	27.52	25.05	23.56	*	*
PLACE300030310	28.37	27.71	24.49	12.33	15.5	11.35	20.66	17.37	21.33	**	*
PLACE300030331	6.68	8.07	7.67	6.55	5.13	3.84	2.57	2.99	0.04	**	*
PLACE300030336	393.24	473.08	270.29	359.87	515.03	306.41	470.48	662.39	717.67	*	*
PLACE30003039	11.78	5.98	6.82	3.79	5.41	4.28	9.74	10.29	11.53	*	*
PLACE300030341	12.2	6.88	6.99	4.2	5.65	4.02	4.35	5.75	4.94	*	*
PLACE300030350	13.71	12.66	10.21	4.86	8.13	4.84	5.77	7.37	4.79	*	*
PLACE300030352	17.23	29.11	20.8	9.42	15.27	8.16	11.43	7.14	13.58	*	*
PLACE300030353	14.74	14.96	16.82	8.78	8.26	6.98	10.37	5.48	6.79	**	*
PLACE300030362	57.42	93.1	72.53	67.02	59.59	35.38	59.68	38.27	60.6	*	*
PLACE300030363	9.44	8.61	10.55	4.39	5.19	4.3	7.06	6.88	6.56	**	*
PLACE300030365	5.59	7.45	4.94	1.48	2.65	3.2	4.78	2.37	2.95	*	*
PLACE300030373	38.45	30.27	25.57	4.05	7.88	3.63	14.16	11.37	15.74	**	*
PLACE300030374	48.65	44.25	34.93	16.2	26.01	11.78	24.23	27.25	23.51	*	*
PLACE300030387	5.55	3.77	3.88	1.58	3.57	4.03	3.58	2.95	3.21	*	*
PLACE300030388	26.03	22.21	15.9	9.86	12.79	6.37	21.94	26.7	24.22	*	*
PLACE300030399	15.37	13.07	9.83	5.64	4.9	3.93	10.68	11.05	8.52	**	*



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	PLACE3000400	42.78	33.52	30.29	11.43	26.51	8.47	52.76	33.47	38.46	*	*	-
	PLACE3000401	137.51	137.03	95.06	91.28	111.28	51.38	81.66	72.2	62.65	*	*	-
5	PLACE3000402	8.43	7.72	4.24	2.44	6.58	2.29	8.31	7.96	5.44			
	PLACE3000405	7.33	4.67	7.44	2.73	3.5	5.1	3.7	5.44	3.66			
	PLACE3000406	4.67	3.39	8.42	4.46	6.89	4.16	3.34	4.69	2.99			
	PLACE3000413	12.33	14.38	16.34	10.31	15.31	7.77	6.83	11.34	9.07	*	*	-
	PLACE3000416	84.6	58.17	41.71	94.16	126.08	86.52	51.61	89.65	63.01			
	PLACE3000425	2.87	4.19	4.03	2.67	4.11	2.12	2.08	0.77	1.54	*	*	-
10	PLACE3000437	6.08	4.62	9.74	3.57	11.5	3	3.57	3.67	4.77			
	PLACE3000455	6.66	7.45	7.23	5.48	5.38	4.19	5.5	5.74	3.82	*	*	-
	PLACE3000475	4.99	6.71	5.08	4.69	5.48	5.91	3.2	5.35	2.87			
	PLACE3000477	12.61	9.21	10.6	8.81	9.19	10.36	8.13	7.94	5.96	*	*	-
	PLACE4000003	30	20.47	39.94	8.43	18.43	9.82	12.11	10.52	8.23	*	*	-
	PLACE4000008	8.19	8.19	9.59	5.97	7.85	6.93	4.18	5.57	3.47	*	*	-
15	PLACE4000009	46.86	36	37.99	37.22	51.39	35.97	11.09	18.85	7.53	**	*	-
	PLACE4000014	18.34	18.57	19.19	16.62	19.49	16.59	6.08	13.2	15.87			
	PLACE4000029	5.3	5.07	5.95	2.91	4.87	2.62	3.69	3.02	2.87	**	*	-
	PLACE4000034	10.02	8.01	6.28	5.12	7.93	4.55	5.88	5.27	5.14			
	PLACE4000049	21.86	18.28	18.64	14.38	19.7	19.05	12.54	13.96	11.08	**	*	-
20	PLACE4000052	47.63	33.03	40.39	17.99	15.08	20.28	24.01	22.07	24.29	**	*	-
	PLACE4000062	53.46	46.6	50.02	32.69	40.48	28.08	39.71	36.99	45	*	*	-
	PLACE4000063	56.25	68.62	67.5	55.27	68.37	73.66	45.78	60.53	44.9			
	PLACE4000089	10.35	13.86	13.41	10.66	10.48	9.25	5.68	5.4	5.66	*	*	-
	PLACE4000093	13.85	18.02	19.57	10.49	13.84	10.33	17.17	14.6	14.04	*	*	-
	PLACE4000100	8.21	7.32	11.21	7.61	6.2	7.32	5.19	5.2	4.71	*	*	-
	PLACE4000103	13.85	15.73	12.84	8.67	14.38	6.43	4.02	8.73	6.65	*	*	-
25	PLACE4000106	32	18.81	23.23	18.35	21.38	15.86	17.78	20.58	18.06			
	PLACE4000128	22.05	18.53	23.14	8.88	10.24	9.57	11.18	17.49	11.76	**	*	-
	PLACE4000131	59.1	45.51	65.57	41.68	34.82	39.78	18.29	19.7	30.83	*	*	-
	PLACE4000147	7.89	7.51	11.76	3.51	5.07	3.96	2.77	6.32	2.52	*	*	-
	PLACE4000156	15.48	18.75	19.37	9.1	12.85	10.65	15.8	15.48	10.02	*	*	-
30	PLACE4000175	12.45	10.41	18.08	11.94	9.67	2.46	6.38	6.69	6.89			
	PLACE4000190	40.84	40.93	32.85	23.06	35.22	26.68	12.42	10.73	11	**	*	-
	PLACE4000192	35.69	24.13	23.88	16.77	21.59	17.59	17.75	19.51	19.4			
	PLACE4000206	33.82	29.03	26.48	11.73	17.97	14.5	17.45	20.16	20.02	**	*	-
	PLACE4000214	13.12	6.23	9.29	7.96	9.94	9.19	6.64	31.04	6.54	**	*	-
35	PLACE4000222	35.35	30.73	34.54	24.03	24.44	20.1	20.58	28.37	25.45	**	*	-
	PLACE4000223	14.88	14.83	15.03	7.36	10.28	5.52	4.16	7.67	5.85	**	*	-
	PLACE4000229	12.38	12.15	12.52	4.51	6.31	4.98	4.32	4.28	3.98	**	*	-
	PLACE4000230	9.56	8.77	9.56	4.68	7.06	5.7	4.97	9.82	3.71	**	*	-
	PLACE4000233	22.71	24.01	29.85	11.57	13.98	13.77	8.53	11.22	9.26	**	*	-
	PLACE4000239	10.07	7.4	9.42	6.8	7.34	6.09	4.49	4.54	3.54	**	*	-
40	PLACE4000247	15	11.82	15.56	9.41	13.91	8.87	8.67	6.24	7.39	**	*	-
	PLACE4000250	16.14	18.27	20.25	16.54	17.86	12.73	10.47	8.04	11.21	*	*	-
	PLACE4000252	10.01	5.15	12.75	1.39	3.96	3.1	2.21	3.92	2.7	*	*	-
	PLACE4000259	25.72	27.31	16.16	12.78	19.39	8.44	8.29	19.39	9.08			
	PLACE4000261	23.52	25.16	22.9	11.05	14.2	9.22	13.61	14.62	13.29	**	*	-
45	PLACE4000264	176.03	156.54	119.76	135.7	191.67	147.27	105.16	95.1	89.72	*	*	-
	PLACE4000269	71.18	49.07	62.08	23.03	41.63	24.74	71.71	82.6	52.18	*	*	-
	PLACE4000270	7.6	6.37	8.9	4.69	5.92	4.81	3.06	3.58	3.44	*	*	-
	PLACE4000281	15.26	16.07	18.29	6.09	10.92	7.61	6.44	6.66	5.1	**	*	-
	PLACE4000300	8.43	9.82	8.78	6.3	8.5	7.03	3.68	2.93	2.96	**	*	-
	PLACE4000320	12.37	11.22	11.92	6.27	10.09	6.43	4.47	4.26	2.85	**	*	-
50	PLACE4000323	15.16	16.25	19.16	9.12	14.06	10.9	6.05	4.54	4.03	**	*	-
	PLACE4000326	11.15	8.97	10.53	4.35	4.69	4.13	4.28	3.68	4.65	**	*	-
	PLACE4000344	27.71	32.93	24.51	14.27	30.44	19.64	5.14	9.78	8.98	**	*	-
	PLACE4000347	156.82	129.54	154.28	89.79	129.04	79.82	138.06	137.09	135.75			
	PLACE4000354	15.47	9.46	11.43	7.01	8.32	6.55	3.28	5.96	4.83	*	*	-
	PLACE4000367	8.63	5.47	7.82	5.38	5.39	6.72	3.84	3.95	3.64	*	*	-
55	PLACE4000369	11.27	6.37	9.31	5.27	4.5	4.05	4.11	4.32	3	*	*	-
	PLACE4000379	6.35	6	4.77	3.22	2.93	2.33	3.1	3.32	2.21	**	*	-
	PLACE4000387	25.99	34.88	32.06	17.28	20.68	16.67	6.75	8.86	3.97	*	*	-

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	PLACE4000392	8.31	9.76	11.03	3.63	5.95	3.64	5.73	2.01	2.93	**	*	-	-
	PLACE4000399	53.9	51.54	53.26	20.64	28.55	18.63	37.94	35.1	44.54	**	*	-	-
5	PLACE4000401	4.22	3.76	3.44	3.96	3.49	2.6	3.5	3.9	1.61	*	-	-	-
	PLACE4000403	5.42	5.82	5.5	4.19	7.87	4.85	3.96	3.29	2.53	*	-	-	-
	PLACE4000411	20.23	15.5	15.73	8.23	11.19	9.81	14.98	10.1	11.34	*	-	-	-
	PLACE4000415	8.15	4.8	4.61	4.06	6.07	4.23	2.98	3.98	4.5	*	-	-	-
	PLACE4000416	35.43	25.11	24.69	17.72	17.34	16.23	24.55	17.6	25.73	*	-	-	-
	PLACE4000424	42.93	33.38	31.83	13.69	19.37	13.98	27.93	23.64	33	**	-	-	-
10	PLACE4000431	10.44	8.78	8.78	5.88	4.85	3.5	4.69	2.33	4.08	**	*	-	-
	PLACE4000443	50.64	44.47	41.43	26.49	37.08	21.33	51.22	33.11	43.74	*	-	-	-
	PLACE4000445	5.42	4.17	3.6	3.57	7.43	5.38	2.23	3.95	2.66	*	-	-	-
	PLACE4000450	9.85	6.68	6.23	4.72	6.64	4.07	3.56	7.58	3.73	*	-	-	-
	PLACE4000455	167.91	132.51	128.81	98.87	124.22	95.79	172.16	139.08	172.24	*	-	-	-
	PLACE4000465	31.84	25.74	18.83	10.79	23.42	11.27	11.29	10.8	17.69	*	-	-	-
15	PLACE4000466	13.01	11.54	9.57	6.56	6.92	4.59	5.76	4.65	5.6	*	**	-	-
	PLACE4000472	165.28	158.69	152.44	150.34	164.09	112.33	151.06	116.56	147.01	*	-	-	-
	PLACE4000487	10.38	6.99	9.12	4.68	4.63	2.93	3.52	2.06	3.49	*	**	-	-
	PLACE4000489	6.8	7.97	5.85	3.99	5.8	4.43	4.22	4.11	4.53	*	-	-	-
	PLACE4000494	70.51	55.91	43.58	29.17	31.84	24.64	72.67	73.79	78.08	*	-	-	-
20	PLACE4000502	204.58	180.8	176.1	156.92	166.08	118.92	216.32	165.78	200.53	*	-	-	-
	PLACE4000521	28.26	22.58	17.07	7.12	15.76	9	21.36	20.06	19.61	*	-	-	-
	PLACE4000522	18.46	20.38	16.27	10.46	14.61	9.51	16.91	13.88	17.23	*	-	-	-
	PLACE4000537	9.79	11.19	9.86	4.99	8.2	4.43	2.5	3.6	0.68	*	**	-	-
	PLACE4000548	12.35	10.52	9.27	3.9	4.07	4.41	4.08	3.04	3.64	**	*	-	-
	PLACE4000558	56.63	61.59	46.82	23.74	32.06	21.71	66.44	39.24	52.93	**	-	-	-
	PLACE4000581	9.34	8.43	8.7	5.21	3.71	3.17	3.73	4.69	4.75	**	*	-	-
25	PLACE4000590	4.28	4.39	2.54	2.29	1.9	1.58	2.69	1.47	1.72	*	-	-	-
	PLACE4000593	9.43	8.29	6.55	6.59	7.86	5.28	9.13	5.16	4.1	*	-	-	-
	PLACE4000612	50.54	44.64	46.86	32.73	32.12	18.75	8.58	0	9.68	*	**	-	-
	PLACE4000638	8.47	6.12	6.11	6.07	5.18	3.4	1.44	4.91	1.37	*	-	-	-
	PLACE4000650	11.71	6	6.58	1.78	5.39	2.69	5.01	3.89	2.3	*	-	-	-
30	PLACE4000651	10.02	10.01	7.85	4.63	8.67	3.43	7.21	6.04	5.23	*	-	-	-
	PLACE4000654	40.79	37.09	26.74	21.7	29.39	18.93	39.41	24.87	38.02	*	-	-	-
	PLACE4000670	7.33	7.03	6.77	5.23	9.34	3.97	6.41	3.63	6.87	*	-	-	-
	PLACE4000685	27.38	21.25	26.71	7.25	13.45	14.89	8.25	13.79	8.57	*	**	-	-
	PLACE4000687	5.87	2.72	5.94	3.75	3.52	3.04	2.8	3.66	2.1	*	-	-	-
	PLACE5000003	13.69	15.66	16.08	8.92	15.85	13.17	6.36	9.93	8.84	**	-	-	-
35	PLACE5000005	17.05	13.38	13.46	14.47	17.35	13.76	5.61	8.29	7.64	**	-	-	-
	PLACE5000010	9.12	11.38	11.73	6.9	5.65	5.55	3.51	3.39	6.14	**	-	-	-
	PLACE5000021	28.4	28.38	31.96	18.99	19.21	16.52	23.2	21.13	21.28	**	*	-	-
	PLACE5000022	44.41	69.47	62.06	68.78	41.05	40.85	49.9	41.64	44.86	**	*	-	-
	PLACE5000024	5.49	3.54	5.62	3.22	3.37	3.62	2.52	4.61	6.39	*	-	-	-
	PLACE5000036	104.88	78.2	100.83	80.5	90.12	87.43	80.46	55.18	59.66	*	-	-	-
40	PLACE5000059	13.88	12.58	10.61	5.28	9.26	6.17	6.41	11.67	8.16	*	-	-	-
	PLACE5000076	102.38	115.06	146.87	71.48	155.46	121.21	73.46	149.18	129.94	*	-	-	-
	PLACE5000117	10.83	17.74	16.15	14.79	20.06	15.63	5.73	9.53	5.57	*	-	-	-
	PLACE5000143	12.99	9.49	15.16	8.13	9.83	8.06	5.81	8.66	8.8	*	-	-	-
	PLACE5000152	183.88	202.8	96.28	147.85	104.4	116.95	74.92	70.73	75.92	*	-	-	-
	PLACE5000154	90.81	108.58	44.13	75.4	77.68	45.59	40.84	23.33	50.85	*	-	-	-
45	PLACE5000155	33.2	24.58	26.07	16.94	31.52	23.72	16.67	17.93	27.02	*	-	-	-
	PLACE5000165	113.75	76.52	82.55	90.32	103.03	88.36	32.72	55.94	39.36	*	-	-	-
	SKNMC1000004	1323.5	940.91	1083.3	665.71	1250.5	673.39	1094.9	1184.2	1060.5	*	-	-	-
	SKNMC1000011	8.28	9.06	11.81	4.48	12.47	5.45	4.79	5.44	8.03	*	-	-	-
	SKNMC1000013	14.72	15.01	20.52	10.84	11.72	12.41	4.74	6.54	6.23	**	-	-	-
	SKNMC1000014	20.79	23.92	26.42	20.23	26.13	18.1	14.76	15.14	11.78	**	-	-	-
50	SKNMC1000018	9.56	8.87	12.44	5.32	9.73	4.54	3.81	4.41	5.25	**	-	-	-
	SKNMC1000020	25.49	27.02	25.39	13.63	25.33	12.68	18.7	20.72	21.65	**	-	-	-
	SKNMC1000046	24.6	15.36	17.74	13.48	22.27	16.07	12.53	14.97	15.86	*	-	-	-
	SKNMC1000050	8.51	7.09	7.49	5.47	4.73	4.3	4.47	21.02	3.74	**	-	-	-
	SKNMC1000062	26.94	17.98	24.61	14.13	15.7	9.74	23.61	36.47	28.61	*	-	-	-
	SKNMC1000075	11.6	7.44	13.24	7.34	10.78	7.51	4.21	5.3	7.09	*	-	-	-
55	SKNMC1000082	22.01	16.02	26.11	8.38	13.04	9.62	12.8	21.17	16.8	*	-	-	-
	SKNMC1000091	36.26	39.39	43.7	12.98	23.22	18.68	24.3	27.26	22.42	**	**	-	-
	SKNMC1000099	11.34	8.86	15.64	6.38	7.5	4.4	5.83	7.15	6.38	*	-	-	-

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	SKNNMC1000104	16.76	17.55	17.05	8.52	14.24	10.52	9.72	10.59	13.24	*	**	-	-
	SKNNMC1000113	45.53	34.91	35.51	20.7	25.14	23.85	18.86	24.14	23.6	*	*	-	-
	SKNNMC1000119	17.58	14.67	21.54	10.33	12.31	8.53	8.83	13.02	8.17	*	*	-	-
5	SKNNMC1000142	16.52	20.57	23.49	7.26	16.72	11.75	8.01	11.68	14.09	*	*	-	-
	SKNNMC1000170	242.49	183.41	211.38	201.28	226.18	182.82	247.45	216.7	250.73	*	*	-	-
	SKNNMC1000178	15.01	12.68	14.32	6.9	9.12	6.49	4.97	7.82	9.01	**	**	-	-
	SKNNMC1000194	7.33	8.61	11.61	2.23	3.73	3.19	2.64	4.74	3.45	*	*	-	-
	SKNNMC1000198	18.76	29.87	24.52	7.87	13.1	9.06	5.41	5.23	5.02	*	*	-	-
10	SKNNMC1000225	100.44	119.68	87.32	52.94	84.28	50.45	35.91	33.78	44.06	**	**	-	-
	SKNNMC1000249	23.35	22.68	30.9	13.07	19.76	17.18	12.83	14.11	14.19	*	*	-	-
	SPLN1000007	10.7	10.7	16.74	6.92	9.27	7.23	6.86	7.37	5.89	*	*	-	-
	SPLN1000012	15.31	13.75	18.53	8.26	13.65	10.56	13.22	11.71	11.02	*	*	-	-
	SPLN1000014	74.22	59.99	63.53	32.33	49.13	32.58	29.87	29.67	37.64	*	**	-	-
	SPLN1000036	14.69	11.54	10.05	7.95	8.19	6.93	3.18	3.76	2.42	*	**	-	-
15	SPLN1000059	39.71	33.5	32.87	12.1	19.81	12.24	19.97	18.35	17.18	**	**	-	-
	SPLN1000068	20.63	22.57	21.07	11.6	16.29	10.46	9.19	11.89	8.79	*	**	-	-
	SPLN1000072	19.88	16.93	14.96	6.06	9.86	7.47	5.18	4.49	6.78	**	**	-	-
	SPLN1000101	71.97	43.16	57.46	18.69	27.56	26.8	32.73	40.27	19.97	*	*	-	-
	SPLN1000108	7.69	6.28	7.07	3.65	4.35	2.67	3.12	2.84	2.04	**	**	-	-
	SPLN1000113	11.47	6.64	12.13	7.54	8.23	7.26	5.5	6.27	7.59	*	*	-	-
20	SPLN1000114	16.01	14.75	14.36	7.29	9.65	6.3	8.14	8.22	8.73	**	**	-	-
	SPLN1000132	5.96	4.51	7.38	2.74	4.42	2.34	1.47	2.25	2.21	*	*	-	-
	SPLN1000135	10.57	8.18	9.19	3.86	4.71	4.73	4.9	2.38	2.97	**	**	-	-
	SPLN1000136	23.91	23.93	20.23	10.77	11.86	10.15	16.69	14.04	13.77	**	**	-	-
	SPLN1000141	42.88	39.73	42.83	27.16	32.91	23.4	23.31	18.41	20.67	**	**	-	-
	SPLN1000164	15.72	13.33	13.69	7.76	12.46	6.69	9.59	8.11	9.12	**	**	-	-
25	SPLN1000166	12.98	9.08	11.45	4.56	6.01	5.04	6.49	5.17	6.32	**	*	-	-
	SPLN1000175	19.25	16.94	15.5	7.48	9.23	6.92	11.34	13.49	13.41	**	*	-	-
	SPLN1000182	67.34	58.35	68.22	30.69	40.43	27.88	28.16	29.1	23.7	**	**	-	-
	SPLN1000185	6.38	8.35	5.56	4.69	4.56	3.06	2.86	2.31	1.51	**	*	-	-
	THYMU1000004	48.79	34.96	41.97	30.97	32.65	27.64	26.98	17.5	12.12	*	**	-	-
	THYMU1000009	14.59	13.55	14.88	8.47	10.1	5	7.34	4.91	5.62	*	*	-	-
30	THYMU1000015	19.34	18.55	12.08	8.34	11.37	5.93	10.34	10.96	13.03	*	*	-	-
	THYMU1000016	6.78	4.3	5.54	2.79	2.51	1.91	5.19	3.5	4.34	*	*	-	-
	THYMU1000023	6.35	6.23	6.53	4.39	3.65	4.2	3.1	5.69	3.98	**	*	-	-
	THYMU1000034	390.65	392.5	375.97	306.71	379.09	270.69	454.49	361.08	369.56	*	*	-	-
	THYMU1000035	8.93	7.8	9.14	5.88	4.95	4.81	5.06	3.93	4.36	**	*	-	-
	THYMU1000037	9.69	6.41	7.36	4.28	3.96	3.33	4.24	3.59	3.83	*	*	-	-
35	THYMU1000042	6.85	3.93	5.82	2.75	3.24	2.02	2.08	1.63	1.09	*	*	-	-
	THYMU1000047	25.64	25.03	24.74	13.43	16.94	11.38	26.77	21.68	23.81	**	*	-	-
	THYMU1000080	20.17	51.54	27.22	17.42	19.98	26.99	13.06	15.8	14.07	*	*	-	-
	THYMU1000094	11.12	6.99	9.51	6.45	6.49	4.35	11.14	9.41	9.31	*	*	-	-
	THYMU1000109	228.62	201.78	195.22	195.65	173.29	154.39	235.81	205.84	221.79	**	*	-	-
40	THYMU1000127	44.2	30.97	37.5	12.05	18.11	17.75	24.49	15.04	18.2	**	*	-	-
	THYMU1000130	21.64	17.3	15.84	7.65	12.45	8	10.24	3.41	8.22	*	*	-	-
	THYMU1000137	6.81	10.03	8.23	3.35	5.2	3.34	4.41	2.7	3.47	*	*	-	-
	THYMU1000146	11.97	7.39	7.48	8.11	7.24	6.17	5.13	3.03	6.19	*	*	-	-
	THYMU1000159	10.45	10.21	8.17	6.28	6.42	3.77	4.54	3.62	4.78	*	**	-	-
	THYMU1000163	8.08	8.93	9.7	5.33	5.95	3.66	7.57	4.17	4.21	**	*	-	-
45	THYMU1000167	67.79	51.53	54.02	27.07	31.06	17.27	75.27	48.55	70.31	**	*	-	-
	THYMU1000186	8.38	8.15	3.89	3.94	4.49	2.65	3.36	2.91	3.02	*	*	-	-
	THYRU1000017	24	17.58	11.71	8.21	11.63	5.25	6.04	5.8	4.42	*	*	-	-
	THYRU1000026	10.24	8.59	6.72	5.28	7.77	4.56	4.15	3.45	6.46	*	*	-	-
	THYRU1000034	39.83	32.92	35.9	29.82	39.02	28.83	26.88	25.91	22.08	*	*	-	-
	THYRU1000035	34.67	27.15	24.29	22.39	30.44	22.35	22.09	19.28	23.65	*	*	-	-
50	THYRU1000036	16.2	14.28	11.79	9.92	10.8	4.36	7.94	4.75	8.23	*	*	-	-
	THYRU1000040	9.47	7.71	9.48	4.32	5.83	3	5.07	3.54	5.01	*	**	-	-
	THYRU1000061	18.28	19.76	15.63	8.28	5.85	4.81	6.42	5.28	9.19	**	*	-	-
	THYRU1000067	16.85	13.02	12.06	8.02	8.96	4.34	7.22	6.1	5.44	**	*	-	-
	THYRU1000070	9.96	13.03	10.58	5.63	9.48	4.69	20.02	18.33	15.63	*	+	-	-
	THYRU1000072	21.57	19.92	18.73	19.89	17.94	12.39	9.77	9.74	9.5	**	*	-	-
55	THYRU1000084	9.91	5.58	5.31	3.9	6.43	2.97	10.41	8.45	10.27	*	*	-	-
	THYRU1000085	29.04	36.56	22.76	13.84	17.05	13.37	10.59	14.52	10.12	*	*	-	-
	THYRU1000086	13.56	10.42	8.08	7.5	9.36	4.87	6.64	6.5	4.47	*	*	-	-

	THYR01000087	51.14	69.3	41.47	29.99	58.4	25.89	61.05	53.08	61.77			
	THYR01000092	26.07	28.19	30.84	13.75	13.51	9.94	17.56	21.51	22.34	**	*	-
	THYR01000093	4.26	2.01	4.16	1.77	3.46	3.25	2.69	3.3	2.41			
5	THYR01000099	9.62	5.87	9.25	3.68	8.63	4.69	5.9	7.16	4.32			
	THYR01000107	70.48	59.74	59.68	39.34	64.57	40.78	35.76	61.82	50.34			
	THYR01000111	13.96	11.92	12.38	7.04	9.78	5.89	9.55	11.53	9.66	*	*	-
	THYR01000121	31.45	32.43	36.13	15.06	18.17	17.71	26.05	28.32	34.79	**	*	-
	THYR01000124	54.83	35.35	48.22	37.6	35.37	31.52	34.87	27.99	31.75			
10	THYR01000129	8.59	9.01	8.49	5.14	9.82	6.86	8.93	8.73	10.55			
	THYR01000130	12.23	8.25	10.06	6.62	6.95	6.32	6.99	9.76	9.68	*	-	-
	THYR01000132	7.93	8.79	12	5.35	7.15	7.04	4.12	4.66	3.86			
	THYR01000134	17.2	6.06	9.3	6.24	6.27	12.5	5.33	7.31	5.41			
	THYR01000144	23.66	30.56	32.27	27.55	32.97	28.83	18.04	19.4	19.02			
	THYR01000155	35.26	37.35	35.3	18.99	24.31	20.42	31.31	40.6	29.86	**	*	-
15	THYR01000156	37.13	43.79	38.99	24.77	34.58	23.66	19.78	36.39	21.81	*	-	-
	THYR01000163	56.18	53.4	58.15	23.96	28.08	23.46	11.7	4.22	4.73	**	**	-
	THYR01000173	8.52	8.35	6.98	5.25	10.18	4.15	3.25	4.41	2.91	**	**	-
	THYR01000186	35.39	31.09	36.48	14.41	13.8	14.41	7.62	12.05	15.91	**	**	-
	THYR01000187	17.39	15.95	24.02	6.63	7.73	8.87	5.49	7.02	6.9	*	**	-
20	THYR01000190	7.06	7.97	10.31	6.43	5.1	6.9	4.78	5.24	5.17	*	-	-
	THYR01000196	8.72	14.15	13.33	14.25	10.93	7.74	3.75	6.65	9.86			
	THYR01000197	13.75	17.13	15.02	14.96	17.34	16.5	8.34	11.47	6.34			
	THYR01000199	6.8	9.71	11.38	6.45	11.32	10.32	5	6.51	7.17	*	-	-
	THYR01000206	20.90	21.74	25.04	13.14	17.5	12.03	7.45	6.8	7.63	*	**	-
	THYR01000221	6.98	7.15	5.44	4.48	8.31	3.29	3.81	4.45	3.66	*	-	-
25	THYR01000222	56.33	56.37	63.27	37.58	40.3	31.94	25.13	33.5	43.65	**	**	-
	THYR01000228	148.64	127.09	184.25	73.36	64.55	57.59	55.06	55.21	55.09	**	**	-
	THYR01000241	7.78	5.72	11.15	4.42	5	4.49	2.68	4.65	4.26	*	-	-
	THYR01000242	18.18	23.99	29.76	25.09	51.85	27.45	12.5	20.02	16.61			
	THYR01000246	21.57	18.12	24.56	19.46	20.13	15.33	9.29	10.17	9.72	**	-	-
	THYR01000253	10.77	13.3	16.4	9.6	16.01	8.45	6.71	8.04	5.73	*	-	-
	THYR01000270	12.58	12.99	17.24	8.11	13.02	8.87	9.06	8.16	7.99	*	-	-
	THYR01000278	15.04	13.53	16	8.28	14.2	7.73	7.71	7.11	4.92	**	**	-
	THYR01000285	1215.2	1221.3	1148.5	961.64	1121.8	817.57	1261.8	1135.7	1518.7			
	THYR01000288	24.11	22.65	22.01	13.89	25.53	14.41	22.83	21.93	20.34			
	THYR01000296	40.26	36.2	38.51	32.51	37.84	29.24	32.78	49.02	40.29			
	THYR01000320	12.29	8.4	14.15	6.59	7.17	0.88	5.28	11.64	9.29	*	-	-
35	THYR01000322	37.49	34.74	36.99	17.69	26.05	19.02	19.43	23.34	20.74	**	**	-
	THYR01000327	29.25	26.35	19.48	16.99	27.29	15.75	10.07	12.24	13.52	*	-	-
	THYR01000343	16.65	12.58	17.82	8.18	11.42	7.21	10.1	9.05	8.44	*	-	-
	THYR01000349	6.25	12.77	6.82	7.74	8.59	3.02	4.68	4.72	4.12	*	-	-
	THYR01000358	13.06	10.31	11.35	6.24	8.76	7.32	8.15	6.51	9.21	*	-	-
	THYR01000368	5.38	5.26	6.26	3.15	2.94	2.68	6.19	3.06	2.43	**	-	-
40	THYR01000375	14.1	11.6	18.84	8.56	5.99	5.1	3.89	3.2	3.55	*	**	-
	THYR01000381	10.31	8.3	9.78	4.37	5.3	5.96	4.17	5.35	3.59	**	**	-
	THYR01000387	11.39	10.61	13.54	4.54	5.97	3.48	10.59	5.84	3.07	**	**	-
	THYR01000394	61.78	50.97	22.02	14.67	26.91	8.08	6.98	9.73	11.33			
	THYR01000395	29.06	37.87	27.54	18.13	24.45	14.15	25.79	23.19	25.7	*	-	-
	THYR01000400	10.51	10.51	9.69	3.23	12.01	5.83	3.72	3.73	3.08	**	**	-
45	THYR01000401	10.42	9.53	10.77	6.74	5.06	4.73	3.24	5.18	5.6	**	**	-
	THYR01000407	111.95	92.99	98.17	63.29	75.05	58.17	51.33	55.33	55.02	**	**	-
	THYR01000420	15.01	13.25	17.92	11.1	11.62	8.56	12.78	12.37	14.41	*	-	-
	THYR01000438	8.38	5.22	8.85	5.12	4.11	4.31	4.22	4.7	3.13	*	-	-
	THYR01000452	15.04	12.59	12.97	5.82	10.6	6.13	2.16	3.93	4.57	*	**	-
	THYR01000455	7.17	8.57	9.52	2.62	3.31	3.44	2.83	2.18	2.11	**	**	-
50	THYR01000471	78.16	81.99	62.01	65.6	82.48	70.86	81.77	51.28	74.06			
	THYR01000481	8.9	7.89	8.46	4.91	7.54	4.12	2.78	3.16	5.02	**	-	-
	THYR01000484	19.83	12.76	16.87	10.37	11.59	9.38	11.21	9.7	11.91			
	THYR01000488	28.64	20.75	23.35	20.89	21.13	19.59	15.6	20.62	19.42			
	THYR01000501	11.59	12.72	13.28	7.74	9.03	6.79	8.05	7.95	10.26	**	*	-
	THYR01000502	55.86	52.65	49.31	44.07	46.78	38.57	44.58	40.93	38.11	*	-	-
55	THYR01000505	5.64	7.65	7.27	5.56	5.82	3.06	3.98	5.47	2.02	*	-	-
	THYR01000535	37.32	41.34	38.41	38.72	38.24	31.02	23.49	20.01	18.32	**	-	-
	THYR01000556	102.92	92.57	85.3	76.31	104.96	62.73	51.56	50.77	49.93	**	-	-

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	THYR01000558	8.54	7.17	6.38	4.15	8.61	3.01	4.26	2.04	3.45	*	-
	THYR01000559	6.63	4.92	4.79	4.77	4	3.41	3.56	3.02	3.94	*	-
	THYR01000570	9.09	6.95	8.33	5.27	6.38	6.54	5.25	4.89	7.09	*	-
5	THYR01000572	52.16	31.52	39.78	12.92	33.15	30.73	30.68	23.84	11.23	*	-
	THYR01000573	8.96	8.49	6.82	4.33	8.49	6.35	13.45	11.85	8.78	*	-
	THYR01000577	9.73	7.83	7.69	3.93	6.26	2.6	2.58	3.82	2.34	*	**
	THYR01000580	40.56	32.54	29.95	22.22	19.86	19.81	24.19	17.34	25.52	*	-
	THYR01000584	35.96	36.8	31.93	19.25	25.5	16.24	26.15	21.02	19.13	*	-
10	THYR01000585	8.99	7.37	6.65	4.18	6.67	4.86	5.4	3.58	2.99	*	-
	THYR01000596	43.85	33.14	32.61	22.94	31.65	11.59	15.52	10.88	14.47	**	-
	THYR01000602	19.04	15.25	10.78	7.23	11.51	11.78	8.87	7.72	10.81	*	-
	THYR01000605	10.06	9.44	5.91	6.29	6.99	4.61	4.9	5.21	5.08	*	-
	THYR01000615	134.15	117.37	85.97	86.81	98.31	67.18	77.31	67	84.37	*	-
	THYR01000625	33.27	24.69	16.68	12.6	10.75	20.13	8.38	6.86	11.76	*	-
15	THYR01000636	17.91	16.49	14.48	12.48	11.49	6.7	8.72	6.17	8.59	*	**
	THYR01000637	18.22	22.2	13.43	10.39	14.05	9.78	9.07	5.2	7.26	*	-
	THYR01000641	7.23	5.87	6.32	4.82	10.06	3.87	8.42	4.55	2.07	*	-
	THYR01000657	10.91	9.86	8.65	6.93	7.74	7.68	9.53	8.35	10.94	*	-
	THYR01000658	14.37	9.48	5.1	6.28	6.83	5.43	4.59	4.62	4.77	*	-
	THYR01000662	10.63	9.43	8.46	6.7	6.85	6.96	7.92	7.09	10.89	*	-
20	THYR01000666	30.51	33.5	45.43	12.9	20.33	13.81	14.6	13.53	16.48	*	**
	THYR01000676	11.56	11.35	8.48	6.32	9.3	8.37	4.16	5.02	6.44	*	-
	THYR01000678	23.44	18.73	20.73	10.13	15.99	8.49	9	7.38	9.87	*	**
	THYR01000684	27.78	27.85	20.27	12.26	16.45	11.06	26.87	17.92	24.98	*	-
	THYR01000694	16.87	11.78	10.72	5.47	10.25	5.99	12.29	9.36	8.6	*	-
	THYR01000699	9.11	6.36	4.55	5.62	6.31	3.48	7.37	3.08	5.06	*	-
25	THYR01000712	17.55	14.87	12.31	9.08	11.99	7.67	12.79	9.26	13.3	*	-
	THYR01000715	29.82	23.25	21.02	20.98	27.37	20.44	15.76	18.98	18.68	**	-
	THYR01000716	13.12	15.14	11.94	8.87	12	7.65	7.48	6.89	6.96	*	-
	THYR01000717	11.89	15.21	12.45	6.9	9.22	5.08	30.93	6.96	7.18	*	-
	THYR01000723	30.36	26.4	21.78	10.82	20.63	14.46	30.94	22.3	30.26	*	-
30	THYR01000734	16.61	19.91	16.12	11.94	17.61	9.39	9.31	6.61	13.3	*	-
	THYR01000748	17.46	14.06	15.87	5	7.52	5.42	7.82	5.84	7.09	**	-
	THYR01000755	20.17	21.24	19.88	13.28	17.61	14.04	14.7	23.04	21.01	*	-
	THYR01000756	369.81	334.57	369.63	298.51	345.41	273.28	259.37	356.07	273.4	*	-
	THYR01000775	4.97	4.89	7.55	4.25	6.18	4.82	2.58	5.02	3.65	*	-
	THYR01000777	5.42	6.63	6.34	5.34	6.01	4.03	3.82	3.75	3.21	**	-
35	THYR01000779	483.37	468.9	483.51	453.87	549.42	449.1	368.6	510.93	458.47	*	-
	THYR01000782	17.27	20.25	23.35	14.58	17.12	13.37	15.61	16.4	16.35	*	-
	THYR01000783	6.74	5.45	6.68	5.43	9.62	4.88	3.62	5.19	3.8	*	-
	THYR01000786	25.62	30.48	26.26	16.78	13.18	14.48	32.89	30.78	26.94	**	-
	THYR01000787	50.52	37.21	54.05	28.71	18.06	26.25	20.11	24.5	22.66	*	-
	THYR01000792	14.11	12.1	15.65	4.55	6.72	7.1	8.13	7.14	8.33	**	-
40	THYR01000793	36.92	35.83	42.61	19.08	27.16	19.55	34.91	38.74	32.64	*	-
	THYR01000795	37.33	45.29	88.32	42.19	57.36	40.15	12.57	21.17	13.38	*	-
	THYR01000796	10.25	11.83	14.01	6.19	10.21	5.98	7	11.89	11.1	*	-
	THYR01000798	9.87	14.22	12.83	9.06	8.1	7.49	5.04	7.33	5.2	*	-
	THYR01000800	37.69	54.75	19.73	33.2	22.36	23.21	13.79	16.89	13.75	*	-
	THYR01000805	8.27	6.21	6.02	5.33	8.39	4.44	3.81	4.14	3.82	*	-
45	THYR01000815	109.41	92.13	90.82	43.51	38.14	25.61	31.76	21.16	31.98	**	-
	THYR01000829	33.86	25.13	34.71	19.68	21.68	18.45	16.87	14.34	12.65	*	-
	THYR01000835	9.51	9.82	10.3	6.71	6.28	4.65	5.41	5.24	6.07	**	-
	THYR01000843	27.06	16.5	24.96	16.28	19.34	15.73	6.22	7.81	8.06	**	-
	THYR01000846	7.86	5.91	13.48	4.53	6.28	7.74	3.89	7.02	5.26	*	-
	THYR01000852	24.69	25.37	23.66	12.87	20.2	12.5	9.33	10.39	11.62	*	**
50	THYR01000855	7.12	7.47	10.43	2.52	5.79	2.98	4.3	6.1	5.2	*	-
	THYR01000865	9.21	5.67	8.64	3.4	6.56	3.18	5.99	8.76	7.67	*	-
	THYR01000868	57.27	46.1	51.69	32.85	43.74	27.97	46.24	39.05	41.55	*	-
	THYR01000881	13.67	12.21	13.18	9.6	10.62	12.24	10.21	16.82	10.91	*	-
	THYR01000894	9.33	7.11	11.4	5.66	6.12	4.31	4.14	4.68	4.75	*	-
	THYR01000895	8.9	5.89	10.11	3.35	4.07	4.72	4.32	4.09	3.46	*	-
55	THYR01000916	9.19	7.72	16.87	5.02	6.67	5.27	4.16	6.12	3.42	*	-
	THYR01000917	6.89	10.63	12.32	4.97	9.51	5.39	6.77	7.94	6.2	*	-
	THYR01000926	14.99	10.81	12.37	6.79	9.95	6.06	7.42	7.03	11.27	*	-

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	THYR01000934	9.21	6.94	9.67	4.17	7.52	4.26	6.41	5.73	4.96	*	*	-
	THYR01000951	21.19	13.82	17.24	10.15	10.71	6.54	7.11	11.34	11.56	*	*	-
5	THYR01000952	38.82	45.17	51.97	24.89	24.37	18.77	17.55	26.97	13.34	**	**	-
	THYR01000956	11.42	8.41	13.85	5.27	6.34	6.15	5.07	6.81	6.85	*	*	-
	THYR01000960	9.97	3.83	8.63	2.78	4.13	2.34	2.46	2.03	6.43	*	*	-
	THYR01000961	33.04	35.26	36.48	15.01	15.48	15.21	21.6	24.41	21.14	**	**	-
	THYR01000964	14.43	12.46	17.93	3.92	6.7	5.62	5.43	7.53	4.58	**	**	-
10	THYR01000971	15.18	16.5	16.14	8.34	13.54	9	9.18	8.59	10.52	*	*	-
	THYR01000974	7.51	5.29	9.43	2.24	6.94	1.8	3.55	5.59	3.45	*	*	-
	THYR01000975	7.71	4.75	6.93	3.36	5.71	4.79	3.77	4.87	3	*	*	-
	THYR01000983	8.4	4.14	7.44	3.86	5.03	3.36	3.1	3.21	4.03	*	*	-
	THYR01000984	9.35	8.4	11.52	6.49	7.32	5.22	5.08	2.55	2.65	*	**	-
	THYR01000988	12.33	6.57	7.62	4.27	4.23	4.6	2.94	2.66	2.92	*	**	-
	THYR01000991	12.33	10.95	12.47	5.27	7.49	7.34	5.57	6.15	6.01	**	**	-
15	THYR01000999	9.77	12.84	10.64	5.68	8.33	5.92	5.68	3.11	2.9	*	**	-
	THYR01001003	324.55	443.5	324.63	353.93	491.59	377.12	509.02	394.65	380.17	*	*	-
	THYR01001015	16.58	13.37	11.66	7.36	13.81	8.4	12.04	9.04	10.47	*	*	-
	THYR01001016	34.7	29.76	32.31	14.48	17.7	10.51	27.97	31.88	30.58	**	**	-
	THYR01001022	27.6	17.2	20.61	6.98	9.39	10.85	5.35	6.58	6.8	*	*	-
20	THYR01001031	15.75	9.57	11.29	5.12	7.05	5.99	8.13	6.39	9.34	*	*	-
	THYR01001033	11.34	7.57	8.58	7.55	5.52	6.01	4.3	4.01	4.9	*	*	-
	THYR01001062	12.86	12.45	12.49	4.68	5.59	4.88	3.54	3.68	2.79	**	**	-
	THYR01001063	10.18	8.38	10.08	5.14	7.17	4.58	3.55	4.32	2.35	*	**	-
	THYR01001071	18.49	15.5	18.23	9.12	10.91	7.86	5.73	5.41	5.84	**	**	-
	THYR01001080	11.77	12.06	11.47	3.65	12.27	3.17	3.08	4.59	4.41	**	**	-
	THYR01001093	12.17	9.63	9.75	5.98	4.91	5	8.58	8.31	7.24	**	*	-
25	THYR01001100	33.06	27.59	26.02	30.29	27.98	30.28	66.02	40.22	70.38	*	†	-
	THYR01001102	10.18	6.7	5.95	5.04	6.9	4.52	4.36	4.71	4.45	*	*	-
	THYR01001104	5.1	2.75	2.78	0.69	0.92	1.62	1.32	0.94	0.7	*	*	-
	THYR01001109	19.62	18.07	14.26	10.98	10.98	9.76	8.55	11.06	8.68	*	*	-
	THYR01001113	10.89	6.97	7.59	2.84	3.69	2.77	2.56	1.4	2.3	*	**	-
30	THYR01001120	9.27	9	8.82	3.46	4.66	2.98	4.02	3.07	2	**	**	-
	THYR01001121	20.41	16.36	16.91	9.1	13.05	6.93	13.22	15.3	13.97	*	*	-
	THYR01001128	25.09	18.24	17.74	8.53	9.61	6.74	3.45	4.7	7.82	**	**	-
	THYR01001133	7.42	6.4	5.88	4	5.05	4.23	3.88	4.14	3.81	*	*	-
	THYR01001134	29.23	23.66	23.28	16.51	20.53	18.49	22.14	16.92	20.47	*	*	-
	THYR01001142	5.04	4.99	5.1	2.78	3.05	3.47	2.44	2.26	1.6	**	**	-
35	THYR01001173	31.85	26.04	28.94	20.36	18.72	13.59	18.5	15.33	18.17	*	*	-
	THYR01001175	95.56	98.04	80.56	104.29	114.18	77.1	51.33	46.56	49.17	**	**	-
	THYR01001177	10.9	11.18	11.71	5.13	7.17	5.9	4.63	5.82	5.02	**	**	-
	THYR01001189	16.52	14.55	11.53	5.76	11.24	3.42	11.07	10.9	8.86	*	*	-
	THYR01001194	11.83	6.2	11.19	5.29	7.22	4.28	5.84	7.01	6.86	*	*	-
40	THYR01001204	52.04	33.32	32.8	18.53	22.19	18.27	39.75	37.94	46.59	*	*	-
	THYR01001205	8.98	12.23	9.39	5.39	8.08	5.04	6.55	6.04	4.85	*	*	-
	THYR01001213	41.54	37.73	35.86	23.36	25.7	20.79	37.67	32.41	38.62	**	**	-
	THYR01001224	10.86	11.43	10.75	5.38	8.69	6.7	7.21	4.53	6.36	*	**	-
	THYR01001237	16.76	20.25	15.97	16.59	13.69	5.38	9.78	5.69	6.27	*	**	-
	THYR01001242	13.1	19.03	16.06	12.27	8.61	6.73	9.21	5.95	9.02	*	*	-
	THYR01001258	27.32	21.68	20.65	9.74	18.76	12.77	10.51	6.86	13.04	*	**	-
45	THYR01001262	8.57	4.74	4.06	3.76	5.55	4.02	4.79	3.93	5.05	*	*	-
	THYR01001266	25.45	17.38	17.48	9.96	11.28	8.76	13.97	15.24	19.55	*	*	-
	THYR01001271	27.85	25.6	17.14	13.77	18.43	9.74	22.54	18.92	23.05	*	*	-
	THYR01001287	126.74	172.63	126.71	56.76	169.06	71.99	103.16	93.81	120.13	*	*	-
	THYR01001290	11.3	8.82	9.68	4.97	7.48	6.55	3.66	5.84	8.41	*	*	-
	THYR01001291	12.9	16.44	13.22	8.85	8.33	3.9	6.83	3.64	6.66	*	**	-
50	THYR01001297	13.17	12.27	11.41	6.73	6.89	4.23	7.87	5.3	8.04	**	**	-
	THYR01001302	28.98	24.47	17.01	9.99	19.11	8.25	41.39	28.42	36.98	*	*	-
	THYR01001313	3.4	2.28	2.86	1.62	1.97	1.71	3.09	2.85	2.3	*	*	-
	THYR01001320	4.85	2.3	4.45	3.81	2.95	2.21	2.67	2.22	1.94	*	*	-
	THYR01001321	84.54	108.43	89.51	45.59	48.9	36.67	60.61	56.13	42.33	**	*	-
	THYR01001322	15.07	13.59	11.8	5.6	6.9	4.45	5.91	6.73	6.71	**	**	-
55	THYR01001327	61.14	62.79	47.56	27.21	36.08	29.25	40.32	44.89	30.36	**	*	-
	THYR01001336	21.04	18.95	13.64	17.33	15.44	11.88	17.21	14.24	12.35	*	*	-
	THYR01001347	42.47	35.49	29.56	20.44	37.43	12.7	20.26	16.34	15.93	**	*	-

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	THYR01001358	6.96	7.77	6.52	4.41	8.39	3.78	5.37	5.5	4.22	**	*	-
	THYR01001363	36.77	35.26	36.97	12.86	20.63	14.65	24.19	31.52	25.12	**	*	-
5	THYR01001365	2.39	1.31	4.42	2.3	2.59	1.42	1.82	2.18	1.5	*	-	-
	THYR01001374	10.11	11.14	11.66	5.19	7.75	3.54	2.84	5.3	4.44	*	**	-
	THYR01001401	11.45	8.59	8.77	5.02	5.3	5.96	5.5	8.56	6.31	*	-	-
	THYR01001403	3.12	3.62	7.98	1.61	2.43	2.61	3.73	1.98	3.91	*	-	-
	THYR01001405	84.82	60.76	92.35	68.75	78.6	50.19	53.53	29.6	47.94	*	-	-
	THYR01001406	13.59	7.57	12.02	4.76	6.87	3.76	11.69	13.59	9.54	*	-	-
10	THYR01001411	4.72	4.15	5.65	3.88	2.4	3.38	2.52	2.5	3.6	*	-	-
	THYR01001420	9.34	4.82	8.71	4.7	4.71	5.55	3.24	4.39	8.81	*	-	-
	THYR01001426	9.26	4.52	12.27	5.65	6.22	4.37	4.27	8.59	6.13	*	-	-
	THYR01001430	10.74	13.91	18.18	13.99	18.28	13.49	6.82	9.48	10.77	*	-	-
	THYR01001434	7.66	6.66	12.91	8.54	10.68	8.13	5.38	8.91	2.99	*	-	-
	THYR01001456	26.49	36.99	36.96	17.02	23.99	16.92	30.71	34.81	38.85	*	-	-
15	THYR01001457	14.33	10.91	13.26	5.72	4.54	3.33	4.05	3.22	4.83	**	*	-
	THYR01001458	15.32	13.83	12.78	10.99	10.13	5.72	4.4	7.29	6.97	*	**	-
	THYR01001459	5.78	4.92	7.16	2.81	3.46	4.24	3.11	4.43	5.51	*	-	-
	THYR01001471	13.48	10.81	13.3	5.13	9.52	6.19	6.36	8.85	9.45	*	-	-
	THYR01001478	8.04	3.79	8.01	2.94	3.62	2.21	4.12	4.22	3.59	*	-	-
20	THYR01001480	16.07	16.86	14.48	6.78	13.68	13.34	3.54	6.61	19.35	*	-	-
	THYR01001481	16.23	13.97	17.19	13.3	15.2	13.73	4.94	6.01	3.76	*	-	-
	THYR01001487	39.34	43.94	45.87	41.49	42.62	34.09	36.78	39.23	41.44	*	-	-
	THYR01001495	6.21	3.33	12.71	2.18	5.51	4.67	3.43	3.46	4.85	*	-	-
	THYR01001498	13.82	15.45	16.61	11.32	20.15	8.37	4.81	6.08	4.31	**	-	-
	THYR01001510	9.97	6.87	19.31	8.41	6.21	3.55	4.99	6.45	19.57	*	-	-
25	THYR01001512	11.51	8.21	10.34	5.87	6.36	6.84	4.43	19.67	5.22	*	-	-
	THYR01001519	12.05	16.47	10.9	4.73	8.69	4.14	4.42	4.28	5.04	*	**	-
	THYR01001522	10.39	6.84	12.83	6.15	7.71	8	5.13	5.33	7.56	*	-	-
	THYR01001523	15.14	10.51	16.01	7.01	9.2	6.38	3.77	3.19	4.5	*	**	-
	THYR01001526	5.67	5.48	12.84	2.85	5.19	3.09	4.51	3.63	4.01	*	-	-
	THYR01001529	70.52	99.68	61.07	73.62	81.82	35.88	29.07	23.9	34.59	*	-	-
30	THYR01001534	10.48	7.92	11.72	6.09	7.42	11.24	6.53	6.35	3.17	*	-	-
	THYR01001537	5.9	3.05	5.93	3.4	3.75	2.75	3.26	2.87	4.91	*	-	-
	THYR01001541	27.84	38.72	38.42	23.51	30.22	18.99	22.01	26.98	14.05	**	-	-
	THYR01001545	12.87	9.76	11.61	3.56	6.9	5.41	4.18	22.14	4.44	**	-	-
	THYR01001559	143.67	217.09	127.43	126.92	211.99	217.97	165.83	143.91	101.7	**	-	-
	THYR01001563	29.66	25.88	28.83	14.46	17.77	19.17	10.82	18.32	17.35	**	**	-
35	THYR01001570	5.85	5.24	10.72	3.21	3.79	2.31	2.47	4.03	3.05	*	-	-
	THYR01001573	10.58	14.52	15.67	7.66	10.98	10.26	4.93	9.17	5.76	*	-	-
	THYR01001584	11.71	9.79	13.05	7.75	12.43	7.3	8.19	4.92	4.88	*	-	-
	THYR01001593	119.63	87.93	122.57	37.27	54.3	33.56	100.89	84.41	119.61	**	-	-
	THYR01001595	9.11	9.13	10.8	7.84	8.88	6.77	4.62	12.97	7.82	*	-	-
	THYR01001596	6.25	3.54	8.97	3.03	4.5	2.76	3.54	3.67	4.02	*	-	-
40	THYR01001602	7.1	6.21	7.8	6.63	4.96	5.02	4.21	4.12	2.97	**	-	-
	THYR01001605	28.22	39.54	25.87	13.48	23.89	22.57	11.83	10.02	13.09	*	-	-
	THYR01001608	19.26	17.94	17.77	8.3	22	8.49	8.07	8.36	11.18	**	-	-
	THYR01001617	7.36	9.07	12.26	4.4	5.61	3.53	3.83	3.37	4.51	*	-	-
	THYR01001634	9.8	9.15	14.08	5.65	9.76	4.62	5.62	3.69	4.86	*	-	-
	THYR01001637	6.56	2.42	6.39	2.18	3.8	2.31	2.41	3.7	6.48	*	-	-
45	THYR01001641	12.87	8.05	12.44	6.03	4.87	6.49	3.32	2.86	2.92	*	**	-
	THYR01001656	20.03	12.66	30.89	7	10.07	5.22	6.32	7.53	5.64	*	-	-
	THYR01001658	7.58	6.85	10.14	4.65	4.77	3.94	3.38	2.8	2.5	*	**	-
	THYR01001661	150.1	98.3	106.51	135.25	166.2	125.8	74	80.32	53.78	*	-	-
	THYR01001671	10.97	8.43	12.21	5	5.04	3.97	5.12	5.12	3.84	**	**	-
	THYR01001672	12.9	11.31	11.75	5.85	6.91	5.08	3.69	2.74	2.72	**	**	-
50	THYR01001673	31.04	28.57	26.79	16.85	19.7	19.9	22.8	23.43	23.51	**	*	-
	THYR01001677	8.63	6.86	9.97	3.55	4.9	4.2	5.4	6.95	6.85	*	-	-
	THYR01001683	39.34	16.85	25.87	16.11	18.7	19.17	8.36	10.76	9.09	*	-	-
	THYR01001700	12.31	7.03	9.15	3.61	4.23	3.04	2.79	3.63	4.8	*	-	-
	THYR01001702	23.7	21.62	17.4	10.57	5.8	11.44	6.01	4.83	2.94	*	**	-
	THYR01001703	7.22	4.23	5.14	2.63	3.23	1.81	2.37	2.42	2.04	*	**	-
55	THYR01001706	8.39	5.62	8.09	3.72	3.11	3.37	3.24	2.65	1.26	*	**	-
	THYR01001721	11.69	10.42	16.73	6.09	4.96	4.46	3.92	2.33	3.87	*	**	-
	THYR01001725	147.69	144.4	144.74	111.99	128.3	86.63	130.43	106.61	93.76	*	*	-

Table 503

	THYR01001730	7.74	3.57	7.41	4.48	4.19	3.07	3.64	4.09	4.72	
	THYR01001738	1.57	3.03	2.24	0.97	0.17	0.58	0.7	0.99	1.64	*
	THYR01001743	5.12	1.48	3.39	1.87	2.12	2.94	1.98	2.6	2.48	*
	THYR01001745	30.25	14.84	20.6	6.81	4.85	9.25	12.7	8.09	11.05	*
	THYR01001746	10.78	5.89	7.69	2.83	3.1	3.64	3.64	1.32	1.23	*
	THYR01001770	20.01	12.02	16.57	10.05	13	10.49	5.67	5.07	5.43	*
	THYR01001772	29.2	56.08	29.11	28.47	34.34	15.95	9.21	8.24	9.37	*
	THYR01001778	39.03	35.61	22.42	13.39	32.45	16.04	9.42	8.03	11.2	*
	THYR01001793	9.35	3.26	5.98	4.02	4.49	3.37	4.45	2.6	5.77	*
	THYR01001796	66.96	62.34	52.36	31.81	31.58	30.68	74.83	63.67	78.59	**
	THYR01001800	25.21	17.42	21.74	19.92	16.43	13.71	5.71	5.48	6.64	**
	THYR01001803	12.96	11.11	10.51	7.04	8.3	3.44	8.62	1.76	1.34	**
	THYR01001809	10.44	7.96	6.8	5.49	3.72	3.71	3.79	4.88	6.37	*
	THYR01001817	18.78	13.28	15.51	15.03	13.53	6.93	8.72	4.29	5.81	*
	THYR01001819	14.15	14.31	9.69	5.8	6.63	6.06	7.27	2.29	2.46	*
	THYR01001828	8.14	8.22	6.65	5.42	7.94	4.29	7.29	2.26	2.47	*
	THYR01001854	50.53	32.68	37.71	33.17	34.18	22.81	22.16	27.13	21.15	*
	THYR01001895	9.86	7.83	3.92	4.41	4.53	2.55	3.7	10.54	3.46	*
	THYR01001907	27.03	13.41	12.49	9.48	10.54	7.02	4.92	4.41	6.47	*
	TRACH1000006	9.54	7.16	8.08	5.68	4.46	3.1	6.46	5.52	6.76	*
	TRACH10000113	9.02	5.8	8.2	2.58	4.66	3.1	3.07	2.02	1.44	*
	TRACH1000074	13.59	9.32	8.63	2.66	5.75	4.06	3.77	3.07	3.63	*
	TRACH1000095	11.28	8.48	10.55	5.54	3.9	3.41	3.79	5.56	3.68	**
	TRACH1000102	26.86	26.3	20.9	15.81	18.57	15.2	32.52	24.6	27.09	*
	TRACH1000108	68.65	59.61	40.48	28.57	26.39	20.9	69.3	56.08	66.91	*
	TRACH1000126	17.36	13.19	13.78	8.07	8.6	6.46	5.91	5.75	6.51	**
	TRACH1000146	7.25	6.83	5.07	5.29	3.75	3.17	3.49	3.25	4.97	*
	TRACH1000160	11.76	11.24	7.7	4.05	5.59	4.95	5.32	4.22	5.87	*
	TRACH1000184	33.51	45.86	50.29	14.82	25.81	22.15	25.29	16.88	23.76	*
	VESENI000004	11.35	8.9	8.13	5.46	9.59	6.32	5.53	6.44	6.01	*
	VESENI000007	32.64	30.13	26.81	16.7	21.99	18.54	37.52	29.73	33.89	**
	VESENI000013	13.16	11.68	12.05	7.19	9.9	4.25	7.18	4.46	8.92	*
	VESENI000028	23.17	20.53	28.94	10.16	15.29	14.76	9.13	12.72	8.48	**
	VESENI000058	4.76	3.32	5.57	3.56	3.32	3.56	1.16	3.33	1.96	*
	VESENI000100	8.85	5.84	8.92	5.55	6.82	4.48	3.69	5.59	3.98	*
	VESENI000107	158.28	125.83	134.47	126.46	135.37	133.6	74.61	79.36	82.66	**
	VESENI000117	3.74	4.02	10.93	3.48	5.02	4.1	2.18	2.11	2.69	*
	VESENI000122	5.84	5.31	7.17	3.91	7.47	3.29	2.52	3.75	2.41	*
	VESENI000137	7.93	10.91	7.7	8.31	5.46	4.02	3.34	3.36	5.77	*
	VESENI000196	12.47	4.75	10.07	4.43	4.22	7.07	3.11	4.32	13.25	*
	VESENI000215	89.55	69.15	78.83	74.46	93.71	81.06	50.08	36.95	43.23	**
	VESENI000279	16.42	11.12	19.97	7.86	19.23	9.52	8.84	13.86	21.34	*
	VESENI000363	40.43	29.46	56.48	41.4	53.72	50.13	17.51	33.82	20.25	*
	VESENI000388	4.51	6.13	9.09	5.56	8.45	6.21	3.44	6.29	2.57	*
	VESENI000394	137.33	123.92	135.03	107.32	177.33	115.58	81.85	76.56	86.04	**
	VESENI000410	7.84	11.73	12.31	7.37	8.85	7.32	8.82	6.16	5.5	*
	VESENI000411	14.34	16.7	11.87	14.26	14.7	9.52	6.54	4.28	7.07	**
	VESENI000415	6.65	6.22	8.5	3.16	5.01	4.35	2.08	3.93	3.73	*
	VESENI000440	7.1	4.56	7.48	10.06	4.69	9.04	3.62	6.97	6.76	*
	VESENI000452	127.08	114.54	102.58	103.33	106.23	122.79	77.87	58.16	82.71	*
	VESENI000539	57.4	47.68	67.32	36.3	45.7	42.57	51.56	51.15	50.18	*
	VESENI000554	7.29	12.24	14.13	6.05	4.57	6.75	3.69	3.4	3.85	*
	VESENI000557	4.5	6.91	10.86	5.64	5.73	4.35	3.05	2.96	4.75	*
	VESENI000575	16	18.27	24.28	11.33	16.07	11.77	13.59	13.83	16.27	*
	VESENI000585	14.4	14.28	13.38	9.87	13.37	6.72	4.91	4.08	5.01	**
	VESENI000592	28.09	20.04	22.75	8.98	11.53	7	7.53	8.48	8.84	**
	VESENI000658	9.27	5.98	6.99	4.92	3.93	3.11	3.31	12.18	6.06	*
	VESENI000668	7.65	11.62	18.09	8.2	9.11	7.91	4.21	6.96	3.61	*
	VESENI000743	27.12	25.27	28.49	19.46	23.17	19.77	12.01	15.14	12.53	*
	VESENI000752	23.77	18.91	24.8	11.19	11.63	9.8	14.24	19.48	18.19	**
	VESENI000761	7.03	8.3	9.9	5.64	5.41	3.65	3.1	8.25	5.47	*
	VESENI2000339	16.58	20.4	16.46	7.12	12.23	7.45	5.23	4.66	6.91	*
	VESENI2000102	15.76	17.97	17.55	7.45	12.52	8.13	11.35	16.16	13.31	*
	VESENI200164	69.66	54.85	57.77	18.32	20.39	15.6	15.69	21.51	20.97	**



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	VESEN2000175	7.45	6.95	7.39	3.43	6.1	3.72	4.64	8.1	4.35	*	-
	VESEN2000186	18.04	20.73	21.8	11.19	14.77	10.58	8.74	12.84	12.61	**	**
	VESEN2000199	11.71	6.48	9.96	8.59	9.24	5.52	6.89	6.26	14.79	*	-
5	VESEN2000200	150.21	142.83	144.63	172.94	215.31	128.05	93.38	87.48	97.05	**	-
	VESEN2000204	7.05	7.07	9.65	4.56	4.24	3	2.19	4.63	3.19	*	*
	VESEN2000218	16.65	12.07	17.29	7.31	8.24	6.18	8.32	5	5.15	**	-
	VESEN2000230	12.09	13.48	13.57	4.57	10.45	4.08	3.93	4.19	2.98	*	*
	VESEN2000272	8.95	9.01	11.14	4.32	3.66	3.22	4.36	3.53	4.22	**	-
10	VESEN2000299	8.61	7.23	11.81	5.04	5.83	4.25	3.6	5.71	4.76	*	*
	VESEN2000323	17.3	12.74	15.22	15.36	17.47	14.24	5.84	6.35	4.65	**	-
	VESEN2000337	18.5	9.19	14.45	6.81	8.17	7.45	3.2	5.07	5.85	*	*
	VESEN2000328	7.53	7.78	8.38	3.45	4.17	4.12	2.35	2.19	1.81	**	-
	VESEN2000330	25.07	20.15	22.73	13.34	18.45	13.16	15.63	15.15	15	*	*
	VESEN2000336	7.29	9.37	11.82	5.86	9.09	5.78	3.64	3.5	5	*	*
15	VESEN2000354	10.99	9.78	10.4	5.27	8.22	4.93	3.58	3.58	2.59	*	*
	VESEN2000378	168.58	110.88	139.59	81.44	99.69	74.23	74.17	76.59	54.75	*	*
	VESEN2000379	32.08	21.47	28.34	16.72	15.12	13	22.77	26.45	21.84	*	*
	VESEN2000397	21.17	10.11	25.4	12.77	12.2	10.8	15.72	16.01	17.99	*	-
	VESEN2000416	5.92	5.21	7.48	3.5	6.28	4.01	2.87	3.94	3.48	*	-
	VESEN2000420	8.47	4.35	7.18	4.04	3.81	2.46	2.31	4.27	1.92	*	-
20	VESEN2000430	8.74	5.76	7.33	2.94	5.32	2.11	1.8	2.27	0.71	*	**
	VESEN2000448	14.67	14.58	16.08	4.71	4.34	2.88	3.91	2.23	2.77	**	**
	VESEN2000449	46.1	50.29	39.97	32.75	32.82	21.56	37.62	28.99	23.73	*	*
	VESEN2000456	45.88	33.52	32.47	18.88	21.08	19.47	15.48	22.28	22.31	*	*
	VESEN2000562	6.11	3.13	4.69	5.4	3.95	3.19	3.24	2.45	2.42	*	*
	VESEN2000573	26.67	20.52	18.39	14.29	11.45	8.79	8.94	7.46	12.2	*	*
25	VESEN2000604	9.02	7.76	4.59	4.65	4.32	4.42	1.84	4.41	1.34	*	*
	VESEN2000614	9.59	7.78	6.05	4.77	5.05	4.35	3	3.94	2.87	*	*
	VESEN2000638	16.75	10.83	10.74	6.38	9.46	6.26	4.67	4.46	3.5	*	*
	VESEN2000641	15.71	14.29	14.25	7.95	7.6	6.71	8.94	7.41	6.5	**	**
	VESEN2000645	9.28	11.51	10.66	5.27	8.03	4.95	5.42	4.96	6.81	*	-
	Y79AA1000013	24.66	15.88	15.09	6.08	5.41	5.53	13.59	13.07	18.88	*	-
30	Y79AA1000030	19.52	16.62	14.47	8.07	7.77	10.99	7.86	7.77	10.02	*	**
	Y79AA1000033	29.91	18.65	28.38	16.37	15.72	11.59	28.15	19.64	28.85	*	-
	Y79AA1000037	4.94	2.8	4.89	5.26	2.24	0.91	1.44	1.94	2.43	*	-
	Y79AA1000041	79.98	53.74	54.87	39.77	36.14	29.21	42.77	30.09	45.97	*	-
	Y79AA1000059	9.8	7.3	8.44	4.37	5.08	2.06	5.32	3.01	5.11	*	-
	Y79AA1000065	116.14	101.03	106.53	93.49	124.96	111.44	68.74	63.93	65.56	**	-
35	Y79AA1000081	7.88	11.03	9.72	7.03	9.28	7.22	5.68	4.38	3.88	**	-
	Y79AA1000127	8	5.82	6.2	3.17	4.25	2.35	5.28	6.34	4.47	*	*
	Y79AA1000130	20.16	11.01	14.68	13.04	8.43	8.05	14.41	16.35	14.16	*	-
	Y79AA1000131	17.14	8.99	11.18	6.93	10.63	6.92	6.82	8.55	6.52	*	-
	Y79AA1000134	6.34	7.52	5.68	7.86	5.61	3.09	4.16	2.2	3.07	*	-
40	Y79AA1000143	8.89	7.38	8.14	3.93	5.83	3.75	3.23	2.53	3.96	*	**
	Y79AA1000144	11.79	8.62	9.18	5.64	6.37	5.56	3.97	3.84	3.36	*	**
	Y79AA1000150	28.57	28.05	20.04	12.4	17.77	10.66	24.46	16.09	20.29	*	-
	Y79AA1000153	11.32	11.62	7.41	5.89	9.36	6.53	6.84	5.59	6.52	*	-
	Y79AA1000166	13.75	6.3	9.45	4.16	5.68	2.88	7.42	8.85	8.76	*	-
	Y79AA1000179	13.15	8.67	7.74	7.91	7.5	4.67	13.52	5.81	9.18	*	-
45	Y79AA1000181	14.37	9.22	8.77	6.64	8.41	3.93	3.41	3.97	4.65	*	-
	Y79AA1000202	22.9	17.78	19.17	14.55	12.31	8.36	18.27	13.59	20.94	*	-
	Y79AA1000207	52.28	63.3	44.9	24.04	38.89	23.79	15.85	13.31	14.27	**	-
	Y79AA1000214	9.44	4.9	5.66	4.71	4.79	4.18	5.54	2.28	3.2	*	-
	Y79AA1000222	11.34	8.61	7.95	5.13	7.04	2.26	4.7	3.53	4.87	*	-
	Y79AA1000226	27.21	25.59	19.24	12.19	15.74	11.35	24.75	16.69	21.48	*	-
50	Y79AA1000227	9.07	6.57	6.62	3.66	4.45	3.9	7.4	6.45	7.51	*	-
	Y79AA1000230	32.97	25.47	29.26	12.55	10.05	6.68	4.18	3.82	4.93	**	**
	Y79AA1000231	65.27	41.2	48.87	47.4	47.89	24.64	28.97	32.14	28.29	*	-
	Y79AA1000239	74.35	85.68	67.35	68.07	52.75	45.41	64.49	54.97	44.91	*	-
	Y79AA1000258	8.42	5.48	5.2	4.36	4.01	3.09	3.34	2.93	4.62	*	-
	Y79AA1000268	80.53	75.19	49.36	22.18	30.03	27.42	30.39	26.87	31.5	*	*
55	Y79AA1000269	73.43	71.24	52.77	41.13	70.01	36.87	77.91	62.7	65.45	*	-
	Y79AA1000270	10.05	7.03	4.1	4.98	7.95	3.4	5.03	5.7	4.72	*	-
	Y79AA1000280	25.49	25.11	28.96	8.6	12.9	9.27	5.74	8.76	6.26	**	**

Table S05

	179AA1000285	22.27	16.31	18.63	6.85	10.3	7.36	15.47	22.31	18.9	**	-
	179AA1000295	4.35	2.68	5.01	1.59	3.76	2.11	2.3	2.59	2.22		
5	179AA1000307	6.82	4.93	8.12	6.39	9.3	7.36	3	5.88	4.49		
	179AA1000313	4.28	2.34	3.94	1.66	3.1	3.25	1.93	2.47	1.62		
	179AA1000314	1.57	1.83	4.11	1.4	1.41	0.98	0.87	0.14	1.73		
	179AA1000328	3.78	3.39	5.43	2.09	10.7	2.68	3.27	3.33	3.32		
	179AA1000334	9.59	9.06	7.49	5.79	6.64	3.5	5.12	3.62	4.02	*	**
	179AA1000342	17.48	13.29	18.31	13.02	15.9	13.67	34.2	31.79	30.43	*	+
10	179AA1000346	17.08	11.48	18.69	8.72	9.82	6.74	5.35	5.97	4.15	*	**
	179AA1000347	28.32	26.71	31.26	22.14	31.96	28.74	20.9	20.82	19.69	*	**
	179AA1000349	15.95	20.35	20.7	17.44	19.4	18.58	5.37	7.08	5.15	**	-
	179AA1000355	11.9	11.6	17.89	14.98	13.2	9.11	5.25	6.54	7.95	*	-
	179AA1000368	5.31	4.56	7.88	4.89	6.47	3.77	2.77	3.21	1.95	*	-
	179AA1000388	9.85	11.63	11.71	9.62	9.75	4.51	5.03	4.57	5.04	**	-
15	179AA1000392	13.05	13.68	11.25	7.92	12.06	6.34	12.1	13.67	13.52		
	179AA1000405	100.68	62.31	79.28	103.67	109.59	81.35	71.19	52.24	66.44		
	179AA1000410	8.13	6.1	10.22	6.13	5.36	5.28	4.83	4.8	5.17		
	179AA1000420	11.1	11.77	13.46	5.41	8.52	5.43	6.77	7.21	5.64	*	**
	179AA1000423	7.61	9.21	8.96	4.46	6.29	5.4	4.36	2.75	3.4	*	**
20	179AA1000426	5.75	6.96	10.06	4.68	5.08	3.97	3.38	2.69	2.24	*	-
	179AA1000432	5.62	5.18	10.2	4.71	5.75	4.03	2.85	3.99	8.12		
	179AA1000453	32.42	33.52	37.01	20.21	25.21	18.7	36.98	32.84	33.05	**	-
	179AA1000465	4.43	1.91	3.14	1.7	4.29	1.76	2.57	2.29	2.11		
	179AA1000469	35.31	28.37	27.42	30.17	34.28	32.32	21.89	31.66	24.15	*	-
	179AA1000480	11.78	8.51	13.38	5.22	5.02	5.9	5.84	10.93	8.28	*	-
25	179AA1000502	19.24	16.15	21.16	8.66	14	12.35	16.39	18.08	18.17	*	-
	179AA1000521	75.16	71.09	84.73	74.85	78.28	67.85	48.04	51.73	45.89	**	-
	179AA1000534	13.31	15.15	20.4	13.25	14.05	10.71	13.15	11.71	11.75		
	179AA1000538	12.36	14.67	20.45	9.58	11.27	5.96	3.97	0	4.64	*	**
	179AA1000539	15.51	16.32	14.99	9.48	12.74	10.1	5.39	5.2	6.13	*	**
	179AA1000540	10.2	7.44	12.08	3.41	6.65	4.35	12.15	10.44	10.32	*	-
30	179AA1000560	180.34	128.09	149.28	162.08	194.06	150.56	118.75	125.1	108.26		
	179AA1000574	12.15	9.72	10.83	5.66	8.8	4.53	10.59	16.21	10.56	*	-
	179AA1000584	40.28	35.5	37.1	23.89	28.68	25.51	26.96	34.59	37.41	**	-
	179AA1000589	9.65	4.15	9.45	2.79	3.53	2.1	3.54	8.38	4.6	*	-
	179AA1000598	34.26	29.42	37.32	17.43	15.95	16.48	24.99	27.55	21.09	*	-
	179AA1000600	44.58	45.66	51.58	51.4	52.23	39.65	32.06	30.08	26.05	**	-
35	179AA1000608	7.91	6.61	8.76	1.95	5.66	3.3	3.74	4.36	7.05	*	-
	179AA1000618	20.27	20.13	21.51	6.61	13.31	6.56	19.86	14.92	16.1	*	-
	179AA1000627	18.35	16.53	18.66	9.09	10.58	9.21	14.78	8.21	19.69	**	-
	179AA1000636	5.21	2.52	7.03	3.36	4.46	4.2	2.54	3.13	1.94	*	-
	179AA1000649	19.51	21.35	25.26	12.58	12.75	9.69	16.99	19.63	19.13	*	-
	179AA1000656	7.37	5.14	7.46	2.86	2.97	2.28	2.83	3.72	2.99	**	-
40	179AA1000673	8.38	7.17	11.58	4.74	3.99	5.74	1.87	4.27	2.18	*	-
	179AA1000674	131.64	157.11	127.73	143.89	140.32	116.2	111.11	118.96	120.08		
	179AA1000678	22.12	27.62	25.96	12.61	21.55	13.08	21.7	19.94	19.36	*	-
	179AA1000682	14.62	11.86	13.44	6.55	8.13	6.38	12.74	13.35	11.29	*	-
	179AA1000683	37.64	24.34	33.28	19.88	16.2	12.73	33.87	33.73	36.17	*	-
	179AA1000697	46.01	35.33	48.41	23.15	27.46	23.15	15.24	20.88	15.95	**	-
45	179AA1000700	3.64	3.69	5.68	3.34	3.06	2.62	3.53	2.27	2.51	*	-
	179AA1000702	50.6	33.01	36	23.71	24.96	18.05	18.21	11.97	15.36	*	-
	179AA1000704	93.86	71.31	88.5	110.92	93.16	106.68	74.22	61.46	46.95	*	-
	179AA1000705	6.23	6.74	7.37	1.82	2.22	2.09	2.28	0.26	2.39	**	-
	179AA1000717	8.36	6.77	8.13	4.96	8.96	4.55	2.44	3.74	2.84	**	-
	179AA1000722	10.83	11.52	10.81	4.97	5.79	3.98	6.28	5.1	5.45	**	-
50	179AA1000724	42.59	35.15	44.52	31.42	30.43	23.04	24.2	29.89	31.56	*	-
	179AA1000726	8.78	4.43	7.31	5.15	4.77	4.25	2.41	3.94	2.09	*	-
	179AA1000734	5.72	4.05	6.45	2.81	2.76	3.46	2.68	2.98	0.96	*	-
	179AA1000748	7.45	7.72	8.69	2.89	2.82	2.75	2.52	2.8	2.36	**	-
	179AA1000750	41.52	33.1	33.65	18.03	22.65	18.6	26.15	29.63	22.6	**	-
	179AA1000752	9.11	9.26	10.14	4.75	3.47	2.23	2.34	2.01	1.29	**	-
55	179AA1000774	19.25	19.31	26.89	10.74	13.71	10.53	12.54	14.59	12.73	*	-
	179AA1000776	12.05	9.97	9.69	5.12	6.81	2.36	10.58	10.24	7.92	*	-
	179AA1000777	17.61	11.59	13.15	7.32	8.15	7.21	6.02	5.12	6.68	*	-

Table 506

	Y79AA1000778	20.06	13.62	11.66	10.8	9.69	8.29	13.52	13.51	12.96			
	Y79AA1000782	13.43	7.55	9.19	7.76	8.46	7.38	6.52	5.21	4.82	*	*	-
5	Y79AA1000784	11.14	10.21	12.84	4.67	5.08	6.71	10.7	9.6	9.71	**	-	-
	Y79AA1000794	46.19	39.88	38.82	22.35	24.71	16.75	37.28	33.24	34.17	*	-	-
	Y79AA1000800	7.18	3.91	5.09	0.48	0.36	0.17	2.34	0	0	**	*	-
	Y79AA1000802	11.45	13.12	10.85	5.78	8.8	4.96	3.89	4.75	3.77	*	**	-
	Y79AA1000805	21.22	18.33	12.77	6.7	11.14	4.1	15.87	12.52	16.72	*	-	-
	Y79AA1000814	27.49	21.74	18.55	16.59	17.35	12.96	22	17.22	22.17	*	-	-
10	Y79AA1000823	14.24	7.73	9.85	4.94	4.36	5.06	6.73	6.96	8.36	*	-	-
	Y79AA1000824	16.24	10	9.76	8.11	9.28	6.16	6.82	5.83	8.72	*	-	-
	Y79AA1000827	9.71	3.82	4.6	3.63	3.22	2.56	3.51	2.06	2.23	*	-	-
	Y79AA1000831	7.38	5.79	7.27	4.13	3.32	2.68	4.43	0.57	1.26	**	*	-
	Y79AA1000833	22.35	19.25	16.88	12.38	7.9	8.89	19.38	11.86	18.04	**	*	-
15	Y79AA1000850	33.44	40.57	26.99	19.52	21.81	14.62	28.93	23.5	32.01	*	-	-
	Y79AA1000856	6.26	7.4	4.9	2.81	6.29	2.12	4.31	2.48	3.63	*	-	-
	Y79AA1000862	8.84	4.04	5.05	7.04	4.31	3.07	5.61	5.34	5.05	*	-	-
	Y79AA1000876	21.17	10.25	11.73	7.67	6.82	6.01	5.79	7.01	6	*	-	-
	Y79AA1000888	32.02	25.94	21.68	17.64	17.29	12.59	18.41	20.33	23.17	*	-	-
	Y79AA1000902	6.26	5.68	6.17	4.27	4.4	2.72	2.73	2.97	2.19	*	**	-
20	Y79AA1000935	76.11	52.08	52.32	70.65	71.58	69.22	39.77	35.2	32.3	*	-	-
	Y79AA1000959	48.22	40.7	37.08	25.45	33.48	19.11	26.33	21.44	21.93	*	-	-
	Y79AA1000962	46.82	45.31	38.99	22.79	24.29	17.48	60.82	38.12	53.14	**	-	-
	Y79AA1000963	25.33	35.17	19.37	13.71	17.32	12.79	14.75	14.39	13.92	*	-	-
	Y79AA1000966	41.31	37.86	31.25	27.6	23.69	23.7	32	18.68	25.22	*	-	-
	Y79AA1000967	19.13	9.69	10.03	8.88	7.99	4.65	1.27	8.2	0.25	*	-	-
25	Y79AA1000968	25.81	16.48	14.41	11.57	12.79	6.94	25.2	19.6	28.68	*	-	-
	Y79AA1000969	40.02	39.97	33.37	23.55	39.74	36.04	32.93	30.52	18.66	*	-	-
	Y79AA1000976	22.75	15.17	16.99	14.98	19.84	15.88	14.85	10.98	11.26	*	-	-
	Y79AA1000978	8.83	7.09	6.8	4.57	5.39	2.66	4.35	3.43	4.33	*	**	-
	Y79AA1000985	8.02	3.9	5.83	4.32	4.39	1.76	4.37	2.17	1.99	*	-	-
	Y79AA1000989	295.68	243.92	218.77	78.52	138.6	77.87	70.03	46.49	61.43	**	**	-
30	Y79AA1000991	12.26	8.35	10.64	5.63	5.93	8.76	7.23	8.65	6.01	*	-	-
	Y79AA1001013	42.37	37.07	51.31	24.72	27.17	18.23	24.27	34.59	22.31	*	*	-
	Y79AA1001014	16.53	17.99	19.41	12.93	20.24	14.74	13.35	18.92	15.51	*	-	-
	Y79AA1001019	8.07	6.21	8.29	4.14	8.05	5.04	2.84	5.3	3.51	*	-	-
	Y79AA1001020	13.89	16.72	13.86	21.03	12.53	10.76	9.5	10.16	11.46	*	-	-
	Y79AA1001023	7.28	6.24	9.28	4.31	8.03	5.29	3.01	3.87	2.51	*	-	-
35	Y79AA1001030	28.41	43.95	33.86	36.62	21.08	22.74	16.86	22.85	18.21	*	-	-
	Y79AA1001035	10.6	13.73	10.93	9.68	10.73	7.69	7.26	7.72	8.91	*	-	-
	Y79AA1001041	14.5	11.14	15.3	8.73	9.96	7.28	9.17	13.51	15.31	*	-	-
	Y79AA1001043	22.79	19.12	22.36	8.78	13.48	10.29	9.42	13.86	17.78	**	*	-
	Y79AA1001048	12.86	13.5	12.88	6.65	11.19	7.59	6.44	7.55	6.3	*	**	-
	Y79AA1001056	6.67	9.77	12.37	5.42	9.5	6.82	2.1	3.99	2.72	*	-	-
40	Y79AA1001061	11.12	17.1	15.18	5.75	10.72	7.78	8.04	10.36	12.77	*	-	-
	Y79AA1001062	4.7	4.96	6.24	2.95	3.71	2.56	2.92	2.19	2.28	*	**	-
	Y79AA1001068	6.22	3.59	5.75	4.34	5.98	4.49	3.29	3.38	3.07	*	-	-
	Y79AA1001073	17.6	17.56	20.08	5.98	13.24	7.19	16.17	13.71	20.42	*	-	-
	Y79AA1001077	7.3	2.86	6.26	7.08	4.43	3.45	1.86	5.22	1.86	*	-	-
	Y79AA1001078	7.29	5.05	6.25	3.73	4.63	2.99	3.3	5.06	3.66	*	-	-
45	Y79AA1001081	7.84	5.5	8.85	3.05	3.81	3.52	2.8	3.1	3.74	*	*	-
	Y79AA1001088	36.17	40.23	42.34	24.5	22.27	19	24.36	30.94	32.13	**	*	-
	Y79AA1001089	332.88	366.62	308.34	284.36	390.54	406.65	237.36	376.46	392	*	-	-
	Y79AA1001090	7.05	4.26	8.66	4.12	3.36	2.71	3.39	1.8	2.5	*	-	-
	Y79AA1001105	22.53	22.64	23.57	8.51	14.07	9.94	17.11	15.32	15.62	**	**	-
	Y79AA1001142	114.5	98.72	131.88	102.55	114.58	143.24	69.56	60.81	74.51	*	-	-
50	Y79AA1001145	98.33	98.57	100.63	125.36	121.38	91.71	78	59.2	74.76	**	-	-
	Y79AA1001162	126.48	83.55	107.65	92.38	93.62	73.32	97.56	124.59	105.84	*	-	-
	Y79AA1001167	12.61	7.85	13.06	7.92	8.82	6.56	7.15	16.96	9.58	*	-	-
	Y79AA1001176	75.12	80.1	84.48	76.52	65.54	64.34	46.71	59.03	47.45	**	*	-
	Y79AA1001177	8.46	7.48	10.23	4.06	5.51	3.51	3.45	4.68	2.96	*	**	-
	Y79AA1001179	54.1	53.61	67.63	28.64	33.09	26.42	13.82	47.33	10.91	**	-	-
55	Y79AA1001185	32.79	30.94	36.04	15.68	21.34	16.32	19.9	17.65	25.06	**	-	-
	Y79AA1001201	45.08	50.33	41.06	13.71	31.35	17.81	48.16	43.78	38.95	*	-	-
	Y79AA1001205	18.73	12.86	21.83	8.38	8.46	6.14	7.31	11.86	11.81	*	-	-

Table 507

	Y79AA1001211	21.15	21.66	22.83	13.08	12.91	10.43	0.44	20.18	19.17	**	-	-
	Y79AA1001212	128.68	116.33	107.84	151.9	151.84	105.91	80.87	83.57	67.14	**	-	-
5	Y79AA1001216	31.68	27.07	33.84	18.3	19.09	14.83	17.05	18.24	23.12	**	-	-
	Y79AA1001228	7.97	5.25	12.95	3.35	3.4	3.64	3.41	10.17	4.89	*	-	-
	Y79AA1001233	8.26	6.53	16.79	3.45	3.77	2.51	2.28	3.79	3.13	*	-	-
	Y79AA1001236	8.84	6.25	11.14	5.02	5.53	3.13	4.08	4.7	2.24	*	-	-
	Y79AA1001239	74.22	59.48	53.54	45.62	41.11	43.05	50.35	42.44	46.18	*	-	-
	Y79AA1001240	70.83	49.07	64.4	30.83	35.04	20.32	48.49	59.48	54.67	*	-	-
10	Y79AA1001255	8.89	10.29	10.55	7.47	6.78	6.42	0.72	6.35	0.76	*	-	-
	Y79AA1001264	14.2	10.19	13.36	9.71	10.05	8.67	4.58	4.84	6.39	**	-	-
	Y79AA1001272	15.16	12.6	13.5	3.77	6.76	5.59	8.86	7.59	6.53	**	-	-
	Y79AA1001281	8.87	7.72	6.68	4.17	4.8	3.47	2.65	2.22	2.28	**	-	-
	Y79AA1001299	9.39	10.08	9.6	4.21	5.3	4.49	3.28	3.68	3.29	**	-	-
	Y79AA1001312	40.47	42.72	35.81	17.92	27.92	14.77	29.7	20.85	26.67	*	-	-
15	Y79AA1001319	31.92	23	20.23	23.19	28.4	16.96	30.43	20.02	18	*	-	-
	Y79AA1001323	32.99	27.82	34.32	14.07	19.03	14.31	25.9	23.32	27.9	**	-	-
	Y79AA1001328	28.33	16.1	28.16	14.56	12.93	12.69	4.94	7.51	4.42	*	-	-
	Y79AA1001343	12.56	8.01	10.99	6.43	7.59	7.49	6.83	9.08	8.27	*	-	-
	Y79AA1001351	6.64	4.21	8.23	2.99	1.8	1.8	2.08	2.52	1.68	*	-	-
20	Y79AA1001364	8.06	5.02	6.83	3.26	2.98	2.12	4.06	2.93	1.74	*	-	-
	Y79AA1001367	145.27	118.42	143.46	117.7	132.8	94.77	76.65	57.61	66.99	**	-	-
	Y79AA1001384	45.86	52.17	41.89	27.43	34.83	21.42	31.33	29.86	26.76	*	-	-
	Y79AA1001391	10.96	12.22	10.34	2.99	9.55	4.77	7.43	7.31	6.01	*	-	-
	Y79AA1001394	24.73	14.05	14.28	9.7	6.32	9.07	6.42	10.16	9.01	*	-	-
	Y79AA1001402	12.42	7.77	9.12	5.62	4.8	4.67	4.74	3.87	4.52	*	-	-
25	Y79AA1001410	5.24	2.77	3.09	3.28	1.53	1.95	2.62	0.78	1.99	*	-	-
	Y79AA1001414	27.49	18.53	20.44	10.78	9.47	10.2	16.16	13.43	11.92	*	-	-
	Y79AA1001426	271.77	221.23	225.78	200.19	221.07	217.77	202.63	211.55	197.64	*	-	-
	Y79AA1001427	15.18	10.97	10.9	6.77	10.81	5.39	6.71	6.07	6.74	*	-	-
	Y79AA1001430	22.25	17.58	19.52	10.25	13.63	7.85	11.32	11.76	10.84	*	-	-
30	Y79AA1001439	6.75	4.58	4.31	2.6	4.23	1.25	2.94	2.35	2.98	*	-	-
	Y79AA1001485	17.57	9.99	14.92	13.26	10.56	8.25	5.32	10.37	14.36	*	-	-
	Y79AA1001493	20.47	12.23	13.25	9.02	11.27	6.64	13.37	13.83	16.06	*	-	-
	Y79AA1001511	14.52	8.05	9.32	8.33	6.58	5.02	5.2	6	5.96	*	-	-
	Y79AA1001523	10.03	6.72	7.33	6.48	4.81	3.84	4.54	3.21	2.59	*	-	-
	Y79AA1001530	11.44	7.57	8.59	6.64	6.84	5.29	6.2	7.76	5.77	*	-	-
	Y79AA1001532	13.55	14.73	11.04	5.35	5.16	4.93	5.08	4.52	6.49	**	-	-
35	Y79AA1001533	56.5	68.51	50.9	29.97	36.82	26.92	69.28	61.19	56.58	*	-	-
	Y79AA1001541	8.12	8.52	5.25	4.02	4.89	2.24	4.69	2.24	2.18	*	-	-
	Y79AA1001548	67.38	47.55	44.48	30.61	26.42	21.92	46.07	51.22	51.86	*	-	-
	Y79AA1001555	14.35	9.75	8.13	8.86	4.86	4.97	8.19	7.68	10.98	*	-	-
	Y79AA1001562	18.44	13.73	12.82	8.99	10.6	7.19	10.2	9.39	15.75	*	-	-
	Y79AA1001581	24.34	18.91	17.62	9.8	12.04	10.4	15.9	9.96	16.33	*	-	-
40	Y79AA1001585	30.32	20.83	22.83	20.22	25.12	15.45	0.69	15.13	0.14	*	-	-
	Y79AA1001592	28.53	25.65	26.36	29.33	16.66	7.28	20.69	8.44	14.72	*	-	-
	Y79AA1001594	23.28	21.85	24.28	14.25	15.59	10.11	22.55	14.53	20.27	**	-	-
	Y79AA1001603	12.47	11.04	10.84	6.8	11.48	6.78	22.63	14.33	27.5	*	-	-
	Y79AA1001613	25.09	18.27	18.81	23.47	16.84	13.34	20.3	16.35	18.99	*	-	-
	Y79AA1001630	22.94	13.91	12.22	13.14	13.53	8.02	11.73	12.98	17.67	*	-	-
45	Y79AA1001647	33.54	24.86	22.66	23.22	25.84	16.49	26.93	21.3	26.55	*	-	-
	Y79AA1001664	12.2	10.56	13.13	7.78	6.05	5.54	10.34	8.1	11.69	**	-	-
	Y79AA1001665	11.52	9	9.75	6.87	7.31	6.13	5.92	6.12	7.69	*	-	-
	Y79AA1001679	24.51	18.98	17.88	11.13	12.84	10.27	24.02	13.28	18.8	*	-	-
	Y79AA1001692	7.23	6.72	8.1	2.24	2.83	2.63	3.64	2.31	3.06	**	-	-
	Y79AA1001696	14.23	12.31	9.21	5.29	8.48	4.61	14.27	13.28	13.01	*	-	-
50	Y79AA1001705	12.04	11.4	8.55	9.76	11.8	6.21	4.61	5.98	4.57	**	-	-
	Y79AA1001711	13.72	7.72	10.63	6.49	4.11	3.08	6.08	4.06	7.4	*	-	-
	Y79AA1001717	4.71	1.55	3.26	3.34	1.71	0.7	1.49	1.53	1.39	*	-	-
	Y79AA1001719	22.12	12.72	16.33	9.89	12.72	6.53	12.21	11.1	11.76	*	-	-
	Y79AA1001727	38.96	27.16	22.35	13.65	17.35	9.31	38.01	28.39	34.23	*	-	-
55	Y79AA1001750	21.5	17.52	18.42	10.15	15.4	8.01	11.94	9.9	11.41	*	-	-
	Y79AA1001760	127.24	115.03	77.78	58.26	73.6	43.62	140.25	100.84	138.73	*	-	-
	Y79AA1001777	6.77	6.32	6.37	2.57	5.24	2.46	5.26	4.15	4.71	*	-	-
	Y79AA1001781	2.86	2.24	2.15	1.61	1.86	2.55	0.74	1.53	1.3	*	-	-

Table 508

	Y79AA1001787	5.04	3.62	6.16	2.83	4.49	3.23	3.33	2.97	2.01			
	Y79AA1001793	120.15	97.84	90.95	70.69	103.02	70.38	56.01	50.79	40.18	**	-	
	Y79AA1001795	5.66	5.4	6.21	4.2	5.9	3.1	3.91	2.49	2.28			
5	Y79AA1001799	15.09	14.95	16.22	8.14	9.02	8.13	5.96	8.67	5.96	**	-	
	Y79AA1001800	25.64	16.41	26.8	14.68	31.06	13.67	17.04	13.04	14.7			
	Y79AA1001801	18.54	13.81	14.73	8.69	14.72	7.61	10.02	6.35	8.81	*	-	
	Y79AA1001803	4.48	5.85	6.44	4.5	2.73	1.98	4.84	2.96	2.69			
	Y79AA1001805	40.28	26.89	34.51	17.56	11.83	10.76	12.11	14.87	11.59	**	-	
	Y79AA1001807	42.38	40.49	41.45	39.87	44.56	37.42	30.19	22.76	22.12	**	-	
10	Y79AA1001827	9.32	11.28	9.81	8.01	8.55	6.68	5.41	8.86	5.83	*	*	
	Y79AA1001846	22.14	19.33	18.59	11.82	17.37	13.61	12.56	15.77	9.7	*	*	
	Y79AA1001848	8.04	9.99	9.11	5.33	6.98	5.01	6.65	6.63	5.92	*	*	
	Y79AA1001853	10.87	10.1	9.06	5.77	8.29	4.56	4.63	5.75	4.91	*	*	
	Y79AA1001863	24.97	27.27	22.17	17.04	22	11.97	13.95	21.02	18.07	*	*	
15	Y79AA1001866	13.46	10.72	11.93	6.28	4.52	4.93	6.56	4.65	4.51	**	-	
	Y79AA1001874	2.1	1.41	2.93	0.78	1.08	0.95	1.46	1.22	1.08	*	*	
	Y79AA1001875	31.78	22.74	37.59	12.11	19.59	16.03	9.16	15	14.61	*	*	
	Y79AA1001907	517.52	778.32	567.93	750.86	875.67	821.68	479.34	605.65	529.63			
	Y79AA1001908	5.27	6.69	9.96	3.58	5.35	3.25	2.93	3.09	1.48	*	-	
	Y79AA1001923	8.48	15.75	14.8	9.28	7.65	3.64	5.48	6.75	5.36	*	-	
	Y79AA1001927	18.05	21.6	19.1	12.29	16.25	12.12	14.45	14.01	14.79	*	*	
	Y79AA1001930	12.23	24.48	15.86	10.91	18.16	6.72	4.54	5.11	5.37	*	-	
	Y79AA1001932	61.74	56.58	52.19	37.44	49.06	33.54	58.52	51.29	51.59	*	-	
	Y79AA1001933	9.52	6.51	10.88	6.04	6.05	6.44	4.27	11.51	4.91	*	-	
	Y79AA1001942	10.76	6.66	7.93	7.97	5.94	4.4	3.29	2.7	3.99	*	-	
25	Y79AA1001963	138.12	106.9	117.87	95.52	130.54	91.9	83.12	67.08	69.04	*	-	
	Y79AA1001968	147.27	91.21	62.32	82.32	49.63	76.26	20.14	2.41	10.4	*	-	
	Y79AA1001983	12.1	16.25	14.99	5.06	8.59	7.83	3.08	3.73	3.02	*	*	
	Y79AA1002000	8.87	9.86	16.46	6.28	9.55	3.45	4.66	4.84	4.51	*	-	
	Y79AA1002004	46.17	58.65	37.42	34.61	47	15.44	17.13	16.13	8.67	**	-	
	Y79AA1002008	16.52	21.1	20.83	11.85	16.14	12.02	7.95	15.74	18.89	*	-	
	Y79AA1002012	13.85	12.54	10.41	5.85	6.84	6.65	8.76	11.21	9.52	**	-	
30	Y79AA1002017	15.21	10.94	15.42	6.73	12.23	8.22	1.29	15.64	2.06			
	Y79AA1002022	42.57	32.77	37.11	21.13	22.85	16.91	21.09	21.59	19.22	**	-	
	Y79AA1002027	10.35	8.04	15.25	2.11	4.6	4.84	5.16	2.67	4.2	*	*	
	Y79AA1002050	13.21	11.11	14.39	7.26	8.9	5.9	6.9	7.16	7.33	**	-	
	Y79AA1002058	167.29	130.21	156.91	193.04	186.39	149.35	127.37	93.56	137.15			
	Y79AA1002060	54.35	76.53	61.68	36.08	41.21	29.16	24.43	9.99	5.28	*	-	
35	Y79AA1002062	49.46	32.53	50.05	16.65	20.72	17.6	35.11	28.1	35.48	*	-	
	Y79AA1002065	113.45	69.34	64.62	65.01	102.96	72.96	82.29	90.04	44.91	*	-	
	Y79AA1002067	33.46	37.19	43.9	21.85	20.1	22.68	15.4	10.55	10.37	**	-	
	Y79AA1002069	5.33	3.94	7.12	3.04	1.49	2.47	3.1	3.24	2.29	*	-	
	Y79AA1002070	67.39	142.78	83.33	77.38	149.87	86.41	153.3	88.92	78.17			
40	Y79AA1002074	1225	1102	498.16	721.59	1162.7	771.32	764.45	491.49	312.45			
	Y79AA1002076	8.24	11.39	15.58	4.01	6.13	3.99	13	9.01	11.16	*	-	
	Y79AA1002083	11.94	6.94	9.48	4.49	4.53	3.15	4.48	1.37	1.78	*	*	
	Y79AA1002084	20.05	13.84	17.88	7.41	8.38	6.24	10.42	8.8	8.13	**	-	
	Y79AA1002086	15.57	8.01	9.58	4.16	3.65	3.41	3.6	4.3	3.59	*	*	
	Y79AA1002087	265.36	258.38	345.6	296.44	355.85	246.9	347.62	322.78	317.34			
45	Y79AA1002089	15.8	12.04	15.08	6.67	9.17	6.14	12.29	9.32	9.91	**	-	
	Y79AA1002093	13.66	12.64	9.33	5.35	6.21	4.47	3.01	2.8	2.77	**	-	
	Y79AA1002101	6.58	7.04	8.08	3.07	2.77	1.96	3.3	4.71	1.21	**	-	
	Y79AA1002103	11.98	11.79	10.9	4.11	5.96	4.92	4.54	2.99	2.4	**	-	
	Y79AA1002115	15.51	18.46	14.58	9.3	11.82	8.45	4.13	9.04	5.86	*	*	
	Y79AA1002121	6.93	5.28	6.92	6.7	3.27	4.36	3.68	3.01	3.29	**	-	
	Y79AA1002125	40.85	21.04	26.11	14.22	18.4	17.66	12.21	8.56	11.75	*	-	
50	Y79AA1002129	7.76	7.25	11.87	4.36	3.94	3.2	3.76	3.8	4.37	*	*	
	Y79AA1002131	5.89	3.57	4.85	1.58	2.79	2.27	3.32	1.61	2.75	*	-	
	Y79AA1002139	8.48	7.22	6.23	4.06	4.42	2.47	3.44	3.86	2.67	*	-	
	Y79AA1002144	53.23	47.33	47.13	32.96	42.65	28.86	30.69	36.28	25.23	*	-	
	Y79AA1002177	14.09	13.17	13.65	5.87	6.08	5.05	5.82	4.1	4.38	**	-	
	Y79AA1002183	76.21	99.47	69.64	24.87	40.12	25.67	26.7	15.32	11.31	**	-	
55	Y79AA1002202	29.69	18.4	18.04	8.22	10.65	9.82	13.41	13.22	16.71	*	-	
	Y79AA1002204	4.17	2.23	3.23	5.04	1.05	2.68	3.28	2.4	2.69	*	-	

Table 509

	Y79AA1002206	7.86	6.79	4.86	2.41	3.6	5.74	5.49	1.51	2.8			
	Y79AA1002208	21.91	17.64	15.14	5.6	4.07	5.57	6.81	5.17	2.55	**	**	-
5	Y79AA1002209	14.82	11.28	11.86	6.23	4.7	2.82	4.71	1.33	3.18	**	**	-
	Y79AA1002210	13.64	7.39	7.59	9.08	4.62	5.18	20.5	2.05	6.37			
	Y79AA1002211	11.76	19.59	13.47	10.43	6.65	6.52	12.32	8.42	11.25			
	Y79AA1002213	40.78	31.99	22.96	18.41	26.57	14.98	45.88	32.4	41.97			
	Y79AA1002215	54.92	41.69	39.55	24.88	24.36	11.26	37.49	23.6	35.98	*		-
10	Y79AA1002220	17.03	11.5	20.58	7.13	5.68	5.31	4.57	4.8	6.51	*	*	-
	Y79AA1002226	48.55	31.27	31.34	7.35	12.72	13.65	9.19	6.65	11.13	*	*	-
	Y79AA1002229	7.88	6.84	5.37	6.02	4.67	2.85	3.67	2.52	3.73	*	*	-
	Y79AA1002234	20.83	13.27	12.39	9.34	6.36	3.6	6.9	3.36	5.84	*	*	-
	Y79AA1002235	28.03	23.84	21.24	15.07	14.87	9.39	10.75	8.42	13.64	*	**	-
	Y79AA1002246	9.72	14.9	10.35	5.25	6.99	4.12	8.31	3.82	6.69	*	*	-
15	Y79AA1002258	12.35	12.02	7.88	7.82	11.57	8.55	9.77	4.5	4.81			
	Y79AA1002279	51.52	49.19	41.11	5.28	2.78	2.07	15.99	20.03	22.13	**	**	-
	Y79AA1002292	13.64	7.58	4.14	5.73	4.43	2.94	6.45	6.01	8.36			
	Y79AA1002298	9.43	8.29	4.77	3.29	5.48	4.2	4.42	4.85	3.79			
20	Y79AA1002307	9.31	8.07	6.62	3.9	4.4	2.44	5.17	1.76	2.58	*	*	-
	Y79AA1002309	8.88	7.96	8.79	3.32	4.26	2.83	4.23	2.88	3.97	**	**	-
	Y79AA1002311	16.51	9.27	11.76	6.9	6.2	3.45	7.45	3.09	6.4	*	*	-
	Y79AA1002334	13.05	8.36	7.7	5.13	4.89	3.36	5.91	4.32	5.92	*	*	-
	Y79AA1002351	13.61	12.49	9.42	7.1	4.15	6.19	7.95	4.93	5.8	*	*	-
	Y79AA1002355	31.74	30.6	21.85	12.21	15.81	9.74	20.54	18.29	18.48	*	*	-
25	Y79AA1002361	23.42	15.4	18.02	12.53	10.73	6.85	25.86	17.1	25.5	*	*	-
	Y79AA1002365	12.42	6.37	7.19	3.15	4.11	3.03	4.29	4.74	4.01			
	Y79AA1002373	8.95	6.89	5.46	5.13	4.81	3.4	9.6	4.57	7.84			
	Y79AA1002376	1550.5	2569.2	1680.8	462.62	827.86	616.71	1477.6	1040.3	1062.1	*	*	-
	Y79AA1002378	20.24	17.32	13.54	5.14	9.41	4.23	19.28	11.07	16.88			
30	Y79AA1002381	116.11	128.86	74.48	110.66	141.78	92.68	155.95	123.08	170.94			
	Y79AA1002388	33.4	33.3	27.31	13.85	26.75	11.62	21.29	16.32	21.24	*	*	-
	Y79AA1002399	11.13	8.22	7.72	4.28	5.54	4.87	7.56	5.9	6.25	*	*	-
	Y79AA1002407	12.66	14.43	18.13	7.72	14.18	6.84	5.83	9.78	4.59	*	*	-
	Y79AA1002413	16.98	12.77	14.95	6.14	9.13	4.62	8.44	10.73	7.99	*	*	-
35	Y79AA1002416	7.52	8.19	8.76	5.47	10.72	5.8	8.2	6.05	6.56			
	Y79AA1002429	17.73	18.61	8.81	5.82	10.24	4.73	3.65	6.89	5.66	*	*	-
	Y79AA1002431	3.38	3.05	6.2	3.01	5.89	1.6	2.81	2.79	1.69			
	Y79AA1002433	9.94	11.67	9.29	5.11	5.57	3.18	3.49	4.6	3.87	**	**	-
	Y79AA1002445	33.47	25.62	23.49	15.99	10.67	7.02	18.92	25.26	13.87	*	*	-
	Y79AA1002461	7.94	6.22	7.84	3.36	7.35	4.7	3.49	2.25	3.85	**	**	-
	Y79AA1002466	778.44	339.4	681.02	542.58	499.15	369	592.67	971	768.71			
40	Y79AA1002471	11.38	8.13	15.35	12.81	13.4	11.43	4.94	6.06	4.47	*	*	-
	Y79AA1002472	31.22	33.06	31.17	18.15	21.85	9.34	16.29	20.14	20.03	*	**	-
	Y79AA1002474	10.68	12.29	10.71	6.77	7.3	7.75	3.17	7.37	4.86	**	*	-
	Y79AA1002482	30.09	33.68	36.63	19.02	23.45	17.38	21.9	25.81	23.08	**	*	-
	Y79AA1002487	8.33	8.29	7.43	7.28	8.45	6.44	5.34	3.78	3.66	**	**	-
45	Y79AA1002490	143.18	106.89	117.63	56.22	71.49	57.31	59.76	51.39	52.37	**	**	-
	Y79AA1002493	44.75	41.56	40.36	20.64	28.52	19.33	38.02	46.19	46.7	**	**	-
	ZRY6C1006278	5.26	7	5.52	3.16	2.97	2.19	2.99	2.6	2.72	**	**	-

## EXAMPLE 16

Selection of novel cDNA clones from cDNA libraries prepared by oligo-capping method

[0246] The following 54 clones were newly selected from cDNA libraries prepared by oligo-capping method, based on the criterion that the 5'-end sequence of a cDNA clone contained a coding region which was initiated with ATG codon and which encoded 50 amino acids or more:

HEMBA1000497, HEMBA1001750, HEMBA1003854, HEMBA1004193, HEMBA1004860, HEMBA1005572, HEMBA1006038, HEMBA1006092, HEMBA1006406, HEMBA1006850, HEMBA1006812, HEMBB1000672, HEMBB1001197, HEMBB1001871, MAMMA1001252, MAMMA1002094, NT2RM4000634, NT2RM4000657,

NT2RM4000783, NT2RM4000857, NT2RM4001178, NT2RM4002420, NT2RP2000198, NT2RP2000551,  
 NT2RP2000660,  
 NT2RP2001214, NT2RP2001460, NT2RP2001756, NT2RP2002056, NT2RP2002677, NT2RP2002755,  
 NT2RP2002843, NT2RP2003101, NT2RP2003799, NT2RP2004095, NT2RP2004732, NT2RP2004920,  
 5 NT2RP2005454, NT2RP2005776, NT2RP2005806, NT2RP2005882, NT2RP3001282, NT2RP3001723,  
 NT2RP3002099, NT2RP3003155, NT2RP3004028, OVARC1000008, OVARC1000724, OVARC1000751,  
 OVARC1001029, PLACE1000814, PLACE1003030, PLACE1005549, PLACE1007218.

Among them, the following 23 clones were predicted to contain a coding region encoding 100 amino acids or more:  
 HEMBA1000497, HEMBA1003854, HEMBA1004193, HEMBA1006812, HEMBB1001871, NT2RM4000657,  
 10 NT2RM4001178, NT2RP2001756, NT2RP2002677, NT2RP2002755, NT2RP2002843, NT2RP2004095,  
 NT2RP2004920, NT2RP2005806, NT2RP3001282, NT2RP3002099, NT2RP3003155, OVARC1000724,  
 OVARC1001029, PLACE1000814, PLACE1003030, PLACE1005549, PLACE1007218. This indicates that the clones  
 encode proteins.

**[0247]** Table 510 shows maximal ATGprl value determined for each clone. Since the respective maximal ATGprl  
 15 values for HEMBA1006812, HEMBB1001871 and NT2RRP3001282 are higher than 0.3, the clones would be full-  
 length. Other clones indicated below have maximal ATGprl values of 0.3 or less, and this means that the fullness ratios  
 of the clones are low.

However, the sequences can still be full-length: HEMBA1000497, HEMBA1001750, HEMBA1003854,  
 HEMBA1004193, HEMBA1004860, HEMBA1005572, HEMBA1006038, HEMBA1006092, HEMBA1006406,  
 20 HEMBA1006650, HEMBB1000672, HEMBB1001197, MAMMA1001252, MAMMA1002094, NT2RM4000634,  
 NT2RM4000657, NT2RM4000783, NT2RM4000857, NT2RM4001178, NT2RM4002420, NT2RP2000198,  
 NT2RP2000551, NT2RP2000660, NT2RP2001214, NT2RP2001460, NT2RP2001756, NT2RP2002056,  
 NT2RP2002677, NT2RP2002755, NT2RP2002843, NT2RP2003101, NT2RP2003799, NT2RP2004095,  
 NT2RP2004732, NT2RP2004920, NT2RP2005454, NT2RP2005776, NT2RP2005806, NT2RP2005882,  
 25 NT2RP3001723, NT2RP3002099, NT2RP3003155, NT2RP3004028, OVARC1000008, OVARC1000724,  
 OVARC1000751, OVARC1001029, PLACE1000814, PLACE1003030, PLACE1005549, PLACE1007218

**[0248]** Table 511 (same as Table 2) shows SEQ ID NOs of the nucleotide sequences located at the 5'-end and 3'-  
 end of each of the 54 clones and the corresponding plasmid clone, which was obtained herein, containing a polynucleotide  
 30 as an insert. SEQ ID NO for a 5'-end sequence is indicated on the right side of the corresponding Sequence  
 name of 5'-end sequence, and SEQ ID NO for a 3'-end sequence is indicated on the right side of the corresponding  
 Sequence name of 3'-end sequence.

**[0249]** Swiss-Prot was searched for data homologous to the 5'-end sequences of the selected 54 clones, and Gen-  
 Bank and UniGene were searched for data homologous to the 5'-end and 3'-end sequences of the same clones. The  
 search results are indicated as Homology search results 1-7 in the last part of this SPECIFICATION.

**[0250]** Based on the matching data obtained by the search, 7 clones presumably encode proteins belonging to any  
 of the categories of secretory or membrane proteins, glycoproteins, signal transduction-associated proteins, transcrip-  
 35 tion-associated proteins, disease-associated proteins, and protein synthesis- and/or protein transport-associated pro-  
 teins. These were clones exhibiting relatively low homology to any of known proteins belonging to said categories.  
 Here, the term "relatively low homology" means that a nucleotide sequence does not satisfy the conditions under which  
 40 the nucleotide sequence exhibits "relatively high homology" (which means that, when the nucleotide sequence is com-  
 pared with the known sequences in Swiss-Prot database, the sequence identity is 60% or higher and the P value is  
 10<sup>-10</sup> or less) and that, when the nucleotide sequence is compared with the known sequences in Swiss-Prot database,  
 the sequence to be compared contains 55 nucleotides or more, the sequence identity is 25% or higher, and the P value  
 is 10<sup>-6</sup> or less.

**[0251]** Among the 7 clones, clones presumably encoding proteins belonging to the category of secretory or mem-  
 45 brane proteins are the two clones, HEMBB1001871 and NT2RM4000857 (which also belong to other categories);  
 clones presumably encoding proteins belonging to the category of glycoproteins are the two clones, HEMBB1001871  
 and NT2RM4000857 (which also belong to other categories); a clone presumably encoding a protein belonging to the  
 category of signal transduction-associated proteins is PLACE1005549; clones presumably encoding proteins belonging  
 50 to the category of transcription-associated proteins are the three clones, HEMBA1005572, NT2RP2001756, and  
 NT2RP2005776; a clone presumably encoding a protein belonging to the category of disease-associated proteins is  
 NT2RM4000857 (which also belong to other categories); a clone presumably encoding a protein belonging to the  
 category of protein synthesis- and/or protein transport-associated proteins is HEMBA1001750 (see Examples 12).

Table 510  
The maximal ATGpr1 value of each clone selected in Example 16

clone name	name of sequence	maximal ATGpr1 score
HEMBA1000497	F-HEMBA1000497	0.25
HEMBA1001750	F-HEMBA1001750	0.08
HEMBA1003854	F-HEMBA1003854	0.23
HEMBA1004193	F-HEMBA1004193	0.22
HEMBA1004860	F-HEMBA1004860	0.29
HEMBA1005572	F-HEMBA1005572	0.24
HEMBA1006038	F-HEMBA1006038	0.29
HEMBA1006092	F-HEMBA1006092	0.28
HEMBA1006406	F-HEMBA1006406	0.26
HEMBA1006650	F-HEMBA1006650	0.22
HEMBA1006812	F-HEMBA1006812	0.71
HEMBA100672	F-HEMBA100672	0.24
HEMBA1001197	F-HEMBA1001197	0.22
HEMBA1001871	F-HEMBA1001871	0.94
MAMMA1001252	F-MAMMA1001252	0.29
MAMMA1002094	F-MAMMA1002094	0.28
NT2RM4000634	F-NT2RM4000634	0.07
NT2RM4000657	F-NT2RM4000657	0.24
NT2RM4000783	F-NT2RM4000783	0.22
NT2RM4000857	F-NT2RM4000857	0.12
NT2RM4001178	F-NT2RM4001178	0.27
NT2RM4002420	F-NT2RM4002420	0.06
NT2RP2000198	F-NT2RP2000198	0.15
NT2RP2000551	F-NT2RP2000551	0.07
NT2RP2000660	F-NT2RP2000660	0.22
NT2RP2001214	F-NT2RP2001214	0.26
NT2RP2001460	F-NT2RP2001460	0.07
NT2RP2001756	F-NT2RP2001756	0.17



	NT2RP2002056	F-NT2RP2002056	0. 12
	NT2RP2002677	F-NT2RP2002677	0. 14
5	NT2RP2002755	F-NT2RP2002755	0. 12
	NT2RP2002843	F-NT2RP2002843	0. 11
	NT2RP2003101	F-NT2RP2003101	0. 13
	NT2RP2003799	F-NT2RP2003799	0. 24
10	NT2RP2004095	F-NT2RP2004095	0. 16
	NT2RP2004732	F-NT2RP2004732	0. 18
	NT2RP2004920	F-NT2RP2004920	0. 15
	NT2RP2005454	F-NT2RP2005454	0. 09
15	NT2RP2005776	F-NT2RP2005776	0. 19
	NT2RP2005806	F-NT2RP2005806	0. 27
	NT2RP2005882	F-NT2RP2005882	0. 11
	NT2RP3001282	F-NT2RP3001282	0. 39
20	NT2RP3001723	F-NT2RP3001723	0. 22
	NT2RP3002099	F-NT2RP3002099	0. 20
	NT2RP3003155	F-NT2RP3003155	0. 29
25	NT2RP3004028	F-NT2RP3004028	0. 13
	OVARC1000008	F-OVARC1000008	0. 23
	OVARC1000724	F-OVARC1000724	0. 27
	OVARC1000751	F-OVARC1000751	0. 28
30	OVARC1001029	F-OVARC1001029	0. 25
	PLACE1000814	F-PLACE1000814	0. 21
	PLACE1003030	F-PLACE1003030	0. 26
	PLACE1005549	F-PLACE1005549	0. 16
35	PLACE1007218	F-PLACE1007218	0. 30

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Table 511

clone name	name of the 5'-end sequence	SEQ ID NO of the 5'-end sequence	name of the 3'-end sequence	SEQ ID NO of the 3'-end sequence
HEMBA1000497	F-HEMBA1000497	16111	R-HEMBA1000497	16165
HEMBA1001750	F-HEMBA1001750	16112	R-HEMBA1001750	16166
HEMBA1003854	F-HEMBA1003854	16113	R-HEMBA1003854	16167
HEMBA1004193	F-HEMBA1004193	16114	R-HEMBA1004193	16168
HEMBA1004860	F-HEMBA1004860	16115	R-HEMBA1004860	16169
HEMBA1005572	F-HEMBA1005572	16116	R-HEMBA1005572	16170
HEMBA1006038	F-HEMBA1006038	16117	R-HEMBA1006038	16171
HEMBA1006092	F-HEMBA1006092	16118	R-HEMBA1006092	16172
HEMBA1006406	F-HEMBA1006406	16119	R-HEMBA1006406	16173
HEMBA1006650	F-HEMBA1006650	16120	R-HEMBA1006650	16174
HEMBA1006812	F-HEMBA1006812	16121	R-HEMBA1006812	16175

	HEMBB1000672	F-HEMBB1000672	16122	R-HEMBB1000672	16176
	HEMBB1001197	F-HEMBB1001197	16123	R-HEMBB1001197	16177
	HEMBB1001871	F-HEMBB1001871	16124	R-HEMBB1001871	16178
5	MAMMA1001252	F-MAMMA1001252	16125	R-MAMMA1001252	16179
	MAMMA1002094	F-MAMMA1002094	16126	R-MAMMA1002094	16180
	NT2RM4000634	F-NT2RM4000634	16127	R-NT2RM4000634	16181
	NT2RM4000657	F-NT2RM4000657	16128	R-NT2RM4000657	16182
10	NT2RM4000783	F-NT2RM4000783	16129	R-NT2RM4000783	16183
	NT2RM4000857	F-NT2RM4000857	16130	R-NT2RM4000857	16184
	NT2RM4001178	F-NT2RM4001178	16131	R-NT2RM4001178	16185
	NT2RM4002420	F-NT2RM4002420	16132	R-NT2RM4002420	16186
15	NT2RP2000198	F-NT2RP2000198	16133	R-NT2RP2000198	16187
	NT2RP2000551	F-NT2RP2000551	16134	R-NT2RP2000551	16188
	NT2RP2000660	F-NT2RP2000660	16135	R-NT2RP2000660	16189
20	NT2RP2001214	F-NT2RP2001214	16136	R-NT2RP2001214	16190
	NT2RP2001460	F-NT2RP2001460	16137	R-NT2RP2001460	16191
	NT2RP2001756	F-NT2RP2001756	16138	R-NT2RP2001756	16192
	NT2RP2002056	F-NT2RP2002056	16139	R-NT2RP2002056	16193
25	NT2RP2002677	F-NT2RP2002677	16140	R-NT2RP2002677	16194
	NT2RP2002755	F-NT2RP2002755	16141	R-NT2RP2002755	16195
	NT2RP2002843	F-NT2RP2002843	16142	R-NT2RP2002843	16196
	NT2RP2003101	F-NT2RP2003101	16143	R-NT2RP2003101	16197
30	NT2RP2003799	F-NT2RP2003799	16144	R-NT2RP2003799	16198
	NT2RP2004095	F-NT2RP2004095	16145	R-NT2RP2004095	16199
	NT2RP2004732	F-NT2RP2004732	16146	R-NT2RP2004732	16200
	NT2RP2004920	F-NT2RP2004920	16147	R-NT2RP2004920	16201
35	NT2RP2005454	F-NT2RP2005454	16148	R-NT2RP2005454	16202
	NT2RP2005776	F-NT2RP2005776	16149	R-NT2RP2005776	16203
	NT2RP2005806	F-NT2RP2005806	16150	R-NT2RP2005806	16204
	NT2RP2005882	F-NT2RP2005882	16151	R-NT2RP2005882	16205
40	NT2RP3001282	F-NT2RP3001282	16152	R-NT2RP3001282	16206
	NT2RP3001723	F-NT2RP3001723	16153	R-NT2RP3001723	16207
	NT2RP3002099	F-NT2RP3002099	16154	R-NT2RP3002099	16208
	NT2RP3003155	F-NT2RP3003155	16155	R-NT2RP3003155	16209
45	NT2RP3004028	F-NT2RP3004028	16156	R-NT2RP3004028	16210
	OVARC1000008	F-OVARC1000008	16157	R-OVARC1000008	16211
	OVARC1000724	F-OVARC1000724	16158	R-OVARC1000724	16212
	OVARC1000751	F-OVARC1000751	16159	R-OVARC1000751	16213
50	OVARC1001029	F-OVARC1001029	16160	R-OVARC1001029	16214
	PLACE1000814	F-PLACE1000814	16161	R-PLACE1000814	16215
	PLACE1003030	F-PLACE1003030	16162	R-PLACE1003030	16216
	PLACE1005549	F-PLACE1005549	16163	R-PLACE1005549	16217
55	PLACE1007218	F-PLACE1007218	16164	R-PLACE1007218	16218

**EXAMPLE 17**

Search for a signal sequence, transmembrane region and functional domain in deduced amino acid sequences

**[0252]** The deduced amino acid sequences from the full-length nucleotide sequences were examined to predict the presence of a signal sequence in their amino-termini as well as the presence of a transmembrane region. The amino acid sequences were also searched for a protein functional domain (motif). The examinations for a signal sequence in the amino-terminus, for a transmembrane region and for a functional domain were performed by using PSORT [K. Nakai & M. Kanehisa, Genomics, 14:897-911 (1992)], SOSUI [T. Hirokawa et al., Bioinformatics, 14:378-379 (1998)] (Mitsui Knowledge Industry Co., Ltd.) and Pfam (<http://www.sanger.ac.uk/Software/Pfam/index.shtml>), respectively. When the presence of a signal sequence or a transmembrane region in the amino-terminus was predicted in the amino acid sequence by PSORT or SOSUI, the protein was predicted to be a secretory protein or a membrane protein. When the amino acid sequence matched a functional domain in the Pfam search for a functional domain, the function of the protein is predictable based on the matching data, for example, by referring to the functional categories in PROSITE (<http://www.expasy.ch/cgi-bin/prosite-list.pl>). The functional domain search can be performed by using PROSITE instead of Pfam.

**[0253]** Search results obtained by using the respective software programs are indicated below.

**[0254]** Clones whose deduced amino acid sequences were predicted to have signal sequences by PSORT search are as follows:

20	HEMBA1001052,	HEMBA1001407,	HEMBA1002486,	HEMBA1002661,	HEMBA1002818,	HEMBA1002876,
	HEMBA1003086,	HEMBA1003711,	HEMBA1004752,	HEMBA1005991,	HEMBA1006067,	HEMBA1006173,
	HEMBA1006198,	HEMBA1006789,	HEMBA1006921,	HEMBA1000054,	HEMBA1000175,	HEMBA1002692,
	MAMMA1000798,	MAMMA1002427,	MAMMA1002881,	MAMMA1003035,	NT2RM1000035,	NT2RM1000742,
	NT2RM1000811,	NT2RM1000905,	NT2RM1001008,	NT2RM2000287,	NT2RM2000609,	NT2RM2001613,
25	NT2RM4000634,	NT2RM4000778,	NT2RM4002339,	NT2RM4002460,	NT2RP1000782,	NT2RP1000856,
	NT2RP1001247,	NT2RP1001546,	NT2RP1001569,	NT2RP2001597,	NT2RP2002537,	NT2RP2004142,
	NT2RP2005752,	NT2RP2005812,	NT2RP3001084,	NT2RP3001589,	NT2RP3002163,	NT2RP3002650,
	NT2RP3003145,	NT2RP3003242,	NT2RP3003621,	NT2RP3004282,	NT2RP3004503,	NT2RP4000051,
	NT2RP4000151,	NT2RP4000243,	NT2RP4000259,	NT2RP4000323,	NT2RP4000417,	NT2RP4001064,
30	NT2RP4001117,	NT2RP4001730,	NT2RP4001739,	NT2RP4002075,	NT2RP5003500,	OVARC1001154,
	PLACE1000611,	PLACE1003030,	PLACE1003044,	PLACE1003369,	PLACE1003596,	PLACE1004258,
	PLACE1005086,	PLACE1006239,	PLACE1006754,	PLACE1006829,	PLACE1007954,	PLACE1008424,
	PLACE1008533,	PLACE1008693,	PLACE1010622,	PLACE1010942,	PLACE2000176,	PLACE2000341,
	PLACE2000379,	PLACE2000427,	PLACE2000477,	PLACE4000431,	PLACE4000593,	THYRC1000156,
35	THYRC1001134,	THYRC1001287,	Y79AA1000258,	Y79AA1001874,	Y79AA1002399,	HEMBA1001871,
	HEMBA1001925,	MAMMA1000778,	MAMMA1000897,	MAMMA1001080,	NT2RP2004300,	NT2RP3002985,
	NT2RP3003059,	OVARC1000689,	OVARC1000890,	PLACE1005162,	PLACE3000399,	PLACE3000455,
	PLACE4000247,	PLACE4000259,	PLACE4000494			

**[0255]** Clones whose deduced amino acid sequences were predicted to have transmembrane regions by SOSUI search are as follows:

40	HEMBA1000005,	HEMBA1000356,	HEMBA1000518,	HEMBA1000531,	HEMBA1000637,	HEMBA1000719,
	HEMBA1000817,	HEMBA1000822,	HEMBA1000870,	HEMBA1000991,	HEMBA1001052,	HEMBA1001085,
	HEMBA1001286,	HEMBA1001351,	HEMBA1001407,	HEMBA1001446,	HEMBA1001510,	HEMBA1001515,
	HEMBA1001557,	HEMBA1001746,	HEMBA1002092,	HEMBA1002125,	HEMBA1002150,	HEMBA1002166,
45	HEMBA1002462,	HEMBA1002477,	HEMBA1002486,	HEMBA1002609,	HEMBA1002659,	HEMBA1002661,
	HEMBA1002780,	HEMBA1002818,	HEMBA1002876,	HEMBA1002921,	HEMBA1003077,	HEMBA1003079,
	HEMBA1003086,	HEMBA1003096,	HEMBA1003281,	HEMBA1003286,	HEMBA1003711,	HEMBA1003742,
	HEMBA1003803,	HEMBA1004143,	HEMBA1004146,	HEMBA1004341,	HEMBA1004461,	HEMBA1004577,
	HEMBA1004637,	HEMBA1004752,	HEMBA1004756,	HEMBA1004850,	HEMBA1004889,	HEMBA1004923,
50	HEMBA1004930,	HEMBA1005029,	HEMBA1005035,	HEMBA1005050,	HEMBA1005552,	HEMBA1005598,
	HEMBA1005616,	HEMBA1005991,	HEMBA1006036,	HEMBA1006067,	HEMBA1006293,	HEMBA1006492,
	HEMBA1006502,	HEMBA1006659,	HEMBA1006758,	HEMBA1006789,	HEMBA1006921,	HEMBA1006926,
	HEMBA1007203,	HEMBA1000050,	HEMBA1000054,	HEMBA1000556,	HEMBA1000593,	HEMBA1000631,
	HEMBA1000763,	HEMBA1000827,	HEMBA1000915,	HEMBA1000975,	HEMBA1001112,	HEMBA1001177,
55	HEMBA1001302,	HEMBA1001348,	HEMBA1001962,	HEMBA1002142,	HEMBA1002190,	HEMBA1002247,
	HEMBA1002387,	HEMBA1002550,	HEMBA1002600,	HEMBA1002692,	MAMMA1000129,	MAMMA1000133,
	MAMMA1000277,	MAMMA1000278,	MAMMA1000410,	MAMMA1000416,	MAMMA1000472,	MAMMA1000714,
	MAMMA1000731,	MAMMA1000734,	MAMMA1000798,	MAMMA1000842,	MAMMA1000956,	MAMMA1001008,

	MAMMA1001030,	MAMMA1001139,	MAMMA1001154,	MAMMA1001388,	MAMMA1001411,	MAMMA1001487,
	MAMMA1001751,	MAMMA1001771,	MAMMA1002461,	MAMMA1002524,	MAMMA1002598,	MAMMA1002684,
	MAMMA1002769,	MAMMA1002890,	MAMMA1002938,	MAMMA1003146,	NT2RM1000035,	NT2RM1000037,
	NT2RM1000062,	NT2RM1000131,	NT2RM1000257,	NT2RM1000260,	NT2RM1000355,	NT2RM1000648,
5	NT2RM1000742,	NT2RM1000900,	NT2RM1000811,	NT2RM1000857,	NT2RM1000867,	NT2RM1000882,
	NT2RM1001008,	NT2RM1001115,	NT2RM1001139,	NT2RM2000259,	NT2RM2000395,	NT2RM2000402,
	NT2RM2000407,	NT2RM2000422,	NT2RM2000566,	NT2RM2000581,	NT2RM2000609,	NT2RM2001370,
	NT2RM2001393,	NT2RM2001499,	NT2RM2001613,	NT2RM2001648,	NT2RM2001659,	NT2RM2001671,
	NT2RM2001718,	NT2RM2001760,	NT2RM2001785,	NT2RM2001823,	NT2RM2001930,	NT2RM2001950,
10	NT2RM2001998,	NT2RM2002049,	NT2RM4000046,	NT2RM4000233,	NT2RM4000433,	NT2RM4000520,
	NT2RM4000634,	NT2RM4000674,	NT2RM4000700,	NT2RM4000764,	NT2RM4000795,	NT2RM4000820,
	NT2RM4000857,	NT2RM4001032,	NT2RM4001054,	NT2RM4001455,	NT2RM4001813,	NT2RM4001930,
	NT2RM4001987,	NT2RM4002054,	NT2RM4002073,	NT2RM4002145,	NT2RM4002146,	NT2RM4002194,
	NT2RM4002339,	NT2RM4002438,	NT2RM4002446,	NT2RM4002452,	NT2RM4002460,	NT2RM4002493,
15	NT2RM4002571,	NT2RP1000191,	NT2RP1000358,	NT2RP1000418,	NT2RP1000547,	NT2RP1000609,
	NT2RP1000767,	NT2RP1000767,	NT2RP1000782,	NT2RP1000856,	NT2RP1001113,	NT2RP1001247,
	NT2RP1001286,	NT2RP1001310,	NT2RP1001311,	NT2RP1001313,	NT2RP1001385,	NT2RP1001449,
	NT2RP1001546,	NT2RP1001569,	NT2RP2000032,	NT2RP2000040,	NT2RP2000070,	NT2RP2000091,
	NT2RP2000114,	NT2RP2000120,	NT2RP2000173,	NT2RP2000175,	NT2RP2000195,	NT2RP2000248,
20	NT2RP2000270,	NT2RP2000283,	NT2RP2000289,	NT2RP2000459,	NT2RP2000516,	NT2RP2000842,
	NT2RP2000892,	NT2RP2001081,	NT2RP2001268,	NT2RP2001295,	NT2RP2001366,	NT2RP2001576,
	NT2RP2001581,	NT2RP2001597,	NT2RP2001947,	NT2RP2001991,	NT2RP2002025,	NT2RP2002312,
	NT2RP2002385,	NT2RP2002479,	NT2RP2002537,	NT2RP2002643,	NT2RP2002701,	NT2RP2002740,
	NT2RP2002857,	NT2RP2003125,	NT2RP2003297,	NT2RP2003433,	NT2RP2003446,	NT2RP2003466,
25	NT2RP2003629,	NT2RP2003777,	NT2RP2003781,	NT2RP2004041,	NT2RP2004194,	NT2RP2004270,
	NT2RP2004861,	NT2RP2004775,	NT2RP2004799,	NT2RP2004936,	NT2RP2005012,	NT2RP2005159,
	NT2RP2005227,	NT2RP2005270,	NT2RP2005344,	NT2RP2005509,	NT2RP2005752,	NT2RP2005781,
	NT2RP2005784,	NT2RP2005812,	NT2RP2006069,	NT2RP2006100,	NT2RP2006141,	NT2RP2006281,
	NT2RP2006571,	NT2RP3000092,	NT2RP3000134,	NT2RP3000333,	NT2RP3000393,	NT2RP3000439,
30	NT2RP3000441,	NT2RP3000631,	NT2RP3000685,	NT2RP3000826,	NT2RP3000852,	NT2RP3001126,
	NT2RP3001176,	NT2RP3001260,	NT2RP3001355,	NT2RP3001383,	NT2RP3001426,	NT2RP3001453,
	NT2RP3001497,	NT2RP3001538,	NT2RP3001716,	NT2RP3001727,	NT2RP3001739,	NT2RP3001799,
	NT2RP3001943,	NT2RP3001944,	NT2RP3002002,	NT2RP3002014,	NT2RP3002054,	NT2RP3002108,
	NT2RP3002163,	NT2RP3002351,	NT2RP3002455,	NT2RP3002549,	NT2RP3002628,	NT2RP3002650,
35	NT2RP3002687,	NT2RP3002701,	NT2RP3002869,	NT2RP3002969,	NT2RP3003008,	NT2RP3003071,
	NT2RP3003101,	NT2RP3003145,	NT2RP3003302,	NT2RP3003353,	NT2RP3003409,	NT2RP3003716,
	NT2RP3003918,	NT2RP3004207,	NT2RP3004454,	NT2RP3004503,	NT2RP4000051,	NT2RP4000151,
	NT2RP4000243,	NT2RP4000259,	NT2RP4000323,	NT2RP4000500,	NT2RP4000560,	NT2RP4000588,
	NT2RP4000713,	NT2RP4000724,	NT2RP4000833,	NT2RP4000878,	NT2RP4000907,	NT2RP4000925,
40	NT2RP4000928,	NT2RP4000973,	NT2RP4000989,	NT2RP4001057,	NT2RP4001064,	NT2RP4001079,
	NT2RP4001117,	NT2RP4001138,	NT2RP4001150,	NT2RP4001174,	NT2RP4001274,	NT2RP4001345,
	NT2RP4001372,	NT2RP4001373,	NT2RP4001379,	NT2RP4001498,	NT2RP4001547,	NT2RP4001571,
	NT2RP4001644,	NT2RP4001677,	NT2RP4001803,	NT2RP4001822,	NT2RP4001975,	NT2RP4002052,
	NT2RP4002075,	NT2RP5003500,	NT2RP5003506,	NT2RP5003522,	NT2RP5003534,	OVARC1000151,
45	OVARC1000241,	OVARC1000335,	OVARC1000700,	OVARC1000722,	OVARC1000751,	OVARC1000850,
	OVARC1000924,	OVARC1000936,	OVARC1000959,	OVARC1000984,	OVARC1001034,	OVARC1001129,
	OVARC1001381,	OVARC1001391,	OVARC1001453,	OVARC1001476,	OVARC1001506,	OVARC1001610,
	OVARC1001702,	OVARC1001703,	OVARC1001713,	OVARC1001745,	OVARC1001767,	OVARC1002127,
	OVARC1002158,	OVARC1002165,	PLACE1000014,	PLACE1000401,	PLACE1000562,	PLACE1000611,
50	PLACE1000656,	PLACE1000712,	PLACE1000909,	PLACE1000948,	PLACE1001241,	PLACE1001257,
	PLACE1001377,	PLACE1001517,	PLACE1001610,	PLACE1001771,	PLACE1001817,	PLACE1001993,
	PLACE1002213,	PLACE1002395,	PLACE1002500,	PLACE1002714,	PLACE1002722,	PLACE1002794,
	PLACE1002851,	PLACE1002908,	PLACE1003045,	PLACE1003238,	PLACE1003296,	PLACE1003369,
	PLACE1003493,	PLACE1003537,	PLACE1003553,	PLACE1003768,	PLACE1003771,	PLACE1003903,
55	PLACE1004197,	PLACE1004258,	PLACE1004270,	PLACE1004289,	PLACE1004473,	PLACE1004743,
	PLACE1004840,	PLACE1004969,	PLACE1005086,	PLACE1005206,	PLACE1005313,	PLACE1005530,
	PLACE1005595,	PLACE1005623,	PLACE1005763,	PLACE1005884,	PLACE1005834,	PLACE1006225,
	PLACE1006754,	PLACE1006901,	PLACE1006935,	PLACE1006956,	PLACE1007014,	PLACE1007111,

	PLACE1007243,	PLACE1007274,	PLACE1007282,	PLACE1007317,	PLACE1007375,	PLACE1007386,
	PLACE1007409,	PLACE1007484,	PLACE1007583,	PLACE1007632,	PLACE1007645,	PLACE1007852,
	PLACE1007877,	PLACE1008331,	PLACE1008424,	PLACE1008531,	PLACE1008532,	PLACE1008568,
	PLACE1008715,	PLACE1009045,	PLACE1009319,	PLACE1009338,	PLACE1009368,	PLACE1009493,
5	PLACE1009639,	PLACE1009708,	PLACE1009731,	PLACE1010089,	PLACE1010231,	PLACE1010321,
	PLACE1010622,	PLACE1010811,	PLACE1010917,	PLACE1010954,	PLACE1011090,	PLACE1011214,
	PLACE1011221,	PLACE1011399,	PLACE1011492,	PLACE1011646,	PLACE1011749,	PLACE2000034,
	PLACE2000111,	PLACE2000176,	PLACE2000187,	PLACE2000341,	PLACE2000379,	PLACE2000425,
	PLACE2000458,	PLACE3000020,	PLACE3000218,	PLACE3000226,	PLACE3000244,	PLACE3000413,
10	PLACE4000052,	PLACE4000129,	PLACE4000300,	PLACE4000387,	PLACE4000581,	PLACE4000593,
	PLACE4000650,	THYRO1000394,	THYRO1000395,	THYRO1000570,	THYRO1000748,	THYRO1000756,
	THYRO1001134,	THYRO1001271,	THYRO1001401,	THYRO1001534,	THYRO1001541,	THYRO1001809,
	Y79AA1000258,	Y79AA1000420,	Y79AA1000469,	Y79AA1000734,	Y79AA1000800,	Y79AA1000976,
	Y79AA1001023,	Y79AA1001177,	Y79AA1001394,	Y79AA1001603,	Y79AA1001647,	Y79AA1001846,
15	Y79AA1001874,	Y79AA1002139,	Y79AA1002351,	Y79AA1002399,	Y79AA1002416,	HEMBA1004055,
	HEMBA1001630,	HEMBA1001872,	HEMBA1002044,	HEMBA1002383,	MAMMA1000778,	MAMMA1000859,
	MAMMA1000897,	MAMMA1001073,	MAMMA1002009,	MAMMA1002844,	MAMMA1002947,	MAMMA1003089,
	NT2RM1000092,	NT2RM1000833,	NT2RP2002105,	NT2RP2003668,	NT2RP2006184,	NT2RP3001282,
	NT2RP3002810,	NT2RP3002985,	NT2RP3003059,	NT2RP3003576,	NT2RP3003665,	NT2RP3003799,
20	NT2RP3003828,	NT2RP3003992,	NT2RP3004051,	NT2RP3004155,	OVARC1000890,	OVARC1001117,
	OVARC1001329,	PLACE1001761,	PLACE1002437,	PLACE1004793,	PLACE1005611,	PLACE1005898,
	PLACE1009935,	PLACE1011896,	PLACE2000132,	PLACE2000335,	PLACE3000373,	PLACE3000406,
	PLACE4000250,	PLACE4000487,	PLACE4000494,	THYRO1001320,	THYRO1001537,	THYRO1001828,
	Y79AA1001384					

[0256] Names of clones whose deduced amino acid sequences were predicted to have functional domains by Pfam search, and names of the matched functional domains are shown below.

When multiple functional domains matched a clone, each domain name was indicated, separated by a double-slash mark, //.

30	HEMBA1000005//DnaJ, prokaryotic heat shock protein
	HEMBA1000020//Tubulin
	HEMBA1000129//Helicases conserved C-terminal domain
	HEMBA1000156//RNA recognition motif. (aka RRM, RBD, or RNP domain)
	HEMBA1000158//Fork head domain, eukaryotic transcription factors //Zinc finger, C2H2 type
35	HEMBA1000303//Src homology domain 3 //Zinc finger, C3HC4 type (RING finger)
	HEMBA1000411//Ank repeat
	HEMBA1000491//Ras family (contains ATP/GTP binding P-loop)
	HEMBA1000531//Heat shock hsp70 proteins
40	HEMBA1000561//Zinc finger, C2H2 type
	HEMBA1000608//Src homology domain 3
	HEMBA1000919//WD domain, G-beta repeats
	HEMBA1001043//Ank repeat
	HEMBA1001088//LIM domain containing proteins
	HEMBA1001137//Zinc finger, C2H2 type
45	HEMBA1001174//ADP-ribosylation factors (Arf family) (contains ATP/GTP binding P-loop)
	HEMBA1001247//WWP domain containing proteins
	HEMBA1001286//Sushi domain
	HEMBA1001510//Basic region plus leucine zipper transcription factors
	HEMBA1001515//Reverse transcriptase (RNA-dependent DNA polymerase)
50	HEMBA1001661//Cadherin
	HEMBA1001723//WD domain, G-beta repeats
	HEMBA1001744//Eukaryotic protein kinase domain
	HEMBA1001804//Zinc finger, C2H2 type
	HEMBA1001819//Zinc finger, C2H2 type
55	HEMBA1001847//Zinc finger, C2H2 type
	HEMBA1002035//Bromodomain
	HEMBA1002102//Ank repeat
	HEMBA1002161//Myosin head (motor domain) (contains ATP/GTP binding P-loop)

HEMBA1002177//GATA family of transcription factors //Zinc finger, C2H2 type  
 HEMBA1002212//Eukaryotic protein kinase domain  
 HEMBA1002215//LIM domain containing proteins  
 HEMBA1002419//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 5 HEMBA1002547//Kazal-type serine protease inhibitor domain //Laminin EGF-like (Domains III and V)  
 HEMBA1002768//Src homology domain 3  
 HEMBA1002810//WWP/rsp5//WWP domain containing proteins  
 HEMBA1002818//EGF-like domain  
 HEMBA1002935//Zinc finger, C2H2 type  
 10 HEMBA1002939//Ank repeat  
 HEMBA1002973//3'-cyclic nucleotide phosphodiesterases  
 HEMBA1003077//Fibronectin type III domain  
 HEMBA1003250//Eukaryotic protein kinase domain  
 HEMBA1003257//Zinc finger, C2H2 type  
 15 HEMBA1003281//IG superfamily  
 HEMBA1003291//Eukaryotic protein kinase domain  
 HEMBA1003433//Forkhead-associated (FHA) domain  
 HEMBA1003545//Homeobox domain //LIM domain containing proteins  
 HEMBA1003591//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 20 HEMBA1003684//Zinc finger, C2H2 type  
 HEMBA1003953//Zinc finger, C2H2 type  
 HEMBA1004202//Ras family (contains ATP/GTP binding P-loop)  
 HEMBA1004227//Protein phosphatase 2C  
 HEMBA1004321//Zinc finger, C2H2 type  
 25 HEMBA1004356//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 HEMBA1004408//Peptidyl-prolyl cis-trans isomerases  
 HEMBA1004596//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 HEMBA1004734//Ubiquitin-conjugating enzymes  
 HEMBA1004973//Fibronectin type III domain  
 30 HEMBA1005009//Actins  
 HEMBA1005101//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 HEMBA1005581//EGF-like domain //Laminin G domain  
 HEMBA1005732//Polyprenyl synthetases  
 HEMBA1005737//EF hand  
 35 HEMBA1006248//Zinc finger, C2H2 type  
 HEMBA1006284//Ubiquitin family  
 HEMBA1006293//IG superfamily  
 HEMBA1006344//Band 4.1 family  
 HEMBA1006445//Ras family (contains ATP/GTP binding P-loop)  
 40 HEMBA1006492//Ank repeat  
 HEMBA1006559//Zinc finger, C3HC4 type (RING finger)  
 HEMBA1006708//WD domain, G-beta repeats  
 HEMBA1006737//Ank repeat  
 HEMBA1006758//Cadherin  
 45 HEMBA1006941//Thioredoxins  
 HEMBA1007243//Purine/pyrimidine phosphoribosyl transferases  
 HEMBA1007300//3'-cyclic nucleotide phosphodiesterases  
 HEMBB1000083//IG superfamily  
 HEMBB1000317//EGF-like domain //Thrombospondin type 1 domain  
 50 HEMBB1000556//Actin-type actin-binding domain containing proteins //LIM domain containing proteins  
 HEMBB1000725//Ras family (contains ATP/GTP binding P-loop)  
 HEMBB1000781//Eukaryotic protein kinase domain  
 HEMBB1000915//Thrombospondin type 1 domain  
 HEMBB1000927//EF hand  
 55 HEMBB1000947//Double-stranded RNA binding motif  
 HEMBB1001112//eubacterial secY protein  
 HEMBB1001175//Ank repeat  
 HEMBB1001234//WWP/rsp5//WWP domain containing proteins

	HEMBB1001282//Ank repeat
	HEMBB1001294//Ras family (contains ATP/GTP binding P-loop)
	HEMBB1001339//Forkhead-associated (FHA) domain
	HEMBB1001673//Forkhead-associated (FHA) domain //Zinc finger, C3HC4 type (RING finger)
5	HEMBB1001802//Intermediate filament proteins
	HEMBB1001839//Zinc finger, C2H2 type
	HEMBB1002217//Zinc finger, C2H2 type
	HEMBB1002342//Thioredoxins
	HEMBB1002600//4 transmembrane segments integral membrane proteins
10	MAMMA1000173//Src homology domain 3
	MAMMA1000388//Zinc finger, C2H2 type
	MAMMA1000402//Reverse transcriptase (RNA-dependent DNA polymerase)
	MAMMA1000612//WD domain, G-beta repeats
	MAMMA1000672//Serine carboxypeptidases
15	MAMMA1000731//SNF2 and others N-terminal domain
	MAMMA1001008//Eukaryotic aspartyl proteases
	MAMMA1001041//Actinin-type actin-binding domain containing proteins
	MAMMA1001059//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
	MAMMA1001105//Zinc finger, C2H2 type
20	MAMMA1001260//Zinc finger, C3HC4 type (RING finger)
	MAMMA1001576//Tubulin
	MAMMA1001735//Tubulin
	MAMMA1001768//ATPases associated with various cellular activities (AAA)
	MAMMA1001837//Zinc finger, C2H2 type
25	MAMMA1002170//Ribosomal protein S5
	MAMMA1002385//RNA recognition motif. (aka RRM, RBD, or RNP domain)
	MAMMA1002619//Ubiquitin carboxyl-terminal hydrolases family 2
	MAMMA1002637//Kinesin light chain repeat
	MAMMA1002650//Zinc finger, C2H2 type
30	MAMMA1002671//AMP-binding enzymes
	MAMMA1002869//LIM domain containing proteins
	MAMMA1002881//SCP-like extracellular Proteins
	MAMMA1002937//Zinc finger, C2H2 type
	MAMMA1002938//Multicopper oxidases
35	MAMMA1003011//Core histones H2A, H2B, H3 and H4
	MAMMA1003057//WD domain, G-beta repeats
	MAMMA1003127//Myosin head (motor domain) (contains ATP/GTP binding P-loop)
	NT2RM1000086//Zinc finger, C3HC4 type (RING finger)
	NT2RM1000199//CUB domain //Sushi domain
40	NT2RM1000256//Glutamine amidotransferases class-I
	NT2RM1000499//Ank repeat
	NT2RM1000555//Cold-shock DNA-binding domain containing proteins
	NT2RM1000666//Cold-shock DNA-binding domain containing proteins //Zinc finger, CCHC class
	NT2RM1000772//WD domain, G-beta repeats
45	NT2RM1000826//Cold-shock DNA-binding domain containing proteins
	NT2RM1000850//Ank repeat //Eukaryotic protein kinase domain
	NT2RM1000852//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
	NT2RM1000882//Heme-binding domain in cytochrome b5 and oxidoreductases
	NT2RM1000885//Zinc finger, C3HC4 type (RING finger)
50	NT2RM1001059//RNA recognition motif. (aka RRM, RBD, or RNP domain)
	NT2RM1001072//C2 domain //Phosphatidylinositol-specific phospholipase C, X domain //Phosphatidylinositol-specific phospholipase C, Y domain
	NT2RM2000092//Ubiquitin carboxyl-terminal hydrolases family 2
	NT2RM2000101//Zinc finger, C3HC4 type (RING finger)
55	NT2RM2000191//3'5'-cyclic nucleotide phosphodiesterases
	NT2RM2000422//Sodium:neurotransmitter symporter family
	NT2RM2000490//C2 domain
	NT2RM2000568//Integrins alpha chain



	NT2RM2000577//tRNA synthetases class I
	NT2RM2000594//C-5 cytosine-specific DNA methylases
	NT2RM2000691//Actins
5	NT2RM2000735//Zinc finger, C2H2 type
	NT2RM2000740//Helicases conserved C-terminal domain
	NT2RM2000951//FGGY family of carbohydrate kinases
	NT2RM2001324//LIM domain containing proteins
	NT2RM2001499//Amino acid permeases
10	NT2RM2001547//DnaJ, prokaryotic heat shock protein //Thioredoxins
	NT2RM2001613//eubacterial secY protein
	NT2RM2001670//Zinc finger, C2H2 type
	NT2RM2001700//Acyl-CoA dehydrogenases
	NT2RM2001730//Ubiquitin carboxyl-terminal hydrolases family 2
	NT2RM2001813//WD domain, G-beta repeats
15	NT2RM2001823//Helicases conserved C-terminal domain //SNF2 and others N-terminal domain
	NT2RM2001896//Cytochrome C oxidase subunit II
	NT2RM2001989//RNA recognition motif. (aka RRM, RBD, or RNP domain)
	NT2RM2001997//Thioredoxins
	NT2RM2002088//KH domain family of RNA binding proteins
20	NT2RM2002100//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
	NT2RM2002109//IG superfamily
	NT2RM4000046//Zinc finger, C3HC4 type (RING finger)
	NT2RM4000104//Zinc finger, C2H2 type
	NT2RM4000167//Kinesin motor domain
25	NT2RM4000191//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
	NT2RM4000202//Zinc finger, C2H2 type
	NT2RM4000229//PH (pleckstrin homology) domain
	NT2RM4000344//ATPases associated with various cellular activities (AAA)
	NT2RM4000356//Ras family (contains ATP/GTP binding P-loop)
30	NT2RM4000471//Aminotransferases class-V
	NT2RM4000496//ATPases associated with various cellular activities (AAA)
	NT2RM4000611//WD domain, G-beta repeats
	NT2RM4000657//C2 domain //Phosphatidylinositol-specific phospholipase C, Y domain
	NT2RM4000712//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
35	NT2RM4000733//Forkhead-associated (FHA) domain
	NT2RM4000734//Zinc finger, C2H2 type
	NT2RM4000751//Zinc finger, C2H2 type
	NT2RM4000795//Carboxylesterases
	NT2RM4000996//Zinc finger, C2H2 type
40	NT2RM4001054//eubacterial secY protein
	NT2RM4001140//Homeobox domain
	NT2RM4001178//DEAD and DEAH box helicases
	NT2RM4001200//Zinc finger, C2H2 type
	NT2RM4001313//Phosphatidylinositol 3- and 4-kinases
45	NT2RM4001316//Acyl-CoA dehydrogenases
	NT2RM4001320//Src homology domain 3
	NT2RM4001411//PH (pleckstrin homology) domain //Src homology domain 2
	NT2RM4001454//PH (pleckstrin homology) domain
	NT2RM4001483//Zinc finger, C2H2 type
50	NT2RM4001629//Src homology domain 3
	NT2RM4001758//Eukaryotic protein kinase domain
	NT2RM4001810//Zinc finger, C2H2 type
	NT2RM4001813//Lectin C-type domain short and long forms
	NT2RM4001823//Zinc finger, C2H2 type
55	NT2RM4001828//Zinc finger, C2H2 type
	NT2RM4001979//Zinc finger, C2H2 type
	NT2RM4001987//IG superfamily
	NT2RM4002013//WD domain, G-beta repeats

	NT2RM4002073//AMP-binding enzymes
	NT2RM4002093//RNA recognition motif. (aka RRM, RBD, or RNP domain)
	NT2RM4002145//IG superfamily
5	NT2RM4002287//Fibronectin type III domain
	NT2RM4002527//WD domain, G-beta repeats
	NT2RM4002623//tRNA synthetases class II
	NT2RP1000101//Zinc finger, C2H2 type
	NT2RP1000202//Ank repeat
	NT2RP1000272//RNA recognition motif. (aka RRM, RBD, or RNP domain)
10	NT2RP1000363//PH (pleckstrin homology) domain
	NT2RP1000376//Ank repeat
	NT2RP1000470//DEAD and DEAH box helicases
	NT2RP1000478//Tubulin
	NT2RP1000522//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
15	NT2RP1000677//Kazal-type serine protease inhibitor domain
	NT2RP1000701//WD domain, G-beta repeats
	NT2RP1000733//Elongation factor Tu family (contains ATP/GTP binding P-loop)
	NT2RP1000782//4 transmembrane segments integral membrane proteins
	NT2RP1000833//3'-cyclic nucleotide phosphodiesterases
20	NT2RP1000856//4 transmembrane segments integral membrane proteins
	NT2RP1000947//Ubiquitin-conjugating enzymes
	NT2RP1000959//60s Acidic ribosomal protein
	NT2RP1000966//RNA recognition motif. (aka RRM, RBD, or RNP domain)
	NT2RP1001033//Tubulin
25	NT2RP1001080//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
	NT2RP1001177//Core histones H2A, H2B, H3 and H4
	NT2RP1001247//Transforming growth factor beta like domain
	NT2RP1001294//WD domain, G-beta repeats
	NT2RP1001302//WD domain, G-beta repeats
30	NT2RP1001313//Heme-binding domain in cytochrome b5 and oxidoreductases
	NT2RP1001457//WD domain, G-beta repeats
	NT2RP1001546//4 transmembrane segments integral membrane proteins
	NT2RP2000008//Zinc finger, C2H2 type
	NT2RP2000040//C2 domain
35	NT2RP2000045//DnaJ, prokaryotic heat shock protein
	NT2RP2000054//Zinc finger, C3HC4 type (RING finger)
	NT2RP2000070//Cadherin
	NT2RP2000126//Helicases conserved C-terminal domain //SNF2 and others N-terminal domain
	NT2RP2000153//RNA recognition motif. (aka RRM, RBD, or RNP domain)
40	NT2RP2000224//PH (pleckstrin, homology) domain
	NT2RP2000257//Mitochondrial carrier proteins
	NT2RP2000329//Adenylate kinases
	NT2RP2000414//RNA recognition motif. (aka RRM, RBD, or RNP domain)
	NT2RP2000448//PH (pleckstrin homology) domain
45	NT2RP2000660//ATPases associated with various cellular activities (AAA)
	NT2RP2000668//Eukaryotic protein kinase domain
	NT2RP2000710//tRNA synthetases class II
	NT2RP2000764//Aminotransferases class-V
	NT2RP2000842//7 transmembrane receptor (rhodopsin family)
50	NT2RP2000880//Elongation factor Tu family (contains ATP/GTP binding P-loop)
	NT2RP2000931//RNA recognition motif. (aka RRM, RBD, or RNP domain)
	NT2RP2000932//Ank repeat
	NT2RP2001081//C2 domain
	NT2RP2001174//Zinc finger, C2H2 type
55	NT2RP2001397//Cyclins
	NT2RP2001520//Mitochondrial carrier proteins
	NT2RP2001597//Zinc finger, C3HC4 type (RING finger)
	NT2RP2001740//Ubiquitin carboxyl-terminal hydrolases family 2

	NT2RP2001748//Polyprenyl synthetases
	NT2RP2001756//Zinc finger, C2H2 type
	NT2RP2001839//Eukaryotic protein kinase domain
	NT2RP2001900//Actins
5	NT2RP2001991//Sodium:neurotransmitter symporter family
	NT2RP2002058//WD domain, G-beta repeats
	NT2RP2002124//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
	NT2RP2002185//Ubiquitin family
	NT2RP2002208//Zinc finger, C3HC4 type (RING finger)
10	NT2RP2002256//Cytochrome P450
	NT2RP2002479//ABC transporters
	NT2RP2002503//Zinc finger, C2H2 type
	NT2RP2002520//Ank repeat
	NT2RP2002591//Zinc finger, C2H2 type
15	NT2RP2002741//Src homology domain 3
	NT2RP2002929//WD domain, G-beta repeats
	NT2RP2002939//Zinc finger, C2H2 type
	NT2RP2002959//Ubiquitin-conjugating enzymes
	NT2RP2002980//Ribosomal protein S10
20	NT2RP2003137//Ubiquitin family
	NT2RP2003164//Eukaryotic protein kinase domain
	NT2RP2003228//MCM2/3/5 family
	NT2RP2003243//Fibronectin type III domain
	NT2RP2003272//Ubiquitin family
25	NT2RP2003307//Kinesin light chain repeat
	NT2RP2003401//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases, family 2
	NT2RP2003433//eubacterial secY protein
	NT2RP2003480//Zinc finger, C2H2 type
	NT2RP2003713//Ubiquitin carboxyl-terminal hydrolases family 2
30	NT2RP2003737//Ubiquitin-conjugating enzymes
	NT2RP2003777//Zinc finger, C3HC4 type (RING finger)
	NT2RP2003840//Ubiquitin-conjugating enzymes
	NT2RP2003857//Ank repeat
	NT2RP2003981//Zinc finger, C3HC4 type (RING finger)
35	NT2RP2004170//WD domain, G-beta repeats
	NT2RP2004187//Zinc finger, C2H2 type
	NT2RP2004232//Phorbol esters / diacylglycerol binding domain //PH (pleckstrin homology) domain //Eukaryotic protein kinase domain
	NT2RP2004389//Ribosomal protein S9
40	NT2RP2004538//PH (pleckstrin homology) domain
	NT2RP2004568//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
	NT2RP2004710//WW/rsp5/WWP domain containing proteins
	NT2RP2004768//Eukaryotic protein kinase domain
	NT2RP2004933//Eukaryotic protein kinase domain
45	NT2RP2004961//Zinc finger, C2H2 type
	NT2RP2005003//Zinc finger, C3HC4 type (RING finger)
	NT2RP2005012//DnaJ, prokaryotic heat shock protein
	NT2RP2005126//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
	NT2RP2005139//Ank repeat
50	NT2RP2005140//PH (pleckstrin homology) domain
	NT2RP2005239//Aminotransferases class-V
	NT2RP2005288//Regulator of chromosome condensation (RCC1)
	NT2RP2005293//PH (pleckstrin homology) domain
	NT2RP2005325//Homeobox domain //LIM domain containing proteins
55	NT2RP2005344//E1-E2 ATPases
	NT2RP2005465//Mitochondrial carrier proteins
	NT2RP2005525//Forkhead-associated (FHA) domain
	NT2RP2005531//Band 4.1 family

NT2RP2005557//Bacterial mutT protein  
 NT2RP2005654//DnaJ, prokaryotic heat shock protein  
 NT2RP2005701//Zinc finger, C3HC4 type (RING finger)  
 NT2RP2005722//Zinc finger, C2H2 type  
 5 NT2RP2005752//TNFR/NGFR cysteine-rich region  
 NT2RP2005763//DEAD and DEAH box helicases //Helicases conserved C-terminal domain  
 NT2RP2005767//HMG (high mobility group) box  
 NT2RP2006312//HMG (high mobility group) box  
 NT2RP2006464//HMG (high mobility group) box  
 10 NT2RP2006571//Cytochrome P450  
 NT2RP3000050//Zinc finger, C2H2 type  
 NT2RP3000068//PH (pleckstrin homology) domain  
 NT2RP3000085//Biotin-requiring enzymes //Carbamoyl-phosphate synthase (CPSase)  
 NT2RP3000299//Src homology domain 3  
 15 NT2RP3000359//Adenylate kinases  
 NT2RP3000366//Ras family (contains ATP/GTP binding P-loop)  
 NT2RP3000403//WW/rsp5/WWP domain containing proteins  
 NT2RP3000487//WW/rsp5/WWP domain containing proteins  
 NT2RP3000512//Homeobox domain  
 20 NT2RP3000527//Zinc finger, C2H2 type  
 NT2RP3000531//IG superfamily  
 NT2RP3000590//Zinc finger, C3HC4 type (RING finger)  
 NT2RP3000603//Helix-loop-helix DNA-binding domain  
 NT2RP3000605//Zinc finger, C2H2 type  
 25 NT2RP3000632//Zinc finger, C2H2 type  
 NT2RP3000742//Phosphatidylinositol-specific phospholipase C, X domain //Phosphatidylinositol-specific phospholipase C, Y domain  
 NT2RP3000759//ADP-ribosylation factors (Arf family) (contains ATP/GTP binding P-loop)  
 NT2RP3000825//EGF-like domain  
 30 NT2RP3000869//ATPases associated with various cellular activities (AAA)  
 NT2RP3000994//Double-stranded RNA binding motif  
 NT2RP3001057//Zinc finger, C2H2 type  
 NT2RP3001084//PH (pleckstrin homology) domain  
 NT2RP3001120//Zinc finger, C2H2 type  
 35 NT2RP3001140//Thrombospondin type 1 domain  
 NT2RP3001150//Forkhead-associated (FHA) domain  
 NT2RP3001155//HMG (high mobility group) box  
 NT2RP3001214//Zinc finger, C2H2 type  
 NT2RP3001268//Zinc finger, C2H2 type  
 40 NT2RP3001338//Zinc finger, C2H2 type  
 NT2RP3001355//Mitochondrial carrier proteins  
 NT2RP3001398//Zinc finger, C2H2 type  
 NT2RP3001426//DnaJ, prokaryotic heat shock protein  
 NT2RP3001453//ABC transporters  
 45 NT2RP3001457//PH (pleckstrin homology) domain  
 NT2RP3001472//HMG (high mobility group) box  
 NT2RP3001495//Alcohol/other dehydrogenases, short chain type //WW/rsp5/WWP domain containing proteins  
 NT2RP3001497//Zinc finger, C3HC4 type (RING finger)  
 NT2RP3001724//Helicases conserved C-terminal domain  
 50 NT2RP3001792//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 NT2RP3001943//Zinc finger, C3HC4 type (RING finger)  
 NT2RP3001944//Zinc finger, C3HC4 type (RING finger)  
 NT2RP3002007//ATPases associated with various cellular activities (AAA)  
 NT2RP3002054//Low-density lipoprotein receptor domain class A  
 55 NT2RP3002151//Elongation factor Tu family (contains ATP/GTP binding P-loop)  
 NT2RP3002399//MCM2/3/5 family  
 NT2RP3002501//Serine/threonine dehydratases  
 NT2RP3002602//Thioredoxins

	NT2RP3002628//DnaJ, prokaryotic heat shock protein //Thioredoxins
	NT2RP3002663//PH (pleckstrin homology) domain
	NT2RP3002909//Ank repeat
5	NT2RP3002953//Cadherin
	NT2RP3002969//AMP-binding enzymes
	NT2RP3003061//Ank repeat
	NT2RP3003145//Zinc carboxypeptidases
	NT2RP3003230//WD domain, G-beta repeats
	NT2RP3003251//Zinc finger, C3HC4 type (RING finger)
10	NT2RP3003278//Ank repeat //Zinc finger, C2H2 type
	NT2RP3003282//PH (pleckstrin homology) domain
	NT2RP3003311//PH (pleckstrin homology) domain
	NT2RP3003385//Ank repeat //Chaperonins dpaB
	NT2RP3003589//Ras family (contains ATP/GTP binding P-loop)
15	NT2RP3003621//CUB domain //Krigle domain
	NT2RP3003701//Thrombospondin type 1 domain
	NT2RP3003716//Fibronectin type III domain
	NT2RP3003809//ATPases associated with various cellular activities (AAA)
	NT2RP3004016//Zinc finger, C3HC4 type (RING finger)
20	NT2RP3004207//CUB domain //Sushi domain
	NT2RP3004209//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
	NT2RP3004242//PH (pleckstrin homology) domain
	NT2RP3004262//DnaJ, prokaryotic heat shock protein
	NT2RP3004566//Zinc finger, C2H2 type
25	NT2RP3004569//Ank repeat
	NT2RP3004594//HMG (high mobility group) box
	NT2RP3004617//Zinc finger, C3HC4 type (RING finger)
	NT2RP4000259//Glutathione peroxidases
	NT2RP4000370//Prokaryotic-type class I peptide chain release factors
30	NT2RP4000376//WD domain, G-beta repeats
	NT2RP4000398//Zinc finger, C2H2 type
	NT2RP4000455//Forkhead-associated (FHA) domain //Zinc finger, C3HC4 type (RING finger)
	NT2RP4000457//Ubiquitin carboxyl-terminal hydrolases family 2
	NT2RP4000518//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
35	NT2RP4000588//Actinin-type actin-binding domain containing proteins
	NT2RP4000614//RNA recognition motif. (aka RRM, RBD, or RNP domain)
	NT2RP4000648//Forkhead-associated (FHA) domain //Zinc finger, C3HC4 type (RING finger)
	NT2RP4000837//Zinc finger, C2H2 type
	NT2RP4000839//WD domain, G-beta repeats
40	NT2RP4000865//Zinc finger, C2H2 type
	NT2RP4000907//Fibronectin type III domain //IG superfamily
	NT2RP4000925//Fibronectin type III domain
	NT2RP4000927//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
	NT2RP4000973//DnaJ, prokaryotic heat shock protein //Thioredoxins
45	NT2RP4001079//E1-E2 ATPases
	NT2RP4001080//RNA recognition motif. (aka RRM, RBD, or RNP domain)
	NT2RP4001117//eubacterial secY protein
	NT2RP4001150//Fibronectin type III domain
	NT2RP4001213//Zinc finger, C2H2 type
50	NT2RP4001219//Thioredoxins
	NT2RP4001235//Zinc finger, CCHC class
	NT2RP4001433//Zinc finger, C2H2 type
	NT2RP4001498//Ank repeat
	NT2RP4001568//Ank repeat
55	NT2RP4001644//Eukaryotic protein kinase domain
	NT2RP4001725//WD domain, G-beta repeats
	NT2RP4001753//Zinc finger, C2H2 type
	NT2RP4001790//Zinc finger, C2H2 type

NT2RP4001822//4 transmembrane segments integral membrane proteins  
 NT2RP4001823//Fibrinogen beta and gamma chains, C-terminal globular domain  
 NT2RP4001893//Ank repeat  
 NT2RP4001896//WD domain, G-beta repeats  
 5 NT2RP4001927//WD domain, G-beta repeats  
 NT2RP4001938//Zinc finger, C2H2 type  
 NT2RP4002047//Elongation factor Tu family (contains ATP/GTP binding P-loop)  
 NT2RP4002078//Zinc finger, C2H2 type  
 NT2RP4002408//Eukaryotic protein kinase domain  
 10 NT2RP4002905//Cyclins  
 NT2RP5003477//WD domain, G-beta repeats  
 OVARC1000006//Core histones H2A, H2B, H3 and H4  
 OVARC1000085//Proteasome A-type and B-type  
 OVARC1000148//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 15 OVARC1000556//Eukaryotic protein kinase domain  
 OVARC1000649//PH (pleckstrin homology) domain //Src homology domain 2  
 OVARC1000746//Double-stranded RNA binding motif  
 OVARC1000885//Alcohol/other dehydrogenases, short chain type  
 OVARC1000937//Cyclins  
 20 OVARC1000999//Ank repeat  
 OVARC1001154//Granulins  
 OVARC1001180//Ubiquitin family  
 OVARC1001306//Helix-loop-helix DNA-binding domain  
 OVARC1001577//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 25 OVARC1001731//Tropomyosins  
 OVARC1001943//Zinc finger, C2H2 type  
 OVARC1002050//Spectrin alpha chain, repeated domain  
 OVARC1002112//Core histones H2A, H2B, H3 and H4  
 OVARC1002138//ATPases associated with various cellular activities (AAA)  
 30 OVARC1002182//WD domain, G-beta repeats  
 PLACE1000014//Zinc finger, C3HC4 type (RING finger)  
 PLACE1000040//Ras family (contains ATP/GTP binding P-loop)  
 PLACE1000050//Zinc finger, C2H2 type  
 PLACE1000081//PH (pleckstrin homology) domain  
 35 PLACE1000142//Enoyl-CoA hydratase/isomerase  
 PLACE1000401//IG superfamily  
 PLACE1000406//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 PLACE1000420//Bacterial mutT protein  
 PLACE1000706//Bromodomain  
 40 PLACE1000769//KH domain family of RNA binding proteins  
 PLACE1000786//PH (pleckstrin homology) domain  
 PLACE1000863//Ribosomal protein S4  
 PLACE1000909//Ank repeat  
 PLACE1000972//Src homology domain 3  
 45 PLACE1000979//Zinc finger, C2H2 type  
 PLACE1001304//Zinc finger, C2H2 type  
 PLACE1001387//Src homology domain 3  
 PLACE1001632//Zinc finger, C2H2 type  
 PLACE1001672//Aminotransferases class-III pyridoxal-phosphate  
 50 PLACE1001716//Zinc finger, CCHC class  
 PLACE1001739//DEAD and DEAH box helicases //Helicases conserved C-terminal domain  
 PLACE1001781//Phosphoglucosyltransferase and phosphomannosyltransferase phosphoserine  
 PLACE1001869//FGGY family of carbohydrate kinases  
 PLACE1002438//Zinc finger, C2H2 type  
 55 PLACE1002450//Zinc finger, C2H2 type  
 PLACE1002474//EGF-like domain //von Willebrand factor type A domain  
 PLACE1002499//Zinc finger, C3HC4 type (RING finger)  
 PLACE1002532//Homeobox domain

PLACE1002571//Actins  
 PLACE1002685//Src homology domain 2  
 PLACE1002722//7 transmembrane receptor (rhodopsin family)  
 PLACE1002775//Bromodomain  
 5 PLACE1002834//Zinc finger, C2H2 type  
 PLACE1003100//Alcohol/other dehydrogenases, short chain type  
 PLACE1003174//Ubiquitin-conjugating enzymes  
 PLACE1003238//7 transmembrane receptor (rhodopsin family)  
 PLACE1003302//Zinc finger, C2H2 type  
 10 PLACE1003334//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 PLACE1003366//C2 domain  
 PLACE1003394//Ras family (contains ATP/GTP binding P-loop)  
 PLACE1003420//Mitochondrial carrier proteins  
 PLACE1003493//C1q domain  
 15 PLACE1003519//KH domain family of RNA binding-proteins  
 PLACE1003723//Src homology domain 2  
 PLACE1003738//Zinc finger, C2H2 type  
 PLACE1003888//C2 domain //Phosphatidylinositol-specific phospholipase C, X domain //Phosphatidylinositol-specific phospholipase C, Y domain  
 20 PLACE1004128//WD domain, G-beta repeats  
 PLACE1004358//PH (pleckstrin homology) domain  
 PLACE1004428//Acyl-CoA dehydrogenases  
 PLACE1004437//isocitrate and isopropylmalate dehydrogenases  
 PLACE1004506//LIM domain containing proteins  
 25 PLACE1004674//EF hand  
 PLACE1004918//L-lactate dehydrogenases  
 PLACE1005243//Eukaryotic protein kinase domain  
 PLACE1005305//Adenylate kinases  
 PLACE1005327//Src homology domain 3  
 30 PLACE1005530//Zinc finger, C3HC4 type (RING finger)  
 PLACE1005646//Helicases conserved C-terminal domain  
 PLACE1005656//Ribonucleotide reductases  
 PLACE1005966//WD domain, G-beta repeats  
 PLACE1006157//Sushi domain  
 35 PLACE1006196//DEAH and DEAR box helicases //Helicases conserved C-terminal domain  
 PLACE1006438//Zinc finger, C2H2 type  
 PLACE1006626//Double-stranded RNA binding motif  
 PLACE1006754//IG superfamily  
 PLACE1006829//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2  
 40 PLACE1006917//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 PLACE1006956//ABC transporters  
 PLACE1006958//Heat shock hsp70 proteins  
 PLACE1007375//C2 domain  
 PLACE1007488//PH (pleckstrin homology) domain  
 45 PLACE1007511//Intermediate filament proteins  
 PLACE1007537//Ank repeat  
 PLACE1007544//Zinc finger, C2H2 type  
 PLACE1007547//Zinc finger, C3HC4 type (RING finger)  
 PLACE1007598//Zinc finger, C2H2 type  
 50 PLACE1007697//ABC transporters  
 PLACE1007958//3'5'-cyclic nucleotide phosphodiesterases  
 PLACE1007969//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 PLACE1008201//Zinc finger, C2H2 type  
 PLACE1008429//Ank repeat  
 55 PLACE1008465//Zinc finger, C2H2 type  
 PLACE1008650//WD domain, G-beta repeats  
 PLACE1009020//Aminotransferases class-V  
 PLACE1009094//von Willebrand factor type C domain

PLACE1009099//Zinc finger, C2H2 type  
 PLACE1009246//LIM domain containing proteins  
 PLACE1009468//WD domain, G-beta repeats  
 PLACE1009476//DEAD and DEAH box helicases //Helicases conserved C-terminal domain  
 5 PLACE1009524//PH (pleckstrin homology) domain  
 PLACE1009596//WD domain, G-beta repeats  
 PLACE1009622//Double-stranded RNA binding motif  
 PLACE1009861//Cysteine proteases  
 PLACE1009925//Helicases conserved C-terminal domain  
 10 PLACE1009992//CUB domain //EGF-like domain //Sushi domain //Trypsin  
 PLACE1010053//Double-stranded RNA binding motif  
 PLACE1010089//Ubiquitin carboxyl-terminal hydrolases family 2  
 PLACE1010702//Zinc finger, C2H2 type  
 PLACE1010833//EF hand  
 15 PLACE1010926//Src homology domain 3  
 PLACE1010960//Actins  
 PLACE1011041//Src homology domain 3  
 PLACE1011046//C2 domain //Phosphatidylinositol-specific phospholipase C, X domain //Phosphatidylinositol-spe-  
 cific phospholipase C, Y domain  
 20 PLACE1011114//Helicases conserved C-terminal domain  
 PLACE1011160//Zinc finger, C3HC4 type (RING finger)  
 PLACE1011263//Ank repeat  
 PLACE1011433//Zinc finger, C2H2 type  
 PLACE1011576//Zinc finger, C2H2 type  
 25 PLACE1011923//Eukaryotic protein kinase domain  
 PLACE2000034//Fibronectin type III domain //IG superfamily  
 PLACE2000072//Zinc finger, C2H2 type  
 PLACE2000111//IG superfamily  
 PLACE2000164//WD domain, G-beta repeats  
 30 PLACE2000216//PH (pleckstrin homology) domain  
 PLACE2000341//Sodium:solute symporter family  
 PLACE2000371//Src homology domain 2  
 PLACE2000373//Thrombospondin type 1 domain  
 PLACE2000398//IG superfamily  
 35 PLACE2000427//Helicases conserved C-terminal domain  
 PLACE2000458//Cadherin  
 PLACE3000020//Guanylate cyclases  
 PLACE3000169//Zinc finger, C2H2 type  
 PLACE4000014//Helicases conserved C-terminal domain  
 40 PLACE4000052//ABC transporters  
 PLACE4000192//Zinc finger, C2H2 type  
 PLACE4000211//Bromodomain  
 PLACE4000431//Helicases conserved C-terminal domain  
 PLACE4000522//Ank repeat  
 45 PLACE4000581//EGF-like domain //Sushi domain  
 PLACE4000654//Ubiquitin-conjugating enzymes  
 THYRO1000072//IG superfamily  
 THYRO1000242//Zinc finger, C2H2 type  
 THYRO1000288//Zinc-binding metalloprotease domain  
 50 THYRO1000488//Zinc finger, C3HC4 type (RING finger)  
 THYRO1000501//Zinc finger, C3HC4 type (RING finger)  
 THYRO1000666//Kinesin motor domain  
 THYRO1000748//Src homology domain 3  
 THYRO1000926//3' 5'-cyclic nucleotide phosphodiesterases  
 55 THYRO1001661//RNA recognition motif. (aka RRM, RBD, or RNP domain)  
 THYRO1001671//Ubiquitin family  
 Y79AA1000037//Zinc finger, C3HC4 type (RING finger)  
 Y79AA1000214//Core histones H2A, H2B, H3 and H4



Y79AA1000342//Zinc finger, C2H2 type  
 Y79AA1000349//Double-stranded RNA binding motif  
 Y79AA1000627//Zinc finger, C2H2 type  
 Y79AA1000705//Helicases conserved C-terminal domain  
 5 Y79AA1000752//KH domain family of RNA binding proteins  
 Y79AA1000833//Tubulin  
 Y79AA1001048//Acyl-CoA dehydrogenases  
 Y79AA1001391//Homeobox domain  
 Y79AA1001394//ATPases associated with various cellular activities (AAA)  
 10 Y79AA1001493//Ubiquitin-conjugating enzymes  
 Y79AA1001613//Zinc finger, C2H2 type  
 Y79AA1001874//TNFR/NGFR cysteine-rich region  
 Y79AA1002027//Ubiquitin-conjugating enzymes  
 Y79AA1002139//DnaJ, prokaryotic heat shock protein  
 15 Y79AA1002208//Ank repeat  
 Y79AA1002246//C2 domain  
 Y79AA1002307//Fibronectin type III domain  
 Y79AA1002472//Zinc finger, C2H2 type  
 HEMBA1003538//CUB domain HEMBA1003645//WD domain, G-beta repeats //Src homology domain 3  
 20 HEMBA1005206//Glutathione S-transferases.  
 HEMBA1006521//Alcohol/other dehydrogenases, short chain type  
 HEMBB1001482//Zinc finger, C2H2 type HEMBB1001915//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubi-  
 quin carboxyl-terminal hydrolases family 2 HEMBB1002044//Caderin MAMMA1000183//Zinc finger, C2H2 type  
 MAMMA1000897//von Willebrand factor type A domain MAMMA1001080//IG superfamily MAMMA1002498//IG  
 25 superfamily MAMMA1002573//KH domain family of RNA binding proteins MAMMA1002617//Zinc finger, C2H2 type  
 NT2RP1000833//eubacterial secY protein NT2RP2001797//Zinc finger, C2H2 type  
 NT2RP1001013//Zinc finger, C2H2 type NT2RP2001233//Zinc finger, C2H2 type  
 NT2RP2001440//14-3-3 proteins NT2RP2002105//7 transmembrane receptor (rhodopsin family)  
 NT2RP3001723//Laminin G domain NT2RP3001938//Eukaryotic protein kinase domain NT2RP3002330//Elonga-  
 30 tion factor Tu family (contains ATP/GTP binding P-loop) NT2RP3003133//Zinc finger, C2H2 type  
 NT2RP3003500//Eukaryotic protein kinase domain NT2RP3003799//C2 domain  
 NT2RP3003800//Eukaryotic protein kinase domain NT2RP3004013//Double-stranded RNA binding motif  
 NT2RP3004125//Zinc finger, C2H2 type  
 OVARC1001244//Bromodomain OVARC1001496//D-isomer specific 2-hydroxyacid dehydrogenases  
 35 PLACE1000007//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2  
 PLACE1001118//Zinc finger, C2H2 type PLACE1010310//Zinc finger, C2H2 type PLACE1011896//wnt family of  
 developmental signaling proteins PLACE3000124//Src homology domain 2  
 PLACE4000100//D-isomer specific 2-hydroxyacid dehydrogenases  
 PLACE4000259//Helicases conserved C-terminal domain PLACE4000261//Bromodomain SKNMC1000013//ABC  
 40 transporters SKNMC1000091//Basic region plus leucine zipper transcription factors THYRO1000343//Src homol-  
 ogy domain 3 THYRO1000569//Zinc finger, C2H2 type THYRO1001189//Zinc finger, C2H2 type Y79AA1002103//  
 Zinc finger, C2H2 type PLACE3000350//Eukaryotic protein kinase domain  
 PLACE4000156//Zinc finger, C2H2 type

#### 45 EXAMPLE 18

Classification of cDNA clones into functional categories based on the full-length nucleotide sequences

50 [0257] Prediction of functions of proteins encoded by the clones and the categorization thereof were performed based  
 on the results of homology search (see Homology search results 6, 12, 13 and 14) of the databases, GenBank, Swiss-  
 Prot and UniGene, for the full-length nucleotide sequences of 4997 clones and based on the results of domain search  
 (see Example 17) of the deduced amino acid sequences encoded by the full-length nucleotide sequences. The target  
 4997 clones are listed below:

55 HEMBA1000005, HEMBA1000012, HEMBA1000020, HEMBA1000030, HEMBA1000042, HEMBA1000046,  
 HEMBA1000050, HEMBA1000076, HEMBA1000129, HEMBA1000141, HEMBA1000150, HEMBA1000156,  
 HEMBA1000158, HEMBA1000168, HEMBA1000185, HEMBA1000193, HEMBA1000201, HEMBA1000213,  
 HEMBA1000216, HEMBA1000227, HEMBA1000231, HEMBA1000243, HEMBA1000244, HEMBA1000251,  
 HEMBA1000264, HEMBA1000280, HEMBA1000282, HEMBA1000288, HEMBA1000290, HEMBA1000302,

	HEMBA1000303,	HEMBA1000304,	HEMBA1000307,	HEMBA1000327,	HEMBA1000333,	HEMBA1000338,
	HEMBA1000351,	HEMBA1000356,	HEMBA1000357,	HEMBA1000369,	HEMBA1000376,	HEMBA1000387,
	HEMBA1000392,	HEMBA1000396,	HEMBA1000411,	HEMBA1000428,	HEMBA1000442,	HEMBA1000456,
	HEMBA1000459,	HEMBA1000460,	HEMBA1000469,	HEMBA1000488,	HEMBA1000491,	HEMBA1000497,
5	HEMBA1000501,	HEMBA1000504,	HEMBA1000505,	HEMBA1000508,	HEMBA1000518,	HEMBA1000519,
	HEMBA1000520,	HEMBA1000523,	HEMBA1000531,	HEMBA1000534,	HEMBA1000542,	HEMBA1000545,
	HEMBA1000555,	HEMBA1000557,	HEMBA1000561,	HEMBA1000568,	HEMBA1000569,	HEMBA1000575,
	HEMBA1000588,	HEMBA1000591,	HEMBA1000592,	HEMBA1000594,	HEMBA1000604,	HEMBA1000608,
	HEMBA1000622,	HEMBA1000636,	HEMBA1000637,	HEMBA1000655,	HEMBA1000657,	HEMBA1000673,
10	HEMBA1000682,	HEMBA1000686,	HEMBA1000702,	HEMBA1000719,	HEMBA1000722,	HEMBA1000726,
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	HEMBA1000817,	HEMBA1000822,	HEMBA1000843,	HEMBA1000851,	HEMBA1000852,	HEMBA1000867,
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	HEMBA1000918,	HEMBA1000919,	HEMBA1000934,	HEMBA1000942,	HEMBA1000943,	HEMBA1000946,
15	HEMBA1000960,	HEMBA1000968,	HEMBA1000971,	HEMBA1000972,	HEMBA1000975,	HEMBA1000985,
	HEMBA1000986,	HEMBA1000991,	HEMBA1001008,	HEMBA1001009,	HEMBA1001019,	HEMBA1001020,
	HEMBA1001022,	HEMBA1001024,	HEMBA1001026,	HEMBA1001043,	HEMBA1001051,	HEMBA1001052,
	HEMBA1001059,	HEMBA1001060,	HEMBA1001071,	HEMBA1001077,	HEMBA1001080,	HEMBA1001085,
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	THYRO1001321,	THYRO1001322,	THYRO1001347,	THYRO1001363,	THYRO1001365,	THYRO1001374,
	THYRO1001401,	THYRO1001403,	THYRO1001405,	THYRO1001406,	THYRO1001411,	THYRO1001426,
	THYRO1001434,	THYRO1001458,	THYRO1001480,	THYRO1001487,	THYRO1001534,	THYRO1001537,
	THYRO1001541,	THYRO1001559,	THYRO1001570,	THYRO1001584,	THYRO1001595,	THYRO1001602,
50	THYRO1001605,	THYRO1001617,	THYRO1001637,	THYRO1001656,	THYRO1001661,	THYRO1001671,
	THYRO1001673,	THYRO1001703,	THYRO1001706,	THYRO1001721,	THYRO1001738,	THYRO1001745,
	THYRO1001746,	THYRO1001772,	THYRO1001793,	THYRO1001809,	THYRO1001828,	THYRO1001854,
	THYRO1001895,	THYRO1001907,	VESEN1000122,	Y79AA1000013,	Y79AA1000033,	Y79AA1000037,
	Y79AA1000059,	Y79AA1000065,	Y79AA1000131,	Y79AA1000181,	Y79AA1000202,	Y79AA1000214,
55	Y79AA1000230,	Y79AA1000231,	Y79AA1000258,	Y79AA1000268,	Y79AA1000313,	Y79AA1000328,
	Y79AA1000342,	Y79AA1000346,	Y79AA1000349,	Y79AA1000355,	Y79AA1000368,	Y79AA1000410,
	Y79AA1000420,	Y79AA1000469,	Y79AA1000480,	Y79AA1000539,	Y79AA1000540,	Y79AA1000560,
	Y79AA1000574,	Y79AA1000589,	Y79AA1000627,	Y79AA1000705,	Y79AA1000734,	Y79AA1000748,

Y79AA1000752,	Y79AA1000774,	Y79AA1000782,	Y79AA1000784,	Y79AA1000794,	Y79AA1000800,
Y79AA1000802,	Y79AA1000805,	Y79AA1000824,	Y79AA1000827,	Y79AA1000833,	Y79AA1000850,
Y79AA1000962,	Y79AA1000966,	Y79AA1000968,	Y79AA1000969,	Y79AA1000976,	Y79AA1000985,
Y79AA1001023,	Y79AA1001041,	Y79AA1001048,	Y79AA1001061,	Y79AA1001068,	Y79AA1001077,
Y79AA1001078,	Y79AA1001145,	Y79AA1001167,	Y79AA1001177,	Y79AA1001185,	Y79AA1001211,
Y79AA1001216,	Y79AA1001228,	Y79AA1001233,	Y79AA1001236,	Y79AA1001281,	Y79AA1001299,
Y79AA1001312,	Y79AA1001323,	Y79AA1001384,	Y79AA1001391,	Y79AA1001394,	Y79AA1001402,
Y79AA1001493,	Y79AA1001511,	Y79AA1001533,	Y79AA1001541,	Y79AA1001548,	Y79AA1001555,
Y79AA1001581,	Y79AA1001585,	Y79AA1001594,	Y79AA1001603,	Y79AA1001613,	Y79AA1001647,
Y79AA1001665,	Y79AA1001679,	Y79AA1001692,	Y79AA1001696,	Y79AA1001705,	Y79AA1001711,
Y79AA1001781,	Y79AA1001805,	Y79AA1001827,	Y79AA1001846,	Y79AA1001866,	Y79AA1001874,
Y79AA1001875,	Y79AA1001923,	Y79AA1001963,	Y79AA1002027,	Y79AA1002083,	Y79AA1002089,
Y79AA1002103,	Y79AA1002115,	Y79AA1002125,	Y79AA1002139,	Y79AA1002204,	Y79AA1002208,
Y79AA1002209,	Y79AA1002210,	Y79AA1002211,	Y79AA1002220,	Y79AA1002229,	Y79AA1002234,
Y79AA1002246,	Y79AA1002258,	Y79AA1002298,	Y79AA1002307,	Y79AA1002311,	Y79AA1002351,
Y79AA1002361,	Y79AA1002399,	Y79AA1002407,	Y79AA1002416,	Y79AA1002431,	Y79AA1002433,
Y79AA1002472,	Y79AA1002482,	Y79AA1002487,			

**[0258]** Among the 4997 clones, there are 2189 clones that presumably encode proteins belonging to any of the categories of secretory or membrane proteins, glycoprotein-associated proteins, signal transduction-associated proteins, transcription-associated proteins, disease-associated proteins, enzymes and/or metabolism-associated proteins, ATP- and/or GTP-binding proteins, nuclear proteins, DNA- and/or RNA-binding proteins, RNA synthesis-associated proteins, protein synthesis- and/or protein transport-associated proteins, cytoskeleton-associated proteins, cell division- and/or cell proliferation-associated proteins, embryogenesis- and/or development-associated proteins, or cellular defense-associated proteins.

**[0259]** The clones that presumably encode proteins belonging to the category of secretory or membrane proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "growth factor", "cytokine", "hormone", "signal", "transmembrane", "membrane", "extracellular matrix", "receptor", "G-protein coupled receptor", "ionic channel", "voltage-gated channel", "calcium channel", "cell adhesion", "collagen", or "connective tissue"; those which matched the data, suggesting that the proteins are secretory or membrane proteins; or those which matched the full-length sequences of GenBank or UniGene database with similar description; and, further, those predicted to have an N-terminal signal sequence or a transmembrane region as a result of domain search for the amino acid sequences deduced from the full-length nucleotide sequences.

**[0260]** The clones that presumably encode proteins belonging to the category of glycoprotein-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "glycoprotein"; those which matched the data, suggesting that the proteins are glycoprotein; or those which matched the full-length sequences of GenBank or UniGene database with similar description.

**[0261]** The clones that presumably encode proteins belonging to the category of signal transduction-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "serine/threonine-protein kinase", "tyrosine-protein kinase", or "SH3 domain"; those which matched the data, suggesting that the proteins are signal transduction-associated proteins (for example, "ADP-ribosylation factor"); or those which matched the full-length sequences of GenBank or UniGene database with similar description.

**[0262]** The clones that presumably encode proteins belonging to the category of transcription-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "transcription regulation", "zinc finger", or "homeobox"; those which matched the data, suggesting that the proteins are transcription-associated proteins; or those which matched the full-length sequences of GenBank or UniGene database with similar description.

**[0263]** The clones that presumably encode proteins belonging to the category of disease-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "disease mutation" or "syndrome"; those which matched the data, suggesting that the proteins are disease-associated proteins; or those which matched the full-length sequences of Swiss-Prot database and GenBank or UniGene database where the matched sequences of genes or proteins which had been registered in the database of Online Mendelian Inheritance in Man (OMIM) (<http://www.ncbi.nlm.nih.gov/OMIM/>), which is a database of human genes and diseases.

**[0264]** The clones that presumably encode proteins belonging to the category of enzymes and/or metabolism-associated proteins are those which showed the terms "metabolism", "oxidoreductase", or "E.C. No. (Enzyme commission number)" in the matching data.

**[0265]** The clones that presumably encode proteins belonging to the category of ATP- and/or GTP-binding proteins are those which matched the data with the terms "ATP-binding" or "GTP-binding".

**[0266]** The clones that presumably encode proteins belonging to the category of nuclear proteins are those which matched the data with the terms "nuclear protein".



**[0267]** The clones that presumably encode proteins belonging to the category of DNA- and/or RNA-binding proteins are those which matched the data with the terms "DNA-binding" or "RNA-binding".

**[0268]** The clones that presumably encode proteins belonging to the category of RNA synthesis-associated proteins are those which matched the data with the terms "RNA splicing", "RNA processing", "RNA helicase", or "polyadenylation".

**[0269]** The clones that presumably encode proteins belonging to the category of protein synthesis- and/or protein transport-associated proteins are those which matched the data with the terms "translation regulation", "protein biosynthesis", "amino-acid biosynthesis", "ribosomal protein", "protein transport", or "signal recognition particle".

**[0270]** The clones that presumably encode proteins belonging to the category of cytoskeleton-associated proteins are those which matched the data with the terms "structural protein", "cytoskeleton", "actin-binding", or "microtubules".

**[0271]** The clones that presumably encode proteins belonging to the category of cell division- and/or cell proliferation-associated proteins are those which matched the data with the terms "cell division", "cell cycle", "mitosis", "chromosomal protein", "cell growth", or "apoptosis".

**[0272]** The clones that presumably encode proteins belonging to the category of embryogenesis- and/or development-associated proteins are those which matched the data with the terms "developmental protein".

**[0273]** The clones that presumably encode proteins belonging to the category of cellular defense-associated proteins are those which matched the data with the terms "heat shock", "DNA repair", or "DNA damage".

**[0274]** When a clone belonged to the above-mentioned multiple functional categories, the clone was classified into the multiple categories. However, the functions of the protein encoded by the clone are not limited to the functions of the categories into which the clone was classified, and therefore, additional functions can be found for the protein by further analyses.

**[0275]** The following 796 clones are categorized into secretory or membrane proteins.

HEMBA1000356,	HEMBA1000518,	HEMBA1000531,	HEMBA1000637,	HEMBA1000719,	HEMBA1000817,
HEMBA1000822,	HEMBA1000852,	HEMBA1000870,	HEMBA1000991,	HEMBA1001052,	HEMBA1001071,
HEMBA1001085,	HEMBA1001286,	HEMBA1001351,	HEMBA1001407,	HEMBA1001446,	HEMBA1001515,
HEMBA1001557,	HEMBA1001569,	HEMBA1001661,	HEMBA1001734,	HEMBA1001746,	HEMBA1001866,
HEMBA1002125,	HEMBA1002150,	HEMBA1002166,	HEMBA1002417,	HEMBA1002462,	HEMBA1002475,
HEMBA1002477,	HEMBA1002486,	HEMBA1002609,	HEMBA1002659,	HEMBA1002661,	HEMBA1002780,
HEMBA1002818,	HEMBA1002876,	HEMBA1002921,	HEMBA1003071,	HEMBA1003077,	HEMBA1003079,
HEMBA1003086,	HEMBA1003096,	HEMBA1003281,	HEMBA1003286,	HEMBA1003538,	HEMBA1003711,
HEMBA1003742,	HEMBA1003803,	HEMBA1004055,	HEMBA1004143,	HEMBA1004146,	HEMBA1004207,
HEMBA1004341,	HEMBA1004461,	HEMBA1004577,	HEMBA1004637,	HEMBA1004752,	HEMBA1004756,
HEMBA1004850,	HEMBA1004889,	HEMBA1004923,	HEMBA1004930,	HEMBA1005029,	HEMBA1005035,
HEMBA1005050,	HEMBA1005552,	HEMBA1005576,	HEMBA1005581,	HEMBA1005588,	HEMBA1005616,
HEMBA1005699,	HEMBA1005991,	HEMBA1006036,	HEMBA1006038,	HEMBA1006067,	HEMBA1006173,
HEMBA1006198,	HEMBA1006293,	HEMBA1006310,	HEMBA1006492,	HEMBA1006502,	HEMBA1006583,
HEMBA1006659,	HEMBA1006758,	HEMBA1006789,	HEMBA1006921,	HEMBA1006926,	HEMBA1006976,
HEMBA1007203,	HEMBA1007301,	HEMBA1000037,	HEMBA1000050,	HEMBA1000054,	HEMBA1000175,
HEMBA1000317,	HEMBA1000556,	HEMBA1000593,	HEMBA1000631,	HEMBA1000763,	HEMBA1000827,
HEMBA1000915,	HEMBA1000975,	HEMBA1001112,	HEMBA1001151,	HEMBA1001177,	HEMBA1001302,
HEMBA1001348,	HEMBA1001564,	HEMBA1001630,	HEMBA1001871,	HEMBA1001872,	HEMBA1001925,
HEMBA1001962,	HEMBA1002042,	HEMBA1002044,	HEMBA1002142,	HEMBA1002190,	HEMBA1002193,
HEMBA1002247,	HEMBA1002383,	HEMBA1002387,	HEMBA1002350,	HEMBA1002600,	HEMBA1002692,
MAMMA1000045,	MAMMA1000129,	MAMMA1000133,	MAMMA1000277,	MAMMA1000278,	MAMMA1000410,
MAMMA1000416,	MAMMA1000472,	MAMMA1000672,	MAMMA1000684,	MAMMA1000714,	MAMMA1000734,
MAMMA1000778,	MAMMA1000798,	MAMMA1000842,	MAMMA1000859,	MAMMA1000897,	MAMMA1000956,
MAMMA1001008,	MAMMA1001030,	MAMMA1001041,	MAMMA1001073,	MAMMA1001080,	MAMMA1001139,
MAMMA1001154,	MAMMA1001322,	MAMMA1001388,	MAMMA1001411,	MAMMA1001487,	MAMMA1001751,
MAMMA1001754,	MAMMA1001771,	MAMMA1002009,	MAMMA1002427,	MAMMA1002428,	MAMMA1002461,
MAMMA1002524,	MAMMA1002573,	MAMMA1002598,	MAMMA1002655,	MAMMA1002684,	MAMMA1002769,
MAMMA1002844,	MAMMA1002881,	MAMMA1002890,	MAMMA1002938,	MAMMA1002947,	MAMMA1003035,
MAMMA1003089,	MAMMA1003146,	MAMMA1003150,	NT2RM1000035,	NT2RM1000037,	NT2RM1000062,
NT2RM1000080,	NT2RM1000092,	NT2RM1000131,	NT2RM1000199,	NT2RM1000257,	NT2RM1000260,
NT2RM1000355,	NT2RM1000430,	NT2RM1000563,	NT2RM1000648,	NT2RM1000742,	NT2RM1000770,
NT2RM1000800,	NT2RM1000811,	NT2RM1000833,	NT2RM1000857,	NT2RM1000867,	NT2RM1000882,
NT2RM1000905,	NT2RM1001008,				
NT2RM1001115,	NT2RM1001139,	NT2RM2000259,	NT2RM2000260,	NT2RM2000287,	NT2RM2000395,
NT2RM2000402,	NT2RM2000407,	NT2RM2000422,	NT2RM2000490,	NT2RM2000522,	NT2RM2000566,

	NT2RM2000581,	NT2RM2000609,	NT2RM2000821,	NT2RM2001370,	NT2RM2001393,	NT2RM2001499,
	NT2RM2001547,	NT2RM2001613,	NT2RM2001648,	NT2RM2001659,	NT2RM2001671,	NT2RM2001688,
	NT2RM2001698,	NT2RM2001718,	NT2RM2001753,	NT2RM2001760,	NT2RM2001785,	NT2RM2001930,
	NT2RM2001950,	NT2RM2001997,	NT2RM2001998,	NT2RM2002049,	NT2RM2002145,	NT2RM4000233,
5	NT2RM4000433,	NT2RM4000457,	NT2RM4000486,	NT2RM4000496,	NT2RM4000520,	NT2RM4000634,
	NT2RM4000674,	NT2RM4000700,	NT2RM4000764,	NT2RM4000778,	NT2RM4000795,	NT2RM4000820,
	NT2RM4000857,	NT2RM4001032,	NT2RM4001054,	NT2RM4001116,	NT2RM4001455,	NT2RM4001666,
	NT2RM4001810,	NT2RM4001813,	NT2RM4001930,	NT2RM4001987,	NT2RM4002054,	NT2RM4002073,
	NT2RM4002145,	NT2RM4002146,	NT2RM4002189,	NT2RM4002194,	NT2RM4002251,	NT2RM4002339,
10	NT2RM4002438,	NT2RM4002446,	NT2RM4002452,	NT2RM4002460,	NT2RM4002493,	NT2RM4002558,
	NT2RM4002565,	NT2RM4002571,	NT2RM4002594,	NT2RP1000130,	NT2RP1000191,	NT2RP1000326,
	NT2RP1000358,	NT2RP1000413,	NT2RP1000418,	NT2RP1000547,	NT2RP1000609,	NT2RP1000677,
	NT2RP1000767,	NT2RP1000782,	NT2RP1000856,	NT2RP1001113,	NT2RP1001247,	NT2RP1001286,
	NT2RP1001310,	NT2RP1001311,	NT2RP1001313,	NT2RP1001385,	NT2RP1001449,	NT2RP1001546,
15	NT2RP1001569,	NT2RP2000032,	NT2RP2000040,	NT2RP2000056,	NT2RP2000070,	NT2RP2000091,
	NT2RP2000114,	NT2RP2000120,	NT2RP2000173,	NT2RP2000175,	NT2RP2000195,	NT2RP2000257,
	NT2RP2000270,	NT2RP2000283,	NT2RP2000288,	NT2RP2000289,	NT2RP2000459,	NT2RP2000516,
	NT2RP2000660,	NT2RP2000684,	NT2RP2000892,	NT2RP2001081,	NT2RP2001268,	NT2RP2001295,
	NT2RP2001366,	NT2RP2001378,	NT2RP2001576,	NT2RP2001581,	NT2RP2001597,	NT2RP2001613,
20	NT2RP2001947,	NT2RP2001991,	NT2RP2002025,	NT2RP2002066,	NT2RP2002078,	NT2RP2002105,
	NT2RP2002312,	NT2RP2002325,	NT2RP2002385,	NT2RP2002479,	NT2RP2002537,	NT2RP2002643,
	NT2RP2002701,	NT2RP2002740,	NT2RP2002857,	NT2RP2003125,	NT2RP2003297,	NT2RP2003433,
	NT2RP2003446,	NT2RP2003466,	NT2RP2003506,	NT2RP2003513,	NT2RP2003629,	NT2RP2003668,
	NT2RP2003760,	NT2RP2003777,	NT2RP2003781,	NT2RP2004041,	NT2RP2004142,	NT2RP2004194,
25	NT2RP2004270,	NT2RP2004300,	NT2RP2004392,	NT2RP2004655,	NT2RP2004681,	NT2RP2004775,
	NT2RP2004799,	NT2RP2004936,	NT2RP2004959,	NT2RP2005012,	NT2RP2005159,	NT2RP2005227,
	NT2RP2005270,	NT2RP2005344,	NT2RP2005465,	NT2RP2005509,	NT2RP2005752,	NT2RP2005781,
	NT2RP2005784,	NT2RP2005812,	NT2RP2006069,	NT2RP2006100,	NT2RP2006141,	NT2RP2006184,
	NT2RP2006261,	NT2RP2006565,	NT2RP2006571,	NT2RP2006573,	NT2RP3000092,	NT2RP3000109,
30	NT2RP3000134,	NT2RP3000207,	NT2RP3000333,	NT2RP3000341,	NT2RP3000393,	NT2RP3000439,
	NT2RP3000441,	NT2RP3000531,	NT2RP3000685,	NT2RP3000825,	NT2RP3000826,	NT2RP3000852,
	NT2RP3000919,	NT2RP3001084,	NT2RP3001096,	NT2RP3001126,	NT2RP3001140,	NT2RP3001176,
	NT2RP3001260,	NT2RP3001282,	NT2RP3001355,	NT2RP3001383,	NT2RP3001426,	NT2RP3001453,
	NT2RP3001497,	NT2RP3001538,	NT2RP3001589,	NT2RP3001642,	NT2RP3001708,	NT2RP3001716,
35	NT2RP3001727,	NT2RP3001739,	NT2RP3001799,	NT2RP3001943,	NT2RP3001944,	NT2RP3002002,
	NT2RP3002007,	NT2RP3002014,	NT2RP3002054,	NT2RP3002108,	NT2RP3002163,	NT2RP3002351,
	NT2RP3002455,	NT2RP3002549,	NT2RP3002602,	NT2RP3002628,	NT2RP3002650,	NT2RP3002687,
	NT2RP3002701,	NT2RP3002810,	NT2RP3002869,	NT2RP3002969,	NT2RP3002985,	NT2RP3003008,
	NT2RP3003059,	NT2RP3003071,	NT2RP3003101,	NT2RP3003145,	NT2RP3003197,	NT2RP3003203,
40	NT2RP3003242,	NT2RP3003302,	NT2RP3003353,	NT2RP3003409,	NT2RP3003576,	NT2RP3003621,
	NT2RP3003665,	NT2RP3003672,	NT2RP3003701,	NT2RP3003716,	NT2RP3003799,	NT2RP3003828,
	NT2RP3003914,	NT2RP3003918,	NT2RP3003992,	NT2RP3004051,	NT2RP3004148,	NT2RP3004155,
	NT2RP3004207,	NT2RP3004282,	NT2RP3004454,	NT2RP3004480,	NT2RP3004503,	NT2RP4000008,
	NT2RP4000051,	NT2RP4000151,	NT2RP4000212,	NT2RP4000243,	NT2RP4000259,	NT2RP4000323,
45	NT2RP4000417,	NT2RP4000500,	NT2RP4000524,	NT2RP4000556,	NT2RP4000560,	NT2RP4000588,
	NT2RP4000713,	NT2RP4000724,	NT2RP4000817,	NT2RP4000833,	NT2RP4000878,	NT2RP4000907,
	NT2RP4000925,	NT2RP4000928,	NT2RP4000973,	NT2RP4000989,	NT2RP4001057,	NT2RP4001064,
	NT2RP4001079,	NT2RP4001117,	NT2RP4001138,	NT2RP4001149,	NT2RP4001150,	NT2RP4001174,
	NT2RP4001219,	NT2RP4001274,	NT2RP4001313,	NT2RP4001345,	NT2RP4001372,	NT2RP4001373,
50	NT2RP4001379,	NT2RP4001498,	NT2RP4001547,	NT2RP4001571,	NT2RP4001574,	NT2RP4001644,
	NT2RP4001656,	NT2RP4001677,	NT2RP4001730,	NT2RP4001739,	NT2RP4001803,	NT2RP4001822,
	NT2RP4001823,	NT2RP4001950,	NT2RP4001975,	NT2RP4002052,	NT2RP4002075,	NT2RP5003500,
	NT2RP5003506,	NT2RP5003522,	NT2RP5003534,	OVARC1000060,	OVARC1000335,	OVARC1000682,
	OVARC1000689,	OVARC1000700,	OVARC1000722,	OVARC1000751,	OVARC1000850,	OVARC1000890,
55	OVARC1000924,	OVARC1000936,	OVARC1000959,	OVARC1000984,	OVARC1000999,	OVARC1001034,
	OVARC1001055,	OVARC1001117,	OVARC1001129,	OVARC1001154,	OVARC1001329,	OVARC1001381,
	OVARC1001391,	OVARC1001453,	OVARC1001476,	OVARC1001506,	OVARC1001610,	OVARC1001702,
	OVARC1001703,	OVARC1001713,	OVARC1001745,	OVARC1001767,	OVARC1002127,	OVARC1002138,

	OVARC1002158,	OVARC1002165,	PLACE1000014,	PLACE1000213,	PLACE1000401,	PLACE1000562,
	PLACE1000611,	PLACE1000656,	PLACE1000712,	PLACE1 000793,	PLACE1000909,	PLACE1000948,
	PLACE1000977,	PLACE1001241,	PLACE1001257,	PLACE1001377,	PLACE1001517,	PLACE1001610,
	PLACE1001761,	PLACE1001771,	PLACE1001817,	PLACE1001983,	PLACE1002046,	PLACE1002140,
5	PLACE1002213,	PLACE1002395,	PLACE1002437,	PLACE1002500,	PLACE1002583,	PLACE1002714,
	PLACE1002722,	PLACE1002782,	PLACE1002794,	PLACE1002851,	PLACE1002908,	PLACE1003030,
	PLACE1003044,	PLACE1003045,	PLACE1003238,	PLACE1003296,	PLACE1003369,	PLACE1003420,
	PLACE1003493,	PLACE1003537,	PLACE1003553,	PLACE1003596,	PLACE1003760,	PLACE1003768,
	PLACE1003771,	PLACE1003903,	PLACE1004149,	PLACE1004197,	PLACE1004203,	PLACE1004258,
10	PLACE1004270,	PLACE1004277,	PLACE1004289,	PLACE1004473,	PLACE1004629,	PLACE1004646,
	PLACE1004743,	PLACE1004751,	PLACE1004793,	PLACE1004840,	PLACE1004969,	PLACE1005086,
	PLACE1005162,	PLACE1005206,	PLACE1005313,	PLACE1005467,	PLACE1005530,	PLACE1005595,
	PLACE1005611,	PLACE1005623,	PLACE1005763,	PLACE1005884,	PLACE1005890,	PLACE1005898,
	PLACE1005934,	PLACE1005953,	PLACE1006157,	PLACE1006225,	PLACE1006239,	PLACE1006288,
15	PLACE1006492,	PLACE1006534,	PLACE1006678,	PLACE1006754,	PLACE1006901,	PLACE1006935,
	PLACE1006956,	PLACE1007111,	PLACE1007243,	PLACE1007274,	PLACE1007282,	PLACE1007317,
	PLACE1007375,	PLACE1007386,	PLACE1007409,	PLACE1007416,	PLACE1007484,	PLACE1007583,
	PLACE1007632,	PLACE1007645,	PLACE1007649,	PLACE1007852,	PLACE1007877,	PLACE1007954,
	PLACE1008273,	PLACE1008309,	PLACE1008331,	PLACE1008402,	PLACE1008424,	PLACE1008429,
20	PLACE1008531,	PLACE1008532,	PLACE1008533,	PLACE1008568,	PLACE1008643,	PLACE1008693,
	PLACE1008715,	PLACE1009045,	PLACE1009094,	PLACE1009298,	PLACE1009319,	PLACE1009338,
	PLACE1009368,	PLACE1009493,	PLACE1009639,	PLACE1009659,	PLACE1009708,	PLACE1009731,
	PLACE1009845,	PLACE1009861,	PLACE1009935,	PLACE1009992,	PLACE1010089,	PLACE1010231,
	PLACE1010321,	PLACE1010362,	PLACE1010599,	PLACE1010622,	PLACE1010662,	PLACE1010811,
25	PLACE1010917,	PLACE1010942,	PLACE1010954,	PLACE1011090,	PLACE1011214,	PLACE1011221,
	PLACE1011371,	PLACE1011399,	PLACE1011492,	PLACE1011646,	PLACE1011749,	PLACE1011896,
	PLACE2000034,	PLACE2000062,	PLACE2000111,	PLACE2000132,	PLACE2000176,	PLACE2000187,
	PLACE2000216,	PLACE2000335,	PLACE2000341,	PLACE2000373,	PLACE2000379,	PLACE2000398,
	PLACE2000399,	PLACE2000425,	PLACE2000436,	PLACE2000458,	PLACE2000477,	PLACE3000020,
30	PLACE3000218,	PLACE3000226,	PLACE3000242,	PLACE3000244,	PLACE3000339,	PLACE3000373,
	PLACE3000399,	PLACE3000406,	PLACE3000413,	PLACE3000455,	PLACE4000052,	PLACE4000063,
	PLACE4000129,	PLACE4000247,	PLACE4000250,	PLACE4000259,	PLACE4000300,	PLACE4000387,
	PLACE4000431,	PLACE4000487,	PLACE4000494,	PLACE4000522,	PLACE4000548,	PLACE4000581,
	PLACE4000593,	PLACE4000650,	THYRO1000156,	THYRO1000327,	THYRO1000394,	THYRO1000395,
35	THYRO1000570,	THYRO1000748,	THYRO1000756,	THYRO1000783,	THYRO1001134,	THYRO1001271,
	THYRO1001287,	THYRO1001320,	THYRO1001401,	THYRO1001534,	THYRO1001537,	THYRO1001541,
	THYRO1001828,	Y79AA1000258,	Y79AA1000420,	Y79AA1000469,	Y79AA1000734,	Y79AA1000800,
	Y79AA1000976,	Y79AA1001023,	Y79AA1001177,	Y79AA1001384,	Y79AA1001394,	Y79AA1001603,
	Y79AA1001647,	Y79AA1001846,	Y79AA1001874,	Y79AA1002139,	Y79AA1002246,	Y79AA1002351,
40	Y79AA1002399,	Y79AA1002416,				
[0276] The following 141 clones are categorized into glycoproteins-associated proteins.						
	HEMBA1000156,	HEMBA1000518,	HEMBA1000852,	HEMBA1001071,	HEMBA1001286,	HEMBA1001661,
	HEMBA1001734,	HEMBA1001866,	HEMBA1003071,	HEMBA1003077,	HEMBA1003281,	HEMBA1003538,
	HEMBA1003679,	HEMBA1003866,	HEMBA1005576,	HEMBA1005581,	HEMBA1005699,	HEMBA1006038,
45	HEMBA1006976,	HEMBA1007301,	HEMBA1008317,	HEMBA1009915,	HEMBA1001871,	HEMBA1001872,
	HEMBA1002193,	MAMMA1000672,	MAMMA1000897,	MAMMA1001030,	MAMMA1001388,	MAMMA1002329,
	MAMMA1002428,	MAMMA1002573,	MAMMA1003150,	MAMMA1000648,	NT2RM1001115,	NT2RM2000260,
	NT2RM2000407,	NT2RM2000422,	NT2RM2000490,	NT2RM2001499,	NT2RM2001659,	NT2RM2001930,
	NT2RM4000820,	NT2RM4000857,	NT2RM4001810,	NT2RM4001813,	NT2RM4001987,	NT2RM4002145,
50	NT2RM4002189,	NT2RM4002251,	NT2RM4002460,	NT2RM4002558,	NT2RP1000677,	NT2RP1000782,
	NT2RP1000856,	NT2RP1001546,	NT2RP2000056,	NT2RP2000070,	NT2RP2001295,	NT2RP2001376,
	NT2RP2001597,	NT2RP2001991,	NT2RP2002025,	NT2RP2002078,	NT2RP2002385,	NT2RP2004587,
	NT2RP2004732,	NT2RP2005531,	NT2RP3000207,	NT2RP3000531,	NT2RP3000825,	NT2RP3001140,
	NT2RP3002810,	NT2RP3003672,	NT2RP3003701,	NT2RP3003716,	NT2RP3003914,	NT2RP3004148,
55	NT2RP4000212,	NT2RP4000417,	NT2RP4000724,	NT2RP4000817,	NT2RP4000925,	NT2RP4001150,
	NT2RP4001372,	NT2RP4001730,	NT2RP4001822,	NT2RP4001823,	NT2RP5003522,	NT2RP5000091,
	OVARC1000288,	OVARC1000682,	OVARC1001055,	OVARC1001506,	OVARC1001713,	OVARC1002127,
	PLACE1000213,	PLACE1000401,	PLACE1002437,	PLACE1002583,		

	PLACE1002722,	PLACE1003045,	PLACE1003238,	PLACE1003258,	PLACE1003493,	PLACE1004197,
	PLACE1004793,	PLACE1005953,	PLACE1005955,	PLACE1006157,	PLACE1006239,	PLACE1006368,
	PLACE1006534,	PLACE1006754,	PLACE1006956,	PLACE1007416,	PLACE1007632,	PLACE1007649,
	PLACE1008643,	PLACE1009094,	PLACE1009992,	PLACE1010231,	PLACE1010662,	PLACE1011371,
5	PLACE2000034,	PLACE2000373,	PLACE2000398,	PLACE2000399,	PLACE2000438,	PLACE2000458,
	PLACE3000339,	PLACE4000063,	PLACE4000230,	PLACE4000522,	PLACE4000548,	PLACE4000581,
	THYRO1003327,	THYRO1000756,	THYRO1001287,	Y79AA1001603,	Y79AA1001874	
	[0277] The following 129 clones are categorized into signal transduction-associated proteins.					
	HEMBA1000303,	HEMBA1000369,	HEMBA1000608,	HEMBA1000657,	HEMBA1000919,	HEMBA1001019,
10	HEMBA1001174,	HEMBA1001822,	HEMBA1001921,	HEMBA1002139,	HEMBA1002212,	HEMBA1002341,
	HEMBA1002417,	HEMBA1002768,	HEMBA1003250,	HEMBA1003291,	HEMBA1003645,	HEMBA1004286,
	HEMBA1005737,	HEMBA1006130,	HEMBA1006708,	HEMBA1000083,	HEMBA1000266,	HEMBA1000632,
	HEMBA1000781,	HEMBA1000831,	HEMBA1002193,	MAMMA1000173,	MAMMA1001038,	MAMMA1001198,
	MAMMA1002842,	MAMMA1003057,	NT2RM1000702,	NT2RM1000772,	NT2RM1001072,	NT2RM2000030,
15	NT2RM2000469,	NT2RM2000612,	NT2RM2001221,	NT2RM2001345,	NT2RM2002128,	NT2RM2000029,
	NT2RM4000354,	NT2RM4000611,	NT2RM4000798,	NT2RM4001411,	NT2RM4001412,	NT2RM4001629,
	NT2RM4001758,	NT2RM4002013,	NT2RM4002527,	NT2RP1000018,	NT2RP1000701,	NT2RP1001294,
	NT2RP1001302,	NT2RP2000668,	NT2RP2001440,	NT2RP2001560,	NT2RP2002058,	NT2RP2002193,
	NT2RP2002408,	NT2RP2002710,	NT2RP2002929,	NT2RP2003164,	NT2RP2003912,	NT2RP2004232,
20	NT2RP2004768,	NT2RP2006071,	NT2RP2006534,	NT2RP3000759,	NT2RP3000845,	NT2RP3001646,
	NT2RP3001857,	NT2RP3001938,	NT2RP3002004,	NT2RP3002785,	NT2RP3002909,	NT2RP3002986,
	NT2RP3003800,	NT2RP3004189,	NT2RP3004544,	NT2RP4000147,	NT2RP4000839,	NT2RP4001122,
	NT2RP4001148,	NT2RP4001336,	NT2RP4001375,	NT2RP4001644,	NT2RP4001725,	NT2RP4001849,
	NT2RP4001896,	NT2RP4001927,	NT2RP4002408,	NT2RP5003477,	OVARC1000013,	OVARC1000437,
25	OVARC1000556,	OVARC1000649,	OVARC1000945,	OVARC1001200,	OVARC1002182,	PLACE1000977,
	PLACE1001387,	PLACE1002493,	PLACE1002591,	PLACE1003190,	PLACE1003353,	PLACE1004128,
	PLACE1004302,	PLACE1004937,	PLACE1005243,	PLACE1008000,	PLACE1008244,	PLACE1008650,
	PLACE1009468,	PLACE1009586,	PLACE1009708,	PLACE1009845,	PLACE1010926,	PLACE1011041,
	PLACE2000164,	PLACE2000371,	PLACE3000145,	PLACE3000350,	THYRO1000072,	THYRO1000748,
30	THYRO1001120,	Y79AA1000328,	Y79AA1002431			
	[0278] The following 309 clones are categorized into transcription-associated proteins.					
	HEMBA1000158,	HEMBA1000201,	HEMBA1000216,	HEMBA1000555,	HEMBA1000561,	HEMBA1000851,
	HEMBA1001077,	HEMBA1001137,	HEMBA1001405,	HEMBA1001510,	HEMBA1001635,	HEMBA1001804,
	HEMBA1001809,	HEMBA1001819,	HEMBA1001847,	HEMBA1001869,	HEMBA1002035,	HEMBA1002092,
35	HEMBA1002177,	HEMBA1002270,	HEMBA1002935,	HEMBA1003408,	HEMBA1003545,	HEMBA1003568,
	HEMBA1003662,	HEMBA1003684,	HEMBA1003760,	HEMBA1003953,	HEMBA1004097,	HEMBA1004321,
	HEMBA1004353,	HEMBA1004389,	HEMBA1004479,	HEMBA1004758,	HEMBA1004973,	HEMBA1005219,
	HEMBA1005359,	HEMBA1005513,	HEMBA1005528,	HEMBA1005548,	HEMBA1005558,	HEMBA1005931,
	HEMBA1006158,	HEMBA1006248,	HEMBA1006278,	HEMBA1006283,	HEMBA1006347,	HEMBA1006359,
40	HEMBA1006559,	HEMBA1006941,	HEMBA1000789,	HEMBA1001011,	HEMBA1001314,	HEMBA1001482,
	HEMBA1001673,	HEMBA1001749,	HEMBA1001839,	HEMBA1001908,	HEMBA1002134,	HEMBA1002217,
	HEMBA1002342,	HEMBA1002607,	MAMMA1000183,	MAMMA1000388,	MAMMA1001105,	MAMMA1001222,
	MAMMA1001260,	MAMMA1001627,	MAMMA1001633,	MAMMA1001743,	MAMMA1001820,	MAMMA1001837,
	MAMMA1002617,	MAMMA1002650,	MAMMA1002937,	NT2RM1000055,	NT2RM1000086,	NT2RM1000746,
45	NT2RM1000885,	NT2RM1000894,	NT2RM1001092,	NT2RM2000013,	NT2RM2000452,	NT2RM2000735,
	NT2RM2000740,	NT2RM2001035,	NT2RM2001105,	NT2RM2001575,	NT2RM2001670,	NT2RM2001716,
	NT2RM2001771,	NT2RM2002091,	NT2RM4000024,	NT2RM4000046,	NT2RM4000104,	NT2RM4000202,
	NT2RM4000531,	NT2RM4000595,	NT2RM4000733,	NT2RM4000734,		
	NT2RM4000741,	NT2RM4000751,	NT2RM4000966,	NT2RM4001092,	NT2RM4001140,	NT2RM4001200,
50	NT2RM4001483,	NT2RM4001592,	NT2RM4001783,	NT2RM4001823,	NT2RM4001828,	NT2RM4001858,
	NT2RM4001979,	NT2RM4002066,	NT2RP1000086,	NT2RP1000111,	NT2RP1000574,	NT2RP1000902,
	NT2RP1001013,	NT2RP2000008,	NT2RP2000126,	NT2RP2000297,	NT2RP2000420,	NT2RP2001174,
	NT2RP2001233,	NT2RP2001756,	NT2RP2001869,	NT2RP2002046,	NT2RP2002252,	NT2RP2002270,
	NT2RP2002464,	NT2RP2002503,	NT2RP2002520,	NT2RP2002591,	NT2RP2002880,	NT2RP2002939,
55	NT2RP2002993,	NT2RP2003243,	NT2RP2003329,	NT2RP2003347,	NT2RP2003480,	NT2RP2003522,
	NT2RP2003564,	NT2RP2003714,	NT2RP2004013,	NT2RP2004066,	NT2RP2004187,	NT2RP2004920,
	NT2RP2004961,	NT2RP2005003,	NT2RP2005139,	NT2RP2005325,	NT2RP2005496,	NT2RP2005701,
	NT2RP2005722,	NT2RP2005776,	NT2RP2005942,	NT2RP2006238,	NT2RP2006436,	NT2RP3000050,

	NT2RP3000320, NT2RP3000632, NT2RP3001268, NT2RP3002165, NT2RP3003313, NT2RP3004428, NT2RP4000455, NT2RP4001080, NT2RP4001638, NT2RP4002078, OVARC1001271, PLACE1000786, PLACE1001383, PLACE1002532, PLACE1003885, PLACE1006318, PLACE1007547, PLACE1009246, PLACE1010771, PLACE100300169, PLACE10040281, THYRO1000488, Y79AA1000013, Y79AA1001299, Y79AA1002102, Y79AA1002229, Y79AA1002433, Y79AA1002472, Y79AA1002482,	NT2RP3000512, NT2RP3001057, NT2RP3001338, NT2RP3002399, NT2RP3003327, NT2RP3004496, NT2RP4000648, NT2RP4001213, NT2RP4001753, NT2RP4002081, OVARC1001417, PLACE1000979, PLACE1001602, PLACE1002775, PLACE1004471, PLACE1006438, PLACE1007598, PLACE1009308, PLACE1010870, PLACE100300254, PLACE100400450, THYRO1000488, Y79AA1000033, Y79AA1001312, Y79AA1001391, Y79AA1002249, Y79AA1002433, Y79AA1002472, Y79AA1002482,	NT2RP3000527, NT2RP3001107, NT2RP3001398, NT2RP3002876, NT2RP3003555, NT2RP3004566, NT2RP4000837, NT2RP4001433, NT2RP4001760, NT2RP5003461, OVARC1000151, PLACE1001118, PLACE1001632, PLACE1002834, PLACE1005584, PLACE1006482, PLACE1007955, PLACE1009398, PLACE1011160, PLACE1000128, PLACE100400450, THYRO1000569, Y79AA1000037, Y79AA1001391, Y79AA1001391, Y79AA1001533, Y79AA1002472, Y79AA1002482,	NT2RP3000590, NT2RP3001111, NT2RP3001527, NT2RP3003133, NT2RP3004016, NT2RP3004617, NT2RP4000865, NT2RP4001529, NT2RP4001790, OVARC1000241, PLACE100133, PLACE1001238, PLACE1002171, PLACE1003302, PLACE1005803, PLACE1007239, PLACE1008132, PLACE1009798, PLACE1011433, PLACE1000156, THYRO1000085, THYRO1001100, Y79AA1000342, Y79AA1001533, Y79AA1001533, Y79AA1001613, Y79AA1002472, Y79AA1002482,	NT2RP3000603, NT2RP3001120, NT2RP3001688, NT2RP3003193, NT2RP3004125, NT2RP4000210, NT2RP4000997, NT2RP4001551, NT2RP4001838, OVARC1000241, PLACE100583, PLACE1001294, PLACE1002438, PLACE1003605, PLACE1005966, PLACE1007346, PLACE1008201, PLACE1010134, PLACE1011576, PLACE1000192, THYRO1000121, THYRO1001189, Y79AA1000627, Y79AA1001613, Y79AA1001613, Y79AA1001613, Y79AA1002472, Y79AA1002482,	NT2RP3000605, NT2RP3001150, NT2RP3001855, NT2RP3003251, NT2RP3004242, NT2RP4000396, NT2RP4001029, NT2RP4001568, NT2RP4001938, OVARC1000479, PLACE1000706, PLACE1001304, PLACE1002450, PLACE1003738, PLACE1006167, PLACE1007488, PLACE1009099, PLACE1010702, PLACE100300009, PLACE1000211, THYRO1000242, THYRO1001809, Y79AA1000705, Y79AA1001866, Y79AA1001866, Y79AA1001866, Y79AA1001866, Y79AA1001866,
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	NT2RP2005288,	NT2RP2005315,	NT2RP2005325,	NT2RP2005336,	NT2RP2005358,	NT2RP2005407,
	NT2RP2005436,	NT2RP2005476,	NT2RP2005525,	NT2RP2005694,	NT2RP2005719,	NT2RP2006043,
	NT2RP2006071,	NT2RP2006219,	NT2RP2006312,	NT2RP2006456,	NT2RP2006050,	NT2RP2006068,
	NT2RP3000085,	NT2RP3000299,	NT2RP3000403,	NT2RP3000596,	NT2RP3000739,	NT2RP3000753,
5	NT2RP3000875,	NT2RP3001057,	NT2RP3001081,	NT2RP3001216,	NT2RP3001307,	NT2RP3001338,
	NT2RP3001427,	NT2RP3001428,	NT2RP3001679,	NT2RP3001723,	NT2RP3001855,	NT2RP3001898,
	NT2RP3001969,	NT2RP3002056,	NT2RP3002062,	NT2RP3002151,	NT2RP3002351,	NT2RP3002399,
	NT2RP3002953,	NT2RP3002988,	NT2RP3003078,	NT2RP3003251,	NT2RP3003282,	NT2RP3003313,
	NT2RP3003327,	NT2RP3003409,	NT2RP3003672,	NT2RP3003831,	NT2RP3004016,	NT2RP3004078,
10	NT2RP3004209,	NT2RP3004258,	NT2RP3004490,	NT2RP3004534,	NT2RP3004569,	NT2RP3004572,
	NT2RP4000109,	NT2RP4000367,	NT2RP4000376,	NT2RP4000449,	NT2RP4000855,	NT2RP4000879,
	NT2RP4000925,	NT2RP4001086,	NT2RP4001126,	NT2RP4001150,	NT2RP4001213,	NT2RP4001276,
	NT2RP4001407,	NT2RP4001433,	NT2RP4001483,	NT2RP4001575,	NT2RP4001760,	NT2RP4001861,
	NT2RP4002078,	NT2RP4002791,	OVARC1000014,	OVARC1000139,	OVARC1000520,	OVARC1000722,
15	OVARC1000771,	OVARC1000834,	OVARC1001051,	OVARC1001113,	OVARC1001244,	OVARC1001372,
	OVARC1001417,	OVARC1001496,	OVARC1001506,	OVARC1001577,	OVARC1001726,	OVARC1001766,
	OVARC1001809,	OVARC1002165,	PLACE1000133,	PLACE1000383,	PLACE1000420,	PLACE1000583,
	PLACE1000588,	PLACE1001171,	PLACE1001387,	PLACE1001602,	PLACE1002046,	PLACE1002140,
	PLACE1002437,	PLACE1002474,	PLACE1002685,	PLACE1002782,	PLACE1002834,	PLACE1002908,
20	PLACE1003045,	PLACE1003302,	PLACE1003353,	PLACE1003366,	PLACE1003493,	PLACE1003669,
	PLACE1003704,	PLACE1003903,	PLACE1003968,	PLACE1004183,	PLACE1004197,	PLACE1004277,
	PLACE1004316,	PLACE1004356,	PLACE1004471,	PLACE1004506,	PLACE1004510,	PLACE1004674,
	PLACE1004777,	PLACE1004814,	PLACE1005494,	PLACE1006040,	PLACE1006170,	PLACE1006438,
	PLACE1006615,	PLACE1007140,	PLACE1007239,	PLACE1007257,	PLACE1007511,	PLACE1007598,
25	PLACE1008177,	PLACE1008356,	PLACE1008402,	PLACE1008696,	PLACE1009027,	PLACE1009113,
	PLACE1009158,	PLACE1009444,	PLACE1009524,	PLACE1010529,	PLACE1010870,	PLACE1010896,
	PLACE1011635,	PLACE1011858,	PLACE1011922,	PLACE2000015,	PLACE2000072,	PLACE2000216,
	PLACE2000399,	PLACE2000438,	PLACE2000458,	PLACE2000242,	PLACE4000009,	PLACE4000014,
	PLACE4000156,	PLACE4000369,	SKNCN1000046,	SKNCN1000050,	THYRO1000034,	THYRO1000327,
30	THYRO1000343,	THYRO1000358,	THYRO1000501,	THYRO1000682,	THYRO1000684,	THYRO1000748,
	THYRO1000934,	THYRO1001120,	THYRO1001189,	THYRO1001204,	THYRO1001458,	THYRO1001617,
	THYRO1001671,	Y79AA1000346,	Y79AA1000469,	Y79AA1000560,	Y79AA1000734,	Y79AA1000782,
	Y79AA1001391,	Y79AA1001548,	Y79AA1001594,	Y79AA1001711,	Y79AA1001874,	Y79AA1002204,
	Y79AA1002210,	Y79AA1002258,	Y79AA1002472,	Y79AA1002482,		
35	[0280] Among them, Swiss-Prot database search and GenBank or UniGene database search revealed that the following 380 clones matched the data of genes or proteins which had been registered in the database of Online Mendelian Inheritance in Man (OMIM) ( <a href="http://www.ncbi.nlm.nih.gov/Omim/">http://www.ncbi.nlm.nih.gov/Omim/</a> ), which is a database of human genes and diseases. (The corresponding OMIM numbers are parenthetically indicated following the clone names.)					
	HEMBB1000985(147485),	HEMBB1001068(603142),	HEMBB1001282(182900),	HEMBB1001339(300080),		
40	HEMBB1001482(603971),	HEMBB1001564(603931),	HEMBB1001802(125660),	HEMBB1001905(190370),		
	HEMBB1001908(601408),	HEMBB1002217(603971),	HEMBB1002477(604439),	MAMMA1000388(604865),		
	MAMMA1000731(602118),	MAMMA1001305(602732),	MAMMA1001633(600834),	MAMMA1001868(190370),		
	MAMMA1002170(603624),	MAMMA1002198(600538),	MAMMA1002268(603730),	MAMMA1002485(603665),		
	MAMMA1002530(603602),	MAMMA1002858(601064),	MAMMA1002869(602567),	MAMMA1002881(602692),		
45	MAMMA1003047(603566),	MAMMA1003146(603094),	MAMMA1003166(604061),	NT2RM1000001(601169),		
	NT2RM1000153(600417),	NT2RM1000252(604108),	NT2RM1000555(191510),	NT2RM1000770(300061),		
	NT2RM1000826(191510),	NT2RM1000850(182900),	NT2RM1001003(604785),	NT2RM1001092(603971),		
	NT2RM1001102(604533),	NT2RM2000191(602973),	NT2RM2000363(151410),	NT2RM2000594(602900),		
	NT2RM2000624(601940),	NT2RM2000714(179555),	NT2RM2000821(600959),	NT2RM2001035(604913),		
50	NT2RM2001575(109092),	NT2RM2001652(604141),	NT2RM2001664(603722),	NT2RM2001668(602952),		
	NT2RM2001698(604327),	NT2RM2001803(603722),	NT2RM2001839(603420),	NT2RM4000155(187790),		
	NT2RM4000471(603485),	NT2RM4000486(168730),	NT2RM4000657(602142),	NT2RM4000775(602277),		
	NT2RM4000996(603971),	NT2RM4001629(601114),	NT2RM4001810(155760),	NT2RM4001819(176873),		
	NT2RM4001876(179555),	NT2RM4001940(603887),	NT2RM4002066(300188),	NT2RM4002093(600693),		
55	NT2RM4002146(602603),	NT2RM4002161(254780),	NT2RM4002558(604194),	NT2RM4002571(602274),		
	NT2RP1000086(602219),	NT2RP1000574(601740),	NT2RP1000825(602732),	NT2RP1000833(602973),		
	NT2RP1000959(180510),	NT2RP1000966(164035),	NT2RP1001013(194558),	NT2RP1001185(243500),		
	NT2RP1001482(600586),	NT2RP1001665(114180),	NT2RP2000070(600976),	NT2RP2000147(603535),		

	NT2RP2000248(603367), NT2RP2000420(600834), NT2RP2001233(603971), NT2RP2001397(603971), NT2RP2001876(601855), NT2RP2002124(603486), NT2RP2003000(191161), NT2RP2003295(603494), NT2RP2003714(603971), NT2RP2004170(300196), NT2RP2005003(109092), NT2RP2005358(603573), NT2RP2005525(602655), NT2RP2006219(601279), NT2RP3000068(182530), NT2RP3000596(190370), NT2RP3001081(603524), NT2RP3001428(189940), NT2RP3001969(190370), NT2RP3002351(604887), NT2RP3003251(109092), NT2RP3003672(313470), NT2RP3004209(125255), NT2RP3004569(106410), NT2RP4000376(603873), NT2RP4000925(600245), NT2RP4001213(602277), NT2RP4001483(203740), NT2RP4002078(603971), OVARC1000520(604126), OVARC1001113(602121), OVARC1001496(602619), OVARC1001766(603910), PLACE1000420(600312), PLACE1001387(600206), PLACE1002347(600046), PLACE1002834(194558), PLACE1003353(604704), PLACE1003704(601940), PLACE1004197(601610), PLACE1004471(194558), PLACE1004777(118423), PLACE1006170(601026), PLACE1007239(604784), PLACE1008177(190370), PLACE1009027(300121), PLACE1009524(602488), PLACE1011635(604058), PLACE2000072(603430), PLACE2000458(600976), PLACE4000156(603971), THYRO1000034(190370), THYRO1000501(109092), THYRO1000934(179035), THYRO1001458(160776), Y79AA1000469(602434), Y79AA1001391(142959),	NT2RP2000297(602277), NT2RP2000523(600130), NT2RP2001327(191161), NT2RP2001460(190370), NT2RP2001898(147264), NT2RP2002325(603866), NT2RP2003157(601940), NT2RP2003517(190040), NT2RP2003737(602962), NT2RP2004587(162250), NT2RP2005144(604730), NT2RP2005315(604039), NT2RP2005407(167040), NT2RP2005719(601178), NT2RP2006312(603111), NT2RP3000085(300032), NT2RP3000739(125370), NT2RP3001216(603121), NT2RP3001723(604569), NT2RP3002056(180201), NT2RP3002399(602638), NT2RP3003282(602378), NT2RP3003831(604051), NT2RP3004258(604347), NT2RP3004572(604912), NT2RP4000449(604479), NT2RP4001086(162230), NT2RP4001276(190370), NT2RP4001575(603443), NT2RP4002791(189940), OVARC1000722(604014), OVARC1001244(601540), OVARC1001506(601313), PLACE1001809(603730), PLACE1000583(194558), PLACE1001602(604913), PLACE1002474(602108), PLACE1002908(604327), PLACE1003366(603681), PLACE1003903(123860), PLACE1004277(603493), PLACE1004506(603450), PLACE1004814(601940), PLACE1006438(600834), PLACE1007257(300108), PLACE1008356(604039), PLACE1009113(600675), PLACE1010529(604834), PLACE1011858(603882), PLACE2000216(182790), PLACE3000242(300132), PLACE4000369(603808), THYRO1000327(603243), THYRO1000662(278750), THYRO1001120(602582), THYRO1001617(602744), Y79AA1000560(601026), Y79AA1001548(600286),	NT2RP2000310(239500), NT2RP2000809(603885), NT2RP2001378(158370), NT2RP2001520(603667), NT2RP2002025(601581), NT2RP2002503(601781), NT2RP2003164(604746), NT2RP2003564(190992), NT2RP2003952(602675), NT2RP2004732(162250), NT2RP2005239(603485), NT2RP2005325(603759), NT2RP2005436(601940), NT2RP2006043(601940), NT2RP2006456(604619), NT2RP3000299(602941), NT2RP3000753(162230), NT2RP3001307(180069), NT2RP3001855(602100), NT2RP3002062(603885), NT2RP3002953(604967), NT2RP3003313(603810), NT2RP3004016(601742), NT2RP3004490(603328), NT2RP4000109(603745), NT2RP4000855(602675), NT2RP4001126(190370), NT2RP4001407(190370), NT2RP4001760(305400), OVARC1000014(603371), OVARC1000771(179509), OVARC1001372(603145), OVARC1001577(603269), PLACE1001333(602542), PLACE1000588(600411), PLACE1002046(151625), PLACE1002685(604515), PLACE1003045(173910), PLACE1003493(601456), PLACE1003968(602742), PLACE1004316(604261), PLACE1004510(604912), PLACE1005494(603652), PLACE1006155(603910), PLACE1007511(148020), PLACE1008402(603344), PLACE1009158(604140), PLACE1010870(603971), PLACE1011922(160776), PLACE2000399(313470), PLACE4000009(160776), SKNMC1000046(603144), THYRO1000343(125370), THYRO1000684(603885), THYRO1001189(603971), THYRO1001617(603281), Y79AA1000734(603867), Y79AA1001594(600936),	NT2RP2000414(601037), NT2RP2000812(160777), NT2RP2001394(300208), NT2RP2001536(600675), NT2RP2002058(604737), NT2RP2002959(602962), NT2RP2003228(602638), NT2RP2003604(604785), NT2RP2004013(602542), NT2RP2004933(603289), NT2RP2005276(602371), NT2RP2005336(190370), NT2RP2005476(602680), NT2RP2006071(604299), NT2RP3000050(603971), NT2RP3000403(604981), NT2RP3001057(603971), NT2RP3001338(314998), NT2RP3001898(604561), NT2RP3002151(139259), NT2RP3002988(603258), NT2RP3003409(604533), NT2RP3004078(142765), NT2RP3004534(600586), NT2RP4000367(603722), NT2RP4000879(314370), NT2RP4001150(601581), NT2RP4001433(602277), NT2RP4001861(190370), OVARC1000139(603486), OVARC1001051(600051), OVARC1001417(300182), OVARC1001726(300103), PLACE1000383(300171), PLACE1001171(310400), PLACE1002140(603748), PLACE1002782(602095), PLACE1003302(194558), PLACE1003669(190370), PLACE1004183(604701), PLACE1004358(603272), PLACE1004674(601057), PLACE1006040(603061), PLACE1007140(190370), PLACE1007598(602277), PLACE1008696(602141), PLACE1009444(600286), PLACE1010896(160776), PLACE2000015(600051), PLACE2000438(602273), PLACE4000014(300032), SKNMC1000050(114230), THYRO1000358(604188), THYRO1000748(300023), THY1001204(603169), Y79AA1000346(604355), Y79AA1000782(600417), Y79AA1001711(600063),
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Y79AA1001874(600315), Y79AA1002204(605033), Y79AA1002210(191161), Y79AA1002472(603971),  
Y79AA1002482(603971),

**[0281]** The following 425 clones presumably belong to enzymes and/or metabolism-associated proteins.

	HEMBA1000012, HEMBA1000129, HEMBA1000141, HEMBA1000150, HEMBA1000542, HEMBA1000852,	
5	HEMBA1001019, HEMBA1001257, HEMBA1001526, HEMBA1001620, HEMBA1001866, HEMBA1001896,	
	HEMBA1002212, HEMBA1002513, HEMBA1002746, HEMBA1002973, HEMBA1003046, HEMBA1003136,	
	HEMBA1003179, HEMBA1003250, HEMBA1003291, HEMBA1003408, HEMBA1003538, HEMBA1003679,	
	HEMBA1003680, HEMBA1004199, HEMBA1004227, HEMBA1004408, HEMBA1004509, HEMBA1004734,	
	HEMBA1004768, HEMBA1005394, HEMBA1005513, HEMBA1005737, HEMBA1005815, HEMBA1006031,	
10	HEMBA1006272, HEMBA1006278, HEMBA1006291, HEMBA1006309, HEMBA1006347, HEMBA1006485,	
	HEMBA1006521, HEMBA1006624, HEMBA1006885, HEMBA1006976, HEMBA1007121, HEMBA1007224,	
	HEMBA1007243, HEMBA1007300, HEMBB1000083, HEMBB1000217, HEMBB1000915, HEMBB1000947,	
	HEMBB1001137, HEMBB1001346, HEMBB1001429, HEMBB1001443, HEMBB1001915, HEMBB1001950,	
	HEMBB1002042, MAMMA1000020, MAMMA1000085, MAMMA1000672, MAMMA1000713, MAMMA1000941,	
15	MAMMA1000897, MAMMA1001008, MAMMA1001038, MAMMA1001059, MAMMA1001476, MAMMA1001501,	
	MAMMA1002268, MAMMA1002470, MAMMA1002530, MAMMA1002573, MAMMA1002619, MAMMA1002655,	
	MAMMA1002671, MAMMA1003013, MAMMA1003035, NT2RM1000039, NT2RM1000132, NT2RM1000153,	
	NT2RM1000256, NT2RM1000280, NT2RM1000377, NT2RM1000553, NT2RM1000648, NT2RM1000702,	
	NT2RM1000894, NT2RM1001072, NT2RM1001115, NT2RM2000013, NT2RM2000092, NT2RM2000322,	
20	NT2RM2000368, NT2RM2000371, NT2RM2000469, NT2RM2000504, NT2RM2000577, NT2RM2000594,	
	NT2RM2000951, NT2RM2001239, NT2RM2001547, NT2RM2001632, NT2RM2001664, NT2RM2001698,	
	NT2RM2001700, NT2RM2001730, NT2RM2001782, NT2RM2001803, NT2RM2001886, NT2RM2001935,	
	NT2RM2001997, NT2RM2002030, NT2RM2002128, NT2RM4000024, NT2RM4000155, NT2RM4000344,	
	NT2RM4000471, NT2RM4000616, NT2RM4000657, NT2RM4000712, NT2RM4000820, NT2RM4001313,	
25	NT2RM4001316, NT2RM4001444, NT2RM4001592, NT2RM4001758, NT2RM4001819, NT2RM4001880,	
	NT2RM4002062, NT2RM4002063, NT2RM4002189, NT2RM4002213, NT2RM4002251, NT2RM4002409,	
	NT2RM4002532, NT2RM4002623, NT2RP1000376, NT2RP1000443, NT2RP1000522, NT2RP1000834,	
	NT2RP1000947, NT2RP1001079, NT2RP1001185, NT2RP1001253, NT2RP1001361, NT2RP1001543,	
	NT2RP2000056, NT2RP2000114, NT2RP2000183, NT2RP2000248, NT2RP2000329, NT2RP2000422,	
30	NT2RP2000448, NT2RP2000668, NT2RP2000710, NT2RP2000816, NT2RP2001070, NT2RP2001392,	
	NT2RP2001601, NT2RP2001663, NT2RP2001740, NT2RP2001748, NT2RP2001898, NT2RP2002124,	
	NT2RP2002256, NT2RP2002609, NT2RP2002618, NT2RP2002959, NT2RP2002993, NT2RP2003230,	
	NT2RP2003286, NT2RP2003401, NT2RP2003506, NT2RP2003543, NT2RP2003643, NT2RP2003702,	
	NT2RP2003704, NT2RP2003713, NT2RP2003737, NT2RP2003840, NT2RP2003912, NT2RP2003952,	
35	NT2RP2004098, NT2RP2004239, NT2RP2004245, NT2RP2004768, NT2RP2004791, NT2RP2004799,	
	NT2RP2004933, NT2RP2005038, NT2RP2005139, NT2RP2005162, NT2RP2005204, NT2RP2005239,	
	NT2RP2005276, NT2RP2005344, NT2RP2005360, NT2RP2005457, NT2RP2005498, NT2RP2005549,	
	NT2RP2005557, NT2RP2005605, NT2RP2005635, NT2RP2005723, NT2RP2005773, NT2RP2005775,	
	NT2RP2005776, NT2RP2005784, NT2RP2005835, NT2RP2005942, NT2RP2006534, NT2RP2006571,	
40	NT2RP2006573, NT2RP3000031, NT2RP3000085, NT2RP3000207, NT2RP3000359, NT2RP3000578,	
	NT2RP3000742, NT2RP3000845, NT2RP3000875, NT2RP3000917, NT2RP3001055, NT2RP3001221,	
	NT2RP3001495, NT2RP3001898, NT2RP3001938, NT2RP3002303, NT2RP3002351, NT2RP3002501,	
	NT2RP3002602, NT2RP3002628, NT2RP3002663, NT2RP3003301, NT2RP3003385, NT2RP3003490,	
	NT2RP3003659, NT2RP3003825, NT2RP3003831, NT2RP3003846, NT2RP3003914, NT2RP3004148,	
45	NT2RP3004209, NT2RP3004378, NT2RP3004669, NT2RP3004670, NT2RP4000259, NT2RP4000312,	
	NT2RP4000367, NT2RP4000417, NT2RP4000457, NT2RP4000657, NT2RP4000817, NT2RP4000855,	
	NT2RP4000879, NT2RP4000927, NT2RP4000973, NT2RP4000997, NT2RP4001041, NT2RP4001079,	
	NT2RP4001095, NT2RP4001143, NT2RP4001219, NT2RP4001375, NT2RP4001389, NT2RP4001483,	
	NT2RP4001555, NT2RP4001592, NT2RP4001644, NT2RP4001730, NT2RP4001946, NT2RP4002408,	
50	NT2RP5003500, NT2RP5003522, OVARC1000013, OVARC1000060, OVARC1000139, OVARC1000288,	
	OVARC1000309, OVARC1000473, OVARC1000556, OVARC1000682, OVARC1000722, OVARC1000751,	
	OVARC1000885, OVARC1000915, OVARC1001107, OVARC1001713, OVARC1001762, OVARC1001809,	
	OVARC1001942, OVARC1002156, OVARC1002165, PLACE1000007, PLACE1000142, PLACE1000185,	
	PLACE1000213, PLACE1000383, PLACE1000420, PLACE1000547, PLACE1000653, PLACE1000755,	
55	PLACE1001054, PLACE1001062, PLACE1001672, PLACE1001692, PLACE1001748, PLACE1001781,	
	PLACE1001817, PLACE1001869, PLACE1001989, PLACE1002073, PLACE1002598, PLACE1002908,	
	PLACE1002981, PLACE1003174, PLACE1003176, PLACE1003709, PLACE1003885, PLACE1003888,	
	PLACE1003903, PLACE1003915, PLACE1004270, PLACE1004428, PLACE1004437, PLACE1004751,	



	PLACE1004804,	PLACE1004918,	PLACE1005243,	PLACE1005305,	PLACE1005373,	PLACE1005656,
	PLACE1005763,	PLACE1005804,	PLACE1005953,	PLACE1005955,	PLACE1006011,	PLACE1006469,
	PLACE1006534,	PLACE1006626,	PLACE1006731,	PLACE1006819,	PLACE1006829,	PLACE1006878,
	PLACE1007226,	PLACE1007416,	PLACE1007649,	PLACE1007706,	PLACE1007729,	PLACE1007954,
5	PLACE1007958,	PLACE1008111,	PLACE1008275,	PLACE1008330,	PLACE1008643,	PLACE1009094,
	PLACE1009310,	PLACE1009444,	PLACE1009763,	PLACE1009861,	PLACE1009992,	PLACE1009997,
	PLACE1010096,	PLACE1010362,	PLACE1010481,	PLACE1010662,	PLACE1011046,	PLACE1011219,
	PLACE1011229,	PLACE1011332,	PLACE1011635,	PLACE1011923,	PLACE2000021,	PLACE2000034,
	PLACE2000398,	PLACE2000404,	PLACE2000438,	PLACE3000009,	PLACE3000020,	PLACE3000059,
10	PLACE3000147,	PLACE3000339,	PLACE3000350,	PLACE4000063,	PLACE4000100,	PLACE4000401,
	PLACE4000548,	PLACE4000654,	SKNMC1000050,	THYRO1000072,	THYRO1000097,	THYRO1000288,
	THYRO1000605,	THYRO1000662,	THYRO1000756,	THYRO1000852,	THYRO1000126,	THYRO 1000934,
	THYRO1000951,	THYRO 1000983,	THYRO1001003,	THYRO1001287,	THYRO1001374,	THYRO1001406,
	THYRO1001617,	THYRO1001671,	THYRO1001738,	Y79AA1000782,	Y79AA1001048,	Y79AA1001233,
15	Y79AA1001394,	Y79AA1001493,	Y79AA1001548,	Y79AA1001581,	Y79AA1001603,	Y79AA1001827,
	Y79AA1002027,	Y79AA1002209,	Y79AA1002211,	Y79AA1002361,	Y79AA1002416,	
	<b>[0282]</b> The following 217 clones presumably belong to a group of cDNAs encoding ATP- and/or GTP-binding proteins.					
	HEMBA1000012,	HEMBA1000129,	HEMBA1000185,	HEMBA1000491,	HEMBA1000531,	HEMBA1001019,
	HEMBA1001174,	HEMBA1001387,	HEMBA1001595,	HEMBA1001723,	HEMBA1001913,	HEMBA1002161,
20	HEMBA1002212,	HEMBA1002876,	HEMBA1002997,	HEMBA1003250,	HEMBA1003291,	HEMBA1003369,
	HEMBA1003555,	HEMBA1003560,	HEMBA1004131,	HEMBA1004199,	HEMBA1004202,	HEMBA1004354,
	HEMBA1004697,	HEMBA1005047,	HEMBA1005595,	HEMBA1007018,	HEMBA1007151,	HEMBA1000083,
	HEMBA1000226,	HEMBA1000264,	HEMBA1000632,	HEMBA1000725,	HEMBA1001294,	HEMBA1002193,
	MAMMA1000085,	MAMMA1000612,	MAMMA1000731,	MAMMA1000738,	MAMMA1001038,	MAMMA1001735,
25	MAMMA1001768,	MAMMA1003127,	NT2RM1000187,	NT2RM1000388,	NT2RM1000702,	NT2RM1000772,
	NT2RM1000924,	NT2RM2000469,	NT2RM2000577,	NT2RM2000740,	NT2RM2001100,	NT2RM2001201,
	NT2RM2001345,	NT2RM2001823,	NT2RM2002128,	NT2RM4000155,	NT2RM4000191,	NT2RM4000356,
	NT2RM4000496,	NT2RM4000611,	NT2RM4000733,	NT2RM4000820,	NT2RM4001084,	NT2RM4001178,
	NT2RM4001344,	NT2RM4001444,	NT2RM4001592,	NT2RM4001714,	NT2RM4001758,	NT2RM4001880,
30	NT2RM4002062,	NT2RM4002174,	NT2RM4002205,	NT2RM4002527,	NT2RM4002594,	NT2RM4002623,
	NT2RP1000470,	NT2RP1000478,	NT2RP1000915,	NT2RP1000958,	NT2RP1001080,	NT2RP1001410,
	NT2RP1001569,	NT2RP2000126,	NT2RP2000258,	NT2RP2000329,	NT2RP2000660,	NT2RP2000668,
	NT2RP2000710,	NT2RP2000812,	NT2RP2000880,	NT2RP2001245,	NT2RP2001392,	NT2RP2002606,
	NT2RP2003277,	NT2RP2003912,	NT2RP2004538,	NT2RP2004568,		
35	NT2RP2004689,	NT2RP2004768,	NT2RP2004791,	NT2RP2004920,	NT2RP2005344,	NT2RP2005393,
	NT2RP2005763,	NT2RP2006534,	NT2RP3000046,	NT2RP3000252,	NT2RP3000350,	NT2RP3000359,
	NT2RP3000366,	NT2RP3000397,	NT2RP3000759,	NT2RP3000845,	NT2RP3000875,	NT2RP3001150,
	NT2RP3001427,	NT2RP3001453,	NT2RP3001529,	NT2RP3001730,	NT2RP3001799,	NT2RP3001857,
40	NT2RP3001938,	NT2RP3002007,	NT2RP3002151,	NT2RP3002330,	NT2RP3002399,	NT2RP3002671,
	NT2RP3003301,	NT2RP3003353,	NT2RP3003589,	NT2RP3003809,	NT2RP3003876,	NT2RP3004189,
	NT2RP3004428,	NT2RP3004578,	NT2RP4000290,	NT2RP4000481,	NT2RP4000518,	NT2RP4000781,
	NT2RP4000938,	NT2RP4000929,	NT2RP4001041,	NT2RP4001079,	NT2RP4001375,	NT2RP4001414,
	NT2RP4001592,	NT2RP4001634,	NT2RP4001644,	NT2RP4001656,	NT2RP4001896,	NT2RP4002047,
	NT2RP4002058,	NT2RP4002408,	NT2RP5003477,	OVARC1000013,	OVARC1000304,	OVARC1000556,
45	OVARC1000771,	OVARC1000800,	OVARC1001068,	OVARC1002138,	OVARC1000040,	OVARC1000588,
	PLACE1001104,	PLACE1001739,	PLACE1002433,	PLACE1002437,	PLACE1002714,	PLACE1003394,
	PLACE1003521,	PLACE1003915,	PLACE1004902,	PLACE1005243,	PLACE1005305,	PLACE1005549,
	PLACE1005739,	PLACE1005921,	PLACE1006119,	PLACE1006196,	PLACE1006552,	PLACE1006956,
	PLACE1007409,	PLACE1007697,	PLACE1007946,	PLACE1008244,	PLACE1009404,	PLACE1009476,
50	PLACE1009596,	PLACE1009908,	PLACE1010134,	PLACE1010720,	PLACE1010896,	PLACE1011109,
	PLACE1011114,	PLACE1011310,	PLACE1011922,	PLACE2000014,	PLACE2000039,	PLACE2000274,
	PLACE2000404,	PLACE2000427,	PLACE3000350,	PLACE4000009,	PLACE4000014,	PLACE4000326,
	SKNMC1000013,	THYRO1000072,	THYRO1001458,	Y79AA1000833,	Y79AA1000962,	Y79AA1001394,
	Y79AA1001875,	Y79AA1001963,	Y79AA1002209,			
55	<b>[0283]</b> The following 320 clones presumably belong to nuclear proteins.					
	HEMBA1000005,	HEMBA1000158,	HEMBA1000216,	HEMBA1000561,	HEMBA1000591,	HEMBA1001088,
	HEMBA1001137,	HEMBA1001405,	HEMBA1001510,	HEMBA1001579,	HEMBA1001809,	HEMBA1001819,
	HEMBA1001824,	HEMBA1001847,	HEMBA1001869,	HEMBA1002177,	HEMBA1002241,	HEMBA1002495,

	HEMBA1002569, HEMBA1003662, HEMBA1004353, HEMBA1005931, HEMBB1000226, HEMBB1001915, MAMMA1001222, MAMMA1002869, NT2RM1000885, NT2RM2000624, NT2RM2001771, NT2RM2002091, NT2RM4000290, NT2RM4001200, NT2RM4001597, NT2RP1000353, NT2RP1000915, NT2RP2000076, NT2RP2000297, NT2RP2001869, NT2RP2002939, NT2RP2003308, NT2RP2004489, NT2RP2005701, NT2RP2006436, NT2RP3000590, NT2RP3001120, NT2RP3001428, NT2RP3002056, NT2RP3003555, NT2RP3004617, NT2RP4000518, NT2RP4001568, NT2RP4002078, OVARC1000241, OVARC1001232, PLACE1000184, PLACE1001383, PLACE1002775, PLACE1003519, PLACE1003923, PLACE1005827, PLACE1006829, PLACE1007688, PLACE1009130, PLACE1010720, PLACE2000427, PLACE4000261, THYRO1000585, Y79AA1000231, Y79AA10001963, Y79AA1002431, Y79AA1002472, Y79AA1002482	HEMBA1002935, HEMBA1003684, HEMBA1004479, HEMBA1006278, HEMBB1000789, HEMBB1002134, MAMMA1001260, MAMMA1002937, NT2RM1000894, NT2RM2000735, NT2RM2001823, NT2RM4000024, NT2RM4000531, NT2RM4001483, NT2RM4001783, NT2RP1000111, NT2RP1000958, NT2RP2000126, NT2RP2000420, NT2RP2002079, NT2RP2002993, NT2RP2003347, NT2RP2004920, NT2RP2005767, NT2RP3000031, NT2RP3000603, NT2RP3001253, NT2RP3001472, NT2RP3002165, NT2RP3004016, NT2RP4000078, NT2RP4000997, NT2RP4001638, NT2RP4002081, OVARC1000326, OVARC1001271, PLACE1000406, PLACE1001632, PLACE1002816, PLACE1003521, PLACE1004302, PLACE1005876, PLACE1006878, PLACE1007969, PLACE1009308, PLACE1010870, PLACE3000009, PLACE4000326, THYRO1001100, Y79AA1000589, Y79AA10002472, Y79AA1002482	HEMBA1002951, HEMBA1003690, HEMBA1004973, HEMBA1006283, HEMBB1001011, MAMMA1002217, MAMMA1001633, MAMMA1003011, NT2RM1001059, NT2RM2000740, NT2RM2001936, NT2RM4000046, NT2RM4000751, NT2RM4001566, NT2RM4001823, NT2RP1000493, NT2RP1000966, NT2RP2000153, NT2RP2000931, NT2RP2002270, NT2RP2003137, NT2RP2003714, NT2RP2005393, NT2RP2005776, NT2RP3000050, NT2RP3000632, NT2RP3001338, NT2RP3001646, NT2RP3002399, NT2RP3004206, NT2RP4000111, NT2RP4001148, NT2RP4001696, NT2RP4002791, OVARC1000556, OVARC1001306, PLACE1000583, PLACE1002171, PLACE1002834, PLACE1003605, PLACE1004471, PLACE1005966, PLACE1006917, PLACE1008044, PLACE1009398, PLACE1011056, PLACE3000169, PLACE4000489, THYRO1001189, Y79AA1000752, Y79AA1001391, Y79AA1002482	HEMBA1002999, HEMBA1003760, HEMBA1005219, HEMBA1006359, HEMBB1001056, MAMMA1000183, MAMMA1001743, MAMMA1000086, NT2RM1001092, NT2RM2001105, NT2RM2001989, NT2RM4000104, NT2RM4000996, NT2RM4001858, NT2RP1000630, NT2RP1001177, NT2RP2000248, NT2RP2001420, NT2RP2002591, NT2RP2003277, NT2RP2004013, NT2RP2005496, NT2RP2005942, NT2RP3000512, NT2RP3001057, NT2RP3001398, NT2RP3001792, NT2RP3003193, NT2RP3004428, NT2RP4000398, NT2RP4001213, NT2RP4001938, OVARC1000086, OVARC1000846, OVARC1001436, OVARC100596, PLACE1002433, PLACE1003100, PLACE1003704, PLACE1004564, PLACE1006167, PLACE1007014, PLACE1008132, PLACE1010134, PLACE1011433, PLACE4000014, SKNMC1000011, THYRO1001809, Y79AA10010037, Y79AA1001613, Y79AA1002482	HEMBA1003545, HEMBA1004321, HEMBA1005558, HEMBA1007087, HEMBB1001482, MAMMA1001105, MAMMA1002617, NT2RM1000666, NT2RM2000588, NT2RM2001670, NT2RM2002088, NT2RM4000215, NT2RM4001140, NT2RM4001979, NT2RP1000902, NT2RP2000008, NT2RP2000258, NT2RP2001756, NT2RP2002880, NT2RP2003286, NT2RP2004187, NT2RP2005539, NT2RP2006043, NT2RP3000527, NT2RP3001107, NT2RP3001427, NT2RP3001855, NT2RP3003212, NT2RP3004566, NT2RP4000481, NT2RP4001433, NT2RP4002058, OVARC1000091, OVARC1001180, PLACE1000133, PLACE1001118, PLACE1002532, PLACE1003302, PLACE1003885, PLACE1004902, PLACE1006482, PLACE1007598, PLACE1009099, PLACE1010702, PLACE2000014, PLACE4000192, THYRO1000242, Y79AA1000214, Y79AA1001705, Y79AA1002482
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[0284] The following 292 clones presumably belong to DNA- and/or RNA-binding proteins.

	HEMBA1000158, HEMBA1001137, HEMBA1001847, HEMBA1003568, HEMBA1003805, HEMBA1004669, HEMBA1000216, HEMBA1001405, HEMBA1001869, HEMBA1003591, HEMBA1003953, HEMBA1004484, HEMBA1000561, HEMBA1001510, HEMBA1002177, HEMBA1003662, HEMBA1004321, HEMBA1004973, HEMBA1000591, HEMBA1001804, HEMBA1002935, HEMBA1003684, HEMBA1004354, HEMBA1005202, HEMBA1000851, HEMBA1001809, HEMBA1003408, HEMBA1003760, HEMBA1004389, HEMBA1005359, HEMBA1001088, HEMBA1001819, HEMBA1003545, HEMBA1003783, HEMBA1004479, HEMBA1005931,
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	HEMBA1006248, HEMBA1007194, HEMBB1001749, MAMMA1001105, MAMMA1002617, NT2RM1000555, NT2RM1001092, NT2RM2001575, NT2RM2002004, NT2RM4000167, NT2RM4000751, NT2RM4001178, NT2RM4001828, NT2RP1000470, NT2RP1001073, NT2RP2001127, NT2RP2002079, NT2RP2003329, NT2RP2004187, NT2RP2005436, NT2RP2006043, NT2RP3000562, NT2RP3001057, NT2RP3001398, NT2RP3001855, NT2RP3003251, NT2RP3004490, NT2RP4000398, NT2RP4001080, NT2RP4001753, OVARC1000241, OVARC1001987, PLACE1001632, PLACE1003302, PLACE1004471, PLACE1006196, PLACE1007547, PLACE1009246, PLACE1010702, PLACE3000009, PLACE4000489, THYRO1001189, Y79AA1001312, Y79AA1001391, Y79AA1001613, Y79AA1002103, Y79AA1002472, Y79AA1002482,	HEMBA1006278, HEMBB1000264, HEMBB1001839, MAMMA1001222, MAMMA1002689, NT2RM1000666, NT2RM2000371, NT2RM2001605, NT2RM2002014, NT2RM4000191, NT2RM4000996, NT2RM4001200, NT2RM4001858, NT2RP1000493, NT2RP1001080, NT2RP2001174, NT2RP2002099, NT2RP2003347, NT2RP2004568, NT2RP2005496, NT2RP2006436, NT2RP3000590, NT2RP3001107, NT2RP3001472, NT2RP3002165, NT2RP3003327, NT2RP3004564, NT2RP4000455, NT2RP4001095, NT2RP4001838, OVARC1000746, OVARC1001732, PLACE1001319, PLACE1003519, PLACE1004564, PLACE1006482, PLACE1007598, PLACE1009398, PLACE1010870, PLACE3000169, SKNMC1000091, THYRO1001809, Y79AA1000037, Y79AA1000349, Y79AA1000373, Y79AA1000377, Y79AA1005876, Y79AA1006818, Y79AA1007969, Y79AA1009622, Y79AA1011114, Y79AA1000156, Y79AA1000242, Y79AA1000349, Y79AA1000752, Y79AA1001211,	HEMBA1006283, HEMBB1000789, HEMBB1002217, MAMMA1001280, MAMMA1002937, NT2RM1000691, NT2RM2000624, NT2RM2001670, NT2RM2002088, NT2RM4000202, NT2RM4000992, NT2RM4001483, NT2RM4001880, NT2RP1000574, NT2RP2000008, NT2RP2001233, NT2RP2002503, NT2RP2003480, NT2RP2004920, NT2RP2005701, NT2RP2006464, NT2RP3000603, NT2RP3001120, NT2RP3001672, NT2RP3002399, NT2RP3003555, NT2RP3004518, NT2RP4000594, NT2RP4001213, NT2RP4001938, OVARC1000846, OVARC1001232, PLACE1000406, PLACE1002438, PLACE1003605, PLACE1004814, PLACE1006488, PLACE1007688, PLACE1009476, PLACE1011056, PLACE4000014, THYRO1000085, Y79AA1000037, Y79AA1000349, Y79AA1000373, Y79AA1000377, Y79AA1005876, Y79AA1006818, Y79AA1007969, Y79AA1009622, Y79AA1011114, Y79AA1000156, Y79AA1000242, Y79AA1000349, Y79AA1000752, Y79AA1001211,	HEMBA1006652, HEMBB1001482, MAMMA1000284, MAMMA1001837, NT2RM1000086, NT2RM1000885, NT2RM2001105, NT2RM2001823, NT2RM4000046, NT2RM4000595, NT2RM4001783, NT2RM4002093, NT2RP1000966, NT2RP2000258, NT2RP2001756, NT2RP2002939, NT2RP2003564, NT2RP2005139, NT2RP2005776, NT2RP2000512, NT2RP3000632, NT2RP3001155, NT2RP3001724, NT2RP3003138, NT2RP3004078, NT2RP4008165, NT2RP4008865, NT2RP4001568, OVARC1000006, OVARC1001271, PLACE1000979, PLACE1002775, PLACE1003738, PLACE1005876, PLACE1006917, PLACE1008132, PLACE1010053, PLACE1011433, PLACE4000192, THYRO1000501, Y79AA1000752, Y79AA1001211,	HEMBA1007089, HEMBB1001736, MAMMA1000371, MAMMA1002385, NT2RM1000599, NT2RM1001459, NT2RM2001024, NT2RM2001989, NT2RM4000104, NT2RM4000703, NT2RM4001823, NT2RM4002109, NT2RP1001013, NT2RP2000289, NT2RP2003157, NT2RP2003714, NT2RP2005168, NT2RP2005942, NT2RP3000527, NT2RP3000984, NT2RP3001398, NT2RP3001792, NT2RP3003193, NT2RP3004428, NT2RP4000111, NT2RP4000929, NT2RP4001696, OVARC1000087, OVARC1001306, PLACE1001118, PLACE1002834, PLACE1003885, PLACE1005951, PLACE1007346, PLACE1009099, PLACE1010194, PLACE2000247, PLACE4000261, THYRO1001100, Y79AA1001211,
	[0285] The following 66 clones presumably belong to the category of RNA synthesis-associated proteins.				
	HEMBA1000591, NT2RM1000187, NT2RM4001178, NT2RP2000153, NT2RP2005539, NT2RP3000361, NT2RP4000481, OVARC1001232, PLACE1003704, PLACE1005646, PLACE1009476, PLACE1009925, PLACE1010194, PLACE101114, THYRO100121, Y79AA1001963,	HEMBA1001579, NT2RM1000852, NT2RM4002093, NT2RP2002928, NT2RP2005605, NT2RP3000397, NT2RP4000518, OVARC1001577, PLACE1003885, PLACE1005876, PLACE1009476, PLACE1009925, PLACE1010194, PLACE101114, THYRO100121, Y79AA1001963,	HEMBA1003179, NT2RM2000624, NT2RP1000035, NT2RP2003157, NT2RP2005776, NT2RP3001671, NT2RP4000614, PLACE1000406, PLACE1004564, PLACE1006818, PLACE1008264, PLACE1009476, PLACE1010194, PLACE101114, THYRO100121, Y79AA1001963,	HEMBA1003591, NT2RM2001989, NT2RP1000272, NT2RP2004568, NT2RP2005942, NT2RP3004504, NT2RP4000929, PLACE1000596, PLACE1004814, PLACE1006818, PLACE1008264, PLACE1009476, PLACE1010194, PLACE101114, THYRO100121, Y79AA1001963,	HEMBA1006278, NT2RM2000210, NT2RP1000470, NT2RP2005126, NT2RP2006043, NT2RP4000078, NT2RP4001696, PLACE1000755, PLACE1009402, PLACE1006878, 

	HEMBA1004276, HEMBA1005202, HEMBA1006973, HEMBB1001831, MAMMA1002219, NT2RM2000504, NT2RM2001648, NT2RM4000344, NT2RM4001382, NT2RP1000522, NT2RP2000710, NT2RP2001613, NT2RP2002959, NT2RP2003401, NT2RP2003981, NT2RP2005360, NT2RP3000759, NT2RP3002529, NT2RP4000370, NT2RP4001313, OVARC1000085, OVARC1001180, PLACE1000863, PLACE1004104, PLACE1006488, PLACE1008790, PLACE1009845, PLACE1012031, SKNMC1000011, TYRO1000983, TYRO1001003, TYRO1001313, Y79AA1000560, Y79AA1000968, Y79AA1001493, Y79AA1001875, Y79AA1002027, Y79AA1002209,	HEMBA1004734, HEMBA1006031, HEMBA1007224, HEMBB1001915, MAMMA1002236, NT2RM2000577, NT2RM2001730, NT2RM4000356, NT2RM4001444, NT2RP1000547, NT2RP2000880, NT2RP2001660, NT2RP2002980, NT2RP2003433, NT2RP2004366, NT2RP2005763, NT2RP3000968, NT2RP3002671, NT2RP4000457, NT2RP4001315, OVARC1000465, OVARC1001342, PLACE1001092, PLACE1004070, PLACE1006829, PLACE1008813, PLACE1010074, PLACE1200404, PLACE2000404, TYRO1000983, TYRO1001003, TYRO1001313, Y79AA1000560, Y79AA1000968, Y79AA1001493, Y79AA1001875, Y79AA1002027, Y79AA1002209,	HEMBA1004847, HEMBA1006272, HEMBB1000915, MAMMA1000085, MAMMA1002619, NT2RM2000821, NT2RM2001760, NT2RM4000421, NT2RM4002062, NT2RP1000746, NT2RP2000943, NT2RP2001740, NT2RP2003137, NT2RP2003704, NT2RP2004389, NT2RP3000366, NT2RP3001690, NT2RP3003846, NT2RP4000879, NT2RP4001574, OVARC1000564, OVARC1000771, PLACE1000061, PLACE1002090, PLACE1005557, PLACE1007729, PLACE1009130, PLACE1011109, PLACE3000121, Y79AA1000560, Y79AA1000968, Y79AA1001493, Y79AA1001875, Y79AA1002027, Y79AA1002209,	HEMBA1004929, HEMBA1006474, HEMBB1001112, MAMMA1000734, NT2RM1000661, NT2RM2001201, NT2RM2002055, NT2RM4000712, NT2RM4002205, NT2RP1000947, NT2RP2001290, NT2RP2002124, NT2RP2003158, NT2RP2003713, NT2RP2004791, NT2RP3001690, NT2RP3003876, NT2RP4001041, OVARC1000013, OVARC1000862, OVARC1000771, PLACE1000081, PLACE1003174, PLACE1005813, PLACE1008273, PLACE1009477, PLACE1011229, PLACE4000269, Y79AA1000560, Y79AA1000968, Y79AA1001493, Y79AA1001875, Y79AA1002027, Y79AA1002209,	HEMBA1005047, HEMBA1006914, HEMBB1001736, MAMMA1002170, NT2RM2000092, NT2RM2001613, NT2RM4000169, NT2RM4001203, NT2RP1000326, NT2RP200147, NT2RP2001601, NT2RP2002862, NT2RP2003394, NT2RP2003760, NT2RP2005116, NT2RP3002045, NT2RP3004209, NT2RP4001117, OVARC1000071, OVARC1001171, PLACE1000492, PLACE1003915, PLACE1006170, PLACE1008402, PLACE1009721, PLACE1011477, PLACE4000654, Y79AA1000784, Y79AA1000968, Y79AA1001493, Y79AA1001875, Y79AA1002027, Y79AA1002209,
	[0287] The following 130 clones presumably belong to cytoskeletal-associated proteins.				
	HEMBA1000156, HEMBA1001068, HEMBA1000411, HEMBA1000588, HEMBA1001043, HEMBA1001651, HEMBA1001661, HEMBA1002102, HEMBA1002161, HEMBA1002939, HEMBA1003235, HEMBA1003581, HEMBA1004499, HEMBA1004344, HEMBA1004697, HEMBA1004929, HEMBA1004972, HEMBA1005582, HEMBA1005595, HEMBA1006354, HEMBA1006737, HEMBB1001175, HEMBB1001282, HEMBB1001562, HEMBB1001802, MAMMA1000824, MAMMA1001041, MAMMA1001576, MAMMA1001679, MAMMA1001735, MAMMA1002297, MAMMA1002351, MAMMA1002622, MAMMA1002637, MAMMA1003127, NT2RM1000850, NT2RM1000898, NT2RM2000030, NT2RM2000260, NT2RM2000691, NT2RP1000202, NT2RP1000348, NT2RP2000812, NT2RP2000478, NT2RM4000515, NT2RM4001217, NT2RP1001302, NT2RP2000070, NT2RP2000812, NT2RP2000814, NT2RP2001168, NT2RP2001245, NT2RP2001634, NT2RP2001900, NT2RP2003307, NT2RP2003394, NT2RP2004041, NT2RP2004242, NT2RP2004538, NT2RP2004587, NT2RP2004681, NT2RP2004732, NT2RP2004978, NT2RP2005491, NT2RP2005531, NT2RP2005712, NT2RP2006275, NT2RP3000753, NT2RP3001113, NT2RP3001216, NT2RP3001239, NT2RP3001272, NT2RP3001554, NT2RP3001690, NT2RP3001799, NT2RP3002688, NT2RP3003061, NT2RP3003185, NT2RP3003230, NT2RP3004569, NT2RP3004578, NT2RP4001004, NT2RP4001086, NT2RP4001256, NT2RP4001567, NT2RP4001927, OVARC1000001, OVARC1000106, OVARC1000437, OVARC1000502, OVARC1000679, OVARC1001731, OVARC1002050, PLACE1001104, PLACE1002571, PLACE1002591, PLACE1002655, PLACE1002714, PLACE1003625, PLACE1005287, PLACE1006552, PLACE1007946, PLACE1008426, PLACE1010148, PLACE1010547, PLACE1010743, PLACE1010896, PLACE1010960, PLACE1011310, PLACE1011922, PLACE2000216, PLACE2000274, PLACE2000371, PLACE2000458, PLACE3000145, PLACE3000416, PLACE4000009, TYRO1000132, TYRO1001405, TYRO1001458, Y79AA1000368, Y79AA1000794, Y79AA1000833, Y79AA1000962, Y79AA1002208,				
	[0288] The following 54 clones presumably belong to cell division-associated and/or cell proliferation-associated proteins.				
	HEMBA1001019, HEMBA1001595, HEMBA1002363, HEMBA1002997, HEMBA1003136, HEMBA1003369, HEMBA1004131, HEMBA1004354, HEMBA1005621, HEMBB1000037, HEMBB1000264, MAMMA1001768, MAMMA1002769, NT2RM1000354, NT2RM1000430, NT2RM1000874, NT2RM2001256, NT2RM2001743,				

NT2RM2001896, NT2RM2002145, NT2RM4000215, NT2RM4001714, NT2RP1000163, NT2RP1000333,  
 NT2RP1000439, NT2RP2000346, NT2RP2001397, NT2RP2002595, NT2RP2003177, NT2RP2003596,  
 NT2RP2003912, NT2RP2004396, NT2RP2005037, NT2RP2005520, NT2RP2005669, NT2RP2005835,  
 NT2RP3001730, NT2RP3002081, NT2RP4000210, NT2RP4000415, NT2RP4001414, NT2RP4001634,  
 5 OVARC1000013, OVARC1000937, PLACE1001383, PLACE1002433, PLACE1004316, PLACE1005287,  
 PLACE1008808, PLACE1010720, PLACE1010833, Y79AA1000748, Y79AA1001236, Y79AA1001394,

**[0289]** The following 36 clones presumably belong to the category of embryogenesis- and/or development-associated proteins.

HEMBA1000518, HEMBA1001847, HEMBA1001869, HEMBA1003545, HEMBA1004973, HEMBB1002442,  
 10 MAMMA1001837, NT2RM2001670, NT2RM4000046, NT2RM4000531, NT2RM4001140, NT2RM4001858,  
 NT2RP2002078, NT2RP2004187, NT2RP2006436, NT2RP3000603, NT2RP3000994, NT2RP3001580,  
 NT2RP3001708, NT2RP3003071, NT2RP3004472, NT2RP3004617, NT2RP4000246, NT2RP4001567,  
 OVARC1000304, OVARC1000746, PLACE1000793, PLACE1002532, PLACE1003258, PLACE1003625,  
 PLACE1004460, PLACE1009622, PLACE4000558, THYRO1000085, Y79AA1001391, Y79AA1001692,

15 **[0290]** The following 30 clones presumably belong to cellular defense-associated proteins.

HEMBA1000005, HEMBA1000531, HEMBA1003417, HEMBA1006253, NT2RM4000354, NT2RM4001880,  
 NT2RP1000333, NT2RP1000493, NT2RP2000006, NT2RP2000045, NT2RP2000809, NT2RP2001536,  
 NT2RP2002464, NT2RP2004920, NT2RP2005037, NT2RP3000590, NT2RP3001426, NT2RP3002062,  
 NT2RP3002785, NT2RP3004262, NT2RP4001555, NT2RP4001638, PLACE1006958, PLACE1008275,  
 20 PLACE1009113, PLACE1011858, PLACE4000014, THYRO1000684, Y79AA1002139, Y79AA1002229,

**[0291]** Although it is unclear whether or not 261 clones out of clones other than the above-mentioned clones belong to any of the above-described categories, these clones are predicted to have some functions, based on the homology search using the full-length sequences thereof. The clone names and the gene definitions found in the result of homology search are shown below, separated with a double-slash mark, //.

25 HEMBA1000030//Homo sapiens ARF GTPase-activating protein GIT1 mRNA, complete cds.

HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1

30 HEMBA1000333//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.

HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).

HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.

HEMBA1001197//Homo sapiens rap2 interacting protein x mRNA, complete cds.

HEMBA1001302//Homo sapiens calcium binding protein precursor, mRNA, complete cds.

35 HEMBA1001455//Mus musculus transposon-derived Buster2 transposase-like protein gene, partial cds.

HEMBA1001675//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.

HEMBA1001714//Homo sapiens mRNA for ATPase inhibitor precursor, complete cds.

HEMBA1001744//SCY1 PROTEIN.

HEMBA1001967//Homo sapiens NY-REN-57 antigen mRNA, partial cds.

40 HEMBA1002151//Rattus norvegicus p34 mRNA, complete cds.

HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].

HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.

HEMBA1002777//Fugu rubripes BAW (BAW) mRNA, complete cds.

HEMBA1003098//Homo sapiens NY-REN-6 antigen mRNA, partial cds.

45 HEMBA1003199//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.

HEMBA1003615//Homo sapiens ART-4 mRNA, complete cds.

HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).

HEMBA1004295//Homo sapiens NY-REN-25 antigen mRNA, partial cds.

HEMBA1004573//Homo sapiens mRNA for HELG protein.

50 HEMBA1004604//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.

HEMBA1004795//COC4-LIKE PROTEIN (FRAGMENT).

HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.

HEMBA1005201//Homo sapiens CGI-07 protein mRNA, complete cds.

HEMBA1005206//Drosophila simulans anon73B1 gene and Su(P) gene.

55 HEMBA1005530//Homo sapiens anaphase-promoting complex subunit 7 (APC7) mRNA, complete cds.

HEMBA1005666//Homo sapiens mRNA for DIPB protein.

HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.

HEMBA1006268//Homo sapiens HQOO24c mRNA, complete cds.

- HEMBA1006398//Human L1 element L1.6 putative p150 gene, complete cds.  
HEMBA1006445//Homo sapiens putative tumor suppressor NOEY2 mRNA, complete cds.  
HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds.  
5 HEMBA1007251//Homo sapiens F-box protein FBX29 (FBX29) mRNA, partial cds. HEMBB1000036//Homo sapiens CGI-51 protein mRNA, complete cds.  
HEMBB1000144//GUANYLATE CYCLASE ACTIVATING PROTEIN 2 (GCAP 2) (RETINAL GUANYLYL CYCLASE ACTIVATOR PROTEIN P24).  
HEMBB1000973//Mus musculus schlafen3 (Sfn3) mRNA, complete cds.  
HEMBB1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds  
10 HEMBB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).  
HEMBB1001288//COPPER HOMEOSTASIS PROTEIN CUTC.  
HEMBB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain: BALB/c.  
HEMBB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.  
HEMBB1002266//NEURONAL PROTEIN.  
15 HEMBB1002510//GYP7 PROTEIN.  
HEMBB1002705//Homo sapiens CGI-27 protein mRNA, complete cds.  
MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TEST)].  
MAMMA1000625//GYP7 PROTEIN.  
MAMMA1001075//Homo sapiens CGI-72 protein mRNA, complete cds.  
20 MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR.  
MAMMA1001259//Mus musculus F-box protein FBX18 mRNA, partial cds.  
MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.  
MAMMA1002143//Homo sapiens Cdc42 effector protein 4 mRNA, complete cds.  
25 MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.  
MAMMA1002972//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27.  
MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.  
NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).  
30 NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).  
NT2RM1000244//Homo sapiens TRAF4 associated factor 1 mRNA, partial cds.  
NT2RM1000421//RIBONUCLEASE INHIBITOR.  
NT2RM1000499//Caenorhabditis elegans mRNA for centaurin gamma 1A.  
35 NT2RM1000623//RIBONUCLEASE INHIBITOR.  
NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.  
NT2RM2000502//Rattus norvegicus W307 mRNA, complete cds.  
NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.  
NT2RM2000718//Homo sapiens endocrine regulator mRNA, complete cds.  
40 NT2RM2001065//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.  
NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).  
NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.  
NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.  
NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.  
45 NT2RM4000030//LAS1 PROTEIN.  
NT2RM4000139//R. norvegicus trg mRNA.  
NT2RM4000156//H. sapiens HPBII-7 gene.  
NT2RM4000386//Mus musculus ODZ3 (Odz3) mRNA, partial cds.  
NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).  
50 NT2RM4001047//MO25 PROTEIN.  
NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN.  
NT2RM4001256//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.  
NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds.  
NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).  
55 NT2RM4001347//Homo sapiens NY-REN-25 antigen mRNA, partial cds.  
NT2RM4001371//Homo sapiens IDN3 mRNA, partial cds.  
NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.  
NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).

- NT2RM4001731//Homo sapiens F-box protein Liliina (LILINA) mRNA, complete cds.  
 NT2RM4001969//R.norvegicus mRNA for IP63 protein.  
 NT2RM4002034//Homo sapiens hiwi mRNA, partial cds.  
 NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).  
 5 NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.  
 NT2RP1000040//Mus musculus donson protein (Donson) mRNA, partial cds.  
 NT2RP1000363//R.norvegicus LL5 mRNA.  
 NT2RP1000481//Homo sapiens antigen NY-CO-3 (NY-CO-3) mRNA, partial cds.  
 NT2RP1000513//Human NifU-like protein (hNifU) mRNA, partial cds.  
 10 NT2RP1000733//Human mRNA for GSPT1-TK protein, complete cds.  
 NT2RP1000860//Homo sapiens KLO4P mRNA, complete cds.  
 NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).  
 NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.  
 NT2RP1001395//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.  
 15 NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).  
 NT2RP1001494//MALE STERILITY PROTEIN 2.  
 NT2RP2000054//Homo sapiens putative ring zinc finger protein NY-REN-43 antigen mRNA, complete cds.  
 NT2RP2000067//Mus musculus ODZ3 (Odz3) mRNA, partial cds.  
 NT2RP2000133//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.  
 20 NT2RP2000157//MLO2 PROTEIN.  
 NT2RP2000764//NIFS PROTEIN.  
 NT2RP2000965//Homo sapiens mRNA for fls353, complete cds.  
 NT2RP2001839//SCY1 PROTEIN.  
 NT2RP2001883//Homo sapiens CGI-01 protein mRNA, complete cds.  
 25 NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds.  
 NT2RP2001985//Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha mRNA, complete cds.  
 NT2RP2002185//Homo sapiens ubiquitin mRNA, complete cds.  
 NT2RP2002442//HESA PROTEIN.  
 30 NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.  
 NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.  
 NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.  
 NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.  
 NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.  
 35 NT2RP2003272//Homo sapiens ubiquitin mRNA, complete cds.  
 NT2RP2003857//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).  
 NT2RP2003871//Homo sapiens transposon-derived Buster1 transposase-like protein gene, complete cds.  
 NT2RP2004425//Mus musculus axotrophin mRNA, complete cds.  
 NT2RP2004476//Homo sapiens cyclin L ania-6a mRNA, complete cds.  
 40 NT2RP2004710//Mus musculus formin binding protein 30 mRNA, complete cds.  
 NT2RP2004816//H58 PROTEIN.  
 NT2RP2005441//Homo sapiens hypothalamus protein HT002 mRNA, complete cds.  
 NT2RP2005490//Mus musculus D3Mm3e (D3Mm3e) mRNA, complete cds.  
 NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.  
 45 NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).  
 NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.  
 NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.  
 NT2RP2005841//Homo sapiens mRNA for ALEX3, complete cds.  
 NT2RP2006598//Homo sapiens retinoid x receptor interacting protein mRNA, complete cds.  
 50 NT2RP3000047//NPL4 PROTEIN.  
 NT2RP3000233//RING CANAL PROTEIN (KELCH PROTEIN).  
 NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.  
 NT2RP3000889//Drosophila melanogaster AAA family protein Bor (bor) mRNA, complete cds.  
 55 NT2RP3001399//SSU72 PROTEIN.  
 NT2RP3001407//SCY1 PROTEIN.  
 NT2RP3001457//Drosophila melanogaster Melted (melt) mRNA, partial cds.  
 NT2RP3001587//Human anthracycline-associated resistance ARX mRNA, complete cds.

- NT2RP3001712//Homo sapiens HP1-BP74 protein mRNA, complete cds.  
 NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN).  
 NT2RP3001854//Homo sapiens novel retinal pigment epithelial cell protein (NORPEG) mRNA, complete cds.  
 NT2RP3001931//Rattus norvegicus clone C48 CDK5 activator-binding protein mRNA, complete cds.  
 5 NT2RP3002273//SCD6 PROTEIN.  
 NT2RP3002631//Homo sapiens Ran binding protein 11 mRNA, complete cds.  
 NT2RP3002682//Homo sapiens CGI-145 protein mRNA, complete cds.  
 NT2RP3002770//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.  
 NT2RP3002818//INSERTION ELEMENT IS2A HYPOTHETICAL 48.2 KD PROTEIN.  
 10 NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).  
 NT2RP3002972//Halocynthia roretzi mRNA for HrPET-1, complete cds.  
 NT2RP3003032//Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds.  
 NT2RP3003290//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.  
 15 NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.  
 NT2RP3003491//Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.  
 NT2RP3003500//SCY1 PROTEIN.  
 NT2RP3003726//Homo sapiens spermatogenesis associated PD1 mRNA, complete cds.  
 NT2RP3003438//R. norvegicus mRNA for cytosolic resiniferatoxin-binding protein.  
 20 NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).  
 NT2RP4000129//Xenopus laevis F-box protein 28 (Fbx28) mRNA, partial cds.  
 NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).  
 NT2RP4000528//NPL4 PROTEIN.  
 NT2RP4000737//Mus musculus F-box protein FBL10 mRNA, partial cds.  
 25 NT2RP4000979//Homo sapiens putative HIV-1 infection related protein mRNA, partial cds.  
 NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds.  
 NT2RP4001207//Homo sapiens Ran binding protein 11 mRNA, complete cds.  
 NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).  
 NT2RP4001260//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.  
 30 NT2RP4001339//Homo sapiens mRNA for AMMER1 protein.  
 NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.  
 NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.  
 NT2RP4001966//Mus musculus ODZ3 (Odz3) mRNA, partial cds.  
 35 NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).  
 OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.  
 OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).  
 OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.  
 OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857O7  
 40 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).  
 OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds.  
 OVARC1001555//NGG1-INTERACTING FACTOR 3.  
 OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).  
 OVARG1001943//Mus musculus DEBT-91 mRNA, complete cds.  
 45 PLACE1000004//Homo sapiens IDN3-B mRNA, complete cds.  
 PLACE1000066//SSU72 PROTEIN.  
 PLACE1000610//MSN5 PROTEIN.  
 PLACE1000636//MALE STERILITY PROTEIN 2.  
 PLACE1000769//Homo sapiens CGI-18 protein mRNA, complete cds.  
 50 PLACE1000987//Rattus norvegicus late gestation lung 2 protein (Lg2) mRNA, complete cds.  
 PLACE1001036//Homo sapiens mRNA for alpha integrin binding protein 63, partial.  
 PLACE1001845//Mus musculus cyclin ania-6a mRNA, complete cds.  
 PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.  
 PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.  
 55 PLACE1003602//Homo sapiens mRNA expressed in placenta.  
 PLACE1003611//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.  
 PLACE1004256//Mus musculus short coiled coil protein SCOCO (Scoc) mRNA, complete cds.  
 PLACE1004550//Homo sapiens CGI-20 protein mRNA, complete cds.



PLACE1004868//MALE STERILITY PROTEIN 2.  
 PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.  
 PLACE1005052//Homo sapiens CGI-16 protein mRNA, complete cds.  
 PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).  
 5 PLACE1005176//Homo sapiens hypothalamus protein HT001 mRNA, complete cds.  
 PLACE1005187//APAG PROTEIN.  
 PLACE1005331//Homo sapiens 7h3 protein mRNA, partial cds.  
 PLACE1005727//Homo sapiens STRIN protein (STRIN) mRNA, complete cds.  
 PLACE1006003//Homo sapiens CGI-94 protein mRNA, complete cds.  
 10 PLACE1006335//Homo sapiens NY-REN-50 antigen mRNA, partial cds.  
 PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.  
 PLACE1006506//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.  
 PLACE1007105//Homo sapiens muskellin (MKLN1) mRNA, complete cds.  
 PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.  
 15 PLACE1007705//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.  
 PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.  
 PLACE1007897//Homo sapiens FLASH mRNA, complete cds.  
 PLACE1008080//Homo sapiens mRNA for HEXIM1 protein, complete cds.  
 PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).  
 20 PLACE1008398//GENE 33 POLYPEPTIDE.  
 PLACE1008465//Homo sapiens mRNA for rapa-1 (rapa gene).  
 PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.  
 PLACE1009020//NIFS PROTEIN.  
 PLACE1009060//BRO1 PROTEIN.  
 25 PLACE1009186//Homo sapiens small zinc finger-like protein (TIM9b) mRNA, complete cds.  
 PLACE1009443//Mus musculus F-box protein FBL8 mRNA, complete cds.  
 PLACE1009571//Homo sapiens PTD002 mRNA, complete cds.  
 PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.  
 PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).  
 30 PLACE1010261//SEGREGATION DISTORTER PROTEIN.  
 PLACE1010310//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).  
 PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds.  
 PLACE1010579//Homo sapiens CED-6 protein (CED-6) mRNA, complete cds.  
 PLACE1010628//Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and  
 35 S171 gene, partial cds.  
 PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS13.  
 PLACE1010761//Homo sapiens mRNA for cisplatin resistance-associated overexpressed protein, complete cds.  
 PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INSB.  
 PLACE1011340//Homo sapiens IDN3-B mRNA, complete cds.  
 40 PLACE1011586//Rattus norvegicus clone C53 CDK5 activator-binding protein mRNA, complete cds.  
 PLACE2000246//RING CANAL PROTEIN (KELCH PROTEIN).  
 PLACE2000411//Homo sapiens epsin 2b mRNA, complete cds.  
 PLACE3000477//Homo sapiens phosphoprotein pp75 mRNA, partial cds.  
 THYRO1000173//Homo sapiens AP-mu chain family member mu1B (HSMU1B) mRNA, complete cds.  
 45 THYRO1000401//Human Tcd37 homolog (HTcd37) mRNA, partial cds.  
 THYRO1000668//Mus musculus mRNA for kinesin like protein 9.  
 THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.  
 THYRO1001347//Homo sapiens RAN binding protein 16 mRNA, complete cds.  
 THYRO1001656//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.  
 50 THYRO1001703//NIFR3-LIKE PROTEIN.  
 THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).  
 Y79AA1000059//Homo sapiens aryl-hydrocarbon interacting protein-like 1 (AIP1) gene, complete cds.  
 Y79AA1000181//Homo sapiens CGI-01 protein mRNA, complete cds.  
 Y79AA1000268//Mus musculus Nip2l mRNA, complete cds.  
 55 Y79AA1000313//CALPHOTIN.  
 Y79AA1000540//CELL POLARITY PROTEIN TEA1.  
 Y79AA1000966//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.  
 Y79AA1000985//Human centrosomal protein kendrin mRNA, complete cds.

Y79AA1001323//Mus musculus mRNA for GSG1, complete cds.

Y79AA1001402//Homo sapiens paraneoplastic cancer-testis-brain antigen (MA4) mRNA, partial cds.

Y79AA1001679//Homo sapiens lambda-crystallin mRNA, complete cds.

Y79AA1001923//Homo sapiens F-box protein Fbx22 (FEX22) gene, partial cds. Y79AA1002083//H. sapiens mRNA for MUF1 protein.

Y79AA1002307//Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds.

Y79AA1002311//R. norvegicus mRNA for cytosolic resiniferatoxin-binding protein.

Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.

**[0292]** Among the clones other than the above-mentioned, there were 36 clones that were similarly classified into the functional categories based on the results of functional domain search using the Pfam program. These clones were categorized as follows.

**[0293]** Clones presumably belonging to the category of secretory or membrane proteins are two clones, MAMMA1002498 and NT2RM4002287, a clone presumably belonging to the category of glycoproteins-associated proteins is a clone MAMMA1002498; clones presumably belonging to the category of signal transduction-associated proteins are 11 clones, HEMBA1001247, NT2RM2001813, NT2RM4001454, NT2RP2005140, NT2RP2005293, NT2RP3000487, NT2RP3003311, PLACE1000972, PLACE1003723, PLACE1005327, and PLACE3000124; clones presumably belonging to the category of transcription-associated proteins are 12 clones, HEMBA1003257, NT2RM2000101, NT2RM2001797, NT2RP1000101, NT2RP2002208, NT2RP3001214, NT2RP3003276, NT2RP4001235, PLACE1000050, PLACE1001716, PLACE1002499, and PLACE1007544; clones presumably belonging to the category of enzymes and/or metabolism-associated proteins are 2 clones, HEMBA1005732 and MAMMA1000402; clones presumably belonging to the category of DNA- and/or RNA-binding proteins are 4 clones, HEMBA1004596, OVARC1000148, PLACE1003334, and THYRO1001661; a clone presumably belonging to the category of protein synthesis- and/or protein transport-associated proteins is a clone, HEMBA1006284.

**[0294]** So far, useful information for presuming the functions is unavailable for the remaining 2511 clones. Their functions will possibly be revealed by further analyses. Names of the clones are listed below.

**[0295]** So far, useful information for presuming the functions are unavailable for the remaining 2511 clones. Their functions will possibly be revealed by further analyses. Names of the clones are listed below.

HEMBA1000042,	HEMBA1000046,	HEMBA1000050,	HEMBA1000076,	HEMBA1000193,	HEMBA1000213,
HEMBA1000227,	HEMBA1000231,	HEMBA1000243,	HEMBA1000244,	HEMBA1000251,	HEMBA1000284,
HEMBA1000280,	HEMBA1000282,	HEMBA1000288,	HEMBA1000290,	HEMBA1000302,	HEMBA1000327,
HEMBA1000338,	HEMBA1000351,	HEMBA1000357,	HEMBA1000376,	HEMBA1000387,	HEMBA1000392,
HEMBA1000396,	HEMBA1000428,	HEMBA1000442,	HEMBA1000456,	HEMBA1000459,	HEMBA1000460,
HEMBA1000469,	HEMBA1000497,	HEMBA1000501,	HEMBA1000504,	HEMBA1000505,	HEMBA1000508,
HEMBA1000519,	HEMBA1000520,	HEMBA1000534,	HEMBA1000545,	HEMBA1000557,	HEMBA1000568,
HEMBA1000575,	HEMBA1000594,	HEMBA1000604,	HEMBA1000622,	HEMBA1000636,	HEMBA1000655,
HEMBA1000673,	HEMBA1000682,	HEMBA1000686,	HEMBA1000702,	HEMBA1000722,	HEMBA1000726,
HEMBA1000727,	HEMBA1000749,	HEMBA1000752,	HEMBA1000769,	HEMBA1000773,	HEMBA1000774,
HEMBA1000843,	HEMBA1000867,	HEMBA1000869,	HEMBA1000872,	HEMBA1000876,	HEMBA1000908,
HEMBA1000918,	HEMBA1000934,	HEMBA1000942,	HEMBA1000943,	HEMBA1000946,	HEMBA1000960,
HEMBA1000968,	HEMBA1000971,	HEMBA1000972,	HEMBA1000975,	HEMBA1000985,	HEMBA1000986,
HEMBA1001008,	HEMBA1001009,	HEMBA1001020,	HEMBA1001022,	HEMBA1001024,	HEMBA1001026,
HEMBA1001051,	HEMBA1001060,	HEMBA1001080,	HEMBA1001094,	HEMBA1001099,	HEMBA1001109,
HEMBA1001121,	HEMBA1001122,	HEMBA1001123,	HEMBA1001133,	HEMBA1001140,	HEMBA1001208,
HEMBA1001213,	HEMBA1001226,	HEMBA1001235,	HEMBA1001281,	HEMBA1001299,	HEMBA1001303,
HEMBA1001310,	HEMBA1001319,	HEMBA1001323,	HEMBA1001326,	HEMBA1001327,	HEMBA1001330,
HEMBA1001361,	HEMBA1001375,	HEMBA1001377,	HEMBA1001383,	HEMBA1001388,	HEMBA1001391,
HEMBA1001398,	HEMBA1001411,	HEMBA1001413,	HEMBA1001415,	HEMBA1001432,	HEMBA1001433,
HEMBA1001435,	HEMBA1001442,	HEMBA1001450,	HEMBA1001463,	HEMBA1001497,	HEMBA1001522,
HEMBA1001533,	HEMBA1001566,	HEMBA1001570,	HEMBA1001581,	HEMBA1001589,	HEMBA1001608,
HEMBA1001636,	HEMBA1001640,	HEMBA1001647,	HEMBA1001655,	HEMBA1001658,	HEMBA1001702,
HEMBA1001711,	HEMBA1001712,	HEMBA1001731,	HEMBA1001745,	HEMBA1001750,	HEMBA1001781,
HEMBA1001784,	HEMBA1001791,	HEMBA1001803,	HEMBA1001815,	HEMBA1001820,	HEMBA1001835,
HEMBA1001864,	HEMBA1001888,	HEMBA1001910,	HEMBA1001912,	HEMBA1001915,	HEMBA1001918,
HEMBA1001939,	HEMBA1001940,	HEMBA1001942,	HEMBA1001950,	HEMBA1001964,	HEMBA1001987,
HEMBA1002018,	HEMBA1002022,	HEMBA1002039,	HEMBA1002049,	HEMBA1002084,	HEMBA1002100,
HEMBA1002113,	HEMBA1002119,	HEMBA1002160,	HEMBA1002162,	HEMBA1002185,	HEMBA1002189,
HEMBA1002191,	HEMBA1002199,	HEMBA1002204,	HEMBA1002229,	HEMBA1002237,	HEMBA1002265,

	HEMBA1002328,	HEMBA1002337,	HEMBA1002348,	HEMBA1002349,	HEMBA1002381,	HEMBA1002430,
	HEMBA1002439,	HEMBA1002460,	HEMBA1002498,	HEMBA1002503,	HEMBA1002508,	HEMBA1002515,
	HEMBA1002538,	HEMBA1002542,	HEMBA1002552,	HEMBA1002558,	HEMBA1002583,	HEMBA1002621,
	HEMBA1002624,	HEMBA1002629,	HEMBA1002645,	HEMBA1002666,	HEMBA1002678,	HEMBA1002679,
5	HEMBA1002688,	HEMBA1002696,	HEMBA1002703,	HEMBA1002712,	HEMBA1002716,	HEMBA1002742,
	HEMBA1002748,	HEMBA1002750,	HEMBA1002779,	HEMBA1002794,	HEMBA1002801,	HEMBA1002816,
	HEMBA1002826,	HEMBA1002833,	HEMBA1002850,	HEMBA1002863,	HEMBA1002934,	HEMBA1002937,
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	THYRO1000787,	THYRO1000793,	THYRO1000796,	THYRO1000805,	THYRO1000815,	THYRO1000843,
	THYRO1000855,	THYRO1000865,	THYRO1000895,	THYRO1000916,	THYRO1000952,	THYRO1000988,
30	THYRO1001031,	THYRO1001062,	THYRO1001133,	THYRO1001142,	THYRO1001173,	THYRO1001213,
	THYRO1001262,	THYRO1001321,	THYRO1001322,	THYRO1001363,	THYRO1001365,	THYRO1001403,
	THYRO1001411,	THYRO1001426,	THYRO1001434,	THYRO1001480,	THYRO1001487,	THYRO1001559,
	THYRO1001570,	THYRO1001584,	THYRO1001595,	THYRO1001602,	THYRO1001605,	THYRO1001637,
	THYRO1001673,	THYRO1001706,	THYRO1001745,	THYRO1001746,	THYRO1001772,	THYRO1001793,
35	THYRO1001854,	THYRO1001895,	THYRO1001907,	VESEN1000122,	Y79AA1000065,	Y79AA1000131,
	Y79AA1000202,	Y79AA1000230,	Y79AA1000355,	Y79AA1000410,	Y79AA1000480,	Y79AA1000539,
	Y79AA1000574,	Y79AA1000774,	Y79AA1000802,	Y79AA1000805,	Y79AA1000824,	Y79AA1000827,
	Y79AA1000850,	Y79AA1000969,	Y79AA1001041,	Y79AA1001061,	Y79AA1001068,	Y79AA1001077,
	Y79AA1001078,	Y79AA1001145,	Y79AA1001167,	Y79AA1001185,	Y79AA1001216,	Y79AA1001228,
40	Y79AA1001281,	Y79AA1001511,	Y79AA1001541,	Y79AA1001555,	Y79AA1001585,	Y79AA1001665,
	Y79AA1001696,	Y79AA1001781,	Y79AA1001805,	Y79AA1002089,	Y79AA1002115,	Y79AA1002125,
	Y79AA1002220,	Y79AA1002234,	Y79AA1002298,	Y79AA1002407,	MAMMA1002215,	MAMMA1002721,
	NT2RP2002070,					

## 45 Homology Search Result Data 1.

[0296] The result of the homology search of the SwissProt using the 5'-end sequence.

[0297] Data include

- 50 the name of clone,  
definition of the top hit data,  
the P-value: the length of the compared sequence: identity (%), and  
the organism and the Accession No. of the top hit data, as in the order separated by //.

55 [0298] Data are not shown for the clones in which the P-value was higher than 1.

[0299] The P-value is a score obtained statistically by taking into account the possible similarity between two sequences. In general, the smaller P-value reflects the higher similarity. (Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410; Gish, W. &

States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3:266-272).

- 5 F-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.8e-85:244:75//MUS MUSCULUS (MOUSE).//Q61712  
F-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINETRNA LIGASE)  
(LEURS).//7.6e-57:231:53//CAENORHABDITIS ELEGANS.//Q09996  
F-HEMBA1000020//TUBULIN BETA CHAIN.//1.0e-92:143:80//AJELLOMYCES CAPSULATA (HISTOPLASMA  
CAPSULATUM).//P41742
- 10 F-HEMBA1000030//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//0.021:136:33//PLASMODIUM  
KNOWLESI (STRAIN NURI).//P04922  
F-HEMBA1000042//METALLOTHIONEIN 10-II (MT-10-II).//0.71:64:32//MYTILUS EDULIS (BLUE MUSSEL).//  
P80247  
F-HEMBA1000046//PROTEIN Q300.//0.92:40:37//MUS MUSCULUS (MOUSE).//Q02722  
F-HEMBA1000050//COMPETENCE PROTEIN S.//0.50:28:35//BACILLUS SUBTILIS.//P80355
- 15 F-HEMBA1000076//ATP SYNTHASE E CHAIN, MITOCHONDRIAL (EC 3.6.1.34).//0.86:41:41//HOMO SAPIENS  
(HUMAN).//P56385  
F-HEMBA1000111  
F-HEMBA1000129//UVSW PROTEIN (DAR PROTEIN).//0.023:68:33//BACTERIOPHAGE T4.//P20703  
F-HEMBA1000141//YSY6 PROTEIN.//0.90:29:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
P38374
- 20 F-HEMBA1000150//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!.//8.4e-16:47:70//HOMO SAPIENS (HUMAN).//  
P39193  
F-HEMBA1000156//IMMEDIATE-EARLY PROTEIN.//8.1e-07:143:28//HERPESVIRUS SAIMIRI (STRAIN 11).//  
Q01042
- 25 F-HEMBA1000158//HYPOTHETICAL PROTEIN KIAA0192 (FRAGMENT).//7.9e-11:129:40//HOMO SAPIENS  
(HUMAN).//Q93074  
F-HEMBA1000168//INSULIN RECEPTOR SUBSTRATE-2 (IRS-2) (4PS).//0.00055:86:36//MUS MUSCULUS  
(MOUSE).//P81122  
F-HEMBA1000180//VPU PROTEIN (U ORF PROTEIN).//0.22:73:28//CHIMPANZEE IMMUNODEFICIENCY VI-  
RUS (SIV(CPZ)) (CIV).//P17286
- 30 F-HEMBA1000185//RAS-1 PROTEIN.//5.1e-10:121:29//NEUROSPORA CRASSA.//P22126  
F-HEMBA1000193//PROLINE-RICH PEPTIDE P-B.//0.00078:56:41//HOMO SAPIENS (HUMAN).//P02814  
F-HEMBA1000201//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.00061:49:42//MUS MUSCULUS  
(MOUSE).//P05142
- 35 F-HEMBA1000213  
F-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PRO-  
TEIN).//1.6e-59:115:53//MUS MUSCULUS (MOUSE).//Q61221  
F-HEMBA1000227//SUPPRESSOR PROTEIN SRP40.//0.000059:135:22//SACCHAROMYCES CEREVISIAE  
(BAKER'S YEAST).//P32583
- 40 F-HEMBA1000231//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME I.//0.024:60:38//  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10264  
F-HEMBA1000243//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.0038:125:34//HOMO SAPIENS (HU-  
MAN).//P08547
- 45 F-HEMBA1000244//HYPOTHETICAL 123.6 KD PROTEIN IN POR2-COX5B INTERGENIC REGION.//3.1e-17:  
149:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40480  
F-HEMBA1000251  
F-HEMBA1000264//PROBABLE E5 PROTEIN.//1.0:49:36//HUMAN PAPILLOMAVIRUS TYPE 58.//P26552  
F-HEMBA1000280//SHORT NEUROTOXIN 1 (TOXIN C-6).//0.98:58:31//NAJA NAJA KAOUTHIA (MONOCLED  
COBRA) (NAJA NAJA SIAMENSIS).//P14613
- 50 F-HEMBA1000282//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!.//0.14:26:65//HOMO SAPIENS (HUMAN).//  
P39188  
F-HEMBA1000288  
F-HEMBA1000290//HYPOTHETICAL 14 KD PROTEIN IN TVRI-6 REPETITIVE REGION.//3.8e-06:98:39//HOMO  
SAPIENS (HUMAN).//P10516
- 55 F-HEMBA1000302  
F-HEMBA1000303//HYPOTHETICAL 104.4 KD PROTEIN F54G8.4 IN CHROMOSOME III.//1.3e-05:69:42//  
CAENORHABDITIS ELEGANS.//Q03601  
F-HEMBA1000304//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!.//0.021:18:83//HOMO SAPIENS (HUMAN).//

- P39194  
F-HEMBA1000307//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//7.1e-06:235.25//HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS).//P39922  
F-HEMBA1000327
- 5 F-HEMBA1000333//SRP1 PROTEIN.//1.0:159:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10193  
F-HEMBA1000338//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/B.8e-26:36.83//HOMO SAPIENS (HUMAN).//P39193  
F-HEMBA1000351
- 10 F-HEMBA1000355//BASIC PROLINE-RICH PEPTIDE P-E (I8-9).//0.99:22:50//HOMO SAPIENS (HUMAN).//P02811  
F-HEMBA1000356//IMMEDIATE-EARLY PROTEIN IE180.//0.11:82:36//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675  
F-HEMBA1000357//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/2.1e-35:105.74//HOMO SAPIENS (HUMAN).//P39192
- 15 F-HEMBA1000366//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR AF1627.//1.0:28:42//ARCHAEOGLOBUS FULGIDUS.//O28646  
F-HEMBA1000369//PRESYNAPTIC DENSITY PROTEIN 95 (PSD-95).//0.013:140:26//HOMO SAPIENS (HUMAN).//P78352
- 20 F-HEMBA1000376//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//6.8e-08:66:42//MUS MUSCULUS (MOUSE).//P11369  
F-HEMBA1000387//HYPOTHETICAL 63.2 KD PROTEIN C1F3.09 IN CHROMOSOME I.//1.5e-15:177:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10414  
F-HEMBA1000390//PARATHYMOSIN.//0.0071:61:29//HOMO SAPIENS (HUMAN).//P20962
- 25 F-HEMBA1000392//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.1e-30:92:69//HOMO SAPIENS (HUMAN).//P39194  
F-HEMBA1000396//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.9e-23:64:57//HOMO SAPIENS (HUMAN).//P08547  
F-HEMBA1000411
- 30 F-HEMBA1000418  
F-HEMBA1000422//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/8.3e-10:90:53//HOMO SAPIENS (HUMAN).//P39188  
F-HEMBA1000428//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.1e-12:72:55//HOMO SAPIENS (HUMAN).//P08547
- 35 F-HEMBA1000434  
F-HEMBA1000442//GENE 11 PROTEIN.//1.0:28:46//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15902  
F-HEMBA1000456//26S PROTEASOME REGULATORY SUBUNIT MTS4 (19S REGULATORY CAP REGION OF 26S PROTEASE SUBUNIT 2).//0.077:118:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87048  
F-HEMBA1000459//HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-) (HRI).//4.8e-62:102:78//ORYCTOLAGUS CUNICULUS (RABBIT).//P33279
- 40 F-HEMBA1000460//LYSIS PROTEIN (E PROTEIN) (GPE).//1.0:24:50//BACTERIOPHAGE ALPHA-3.//P31280  
F-HEMBA1000464  
F-HEMBA1000469//PILI PROTEIN.//1.0:27:44//PSEUDOMONAS AERUGINOSA.//P43502  
F-HEMBA1000488//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//1.1e-07:90:38//HOMO SAPIENS (HUMAN).//Q13105
- 45 F-HEMBA1000490//PLECTIN.//0.74:254:25//RATTUS NORVEGICUS (RAT).//P30427  
F-HEMBA1000491//RAS-RELATED PROTEIN M-RAS.//3.0e-14:100:36//RATTUS NORVEGICUS (RAT).//P97538  
F-HEMBA1000501//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.5e-20:81:54//HOMO SAPIENS (HUMAN).//P39194
- 50 F-HEMBA1000504  
F-HEMBA1000505//NEURON-SPECIFIC X11 PROTEIN (FRAGMENT).//0.00028:128:32//HOMO SAPIENS (HUMAN).//Q02410  
F-HEMBA1000508//CHITIN SYNTHASE 3 (EC 2.4.1.16) (CHITIN-UDP ACETYL-GLUCOSAMINYL TRANSFERASE 3).//0.61:132:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P29465
- 55 F-HEMBA1000518  
F-HEMBA1000519//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.8e-37:68:75//HOMO SAPIENS (HUMAN).//P39189

- F-HEMBA1000520//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/5.2e-09:75:49//HOMO SAPIENS (HUMAN).//P39192
- F-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.//1.5e-35:257:36//MUS MUSCULUS (MOUSE).//Q01755
- 5 F-HEMBA1000531//HEAT SHOCK PROTEIN 70 B2.//1.6e-14:72:44//ANOPHELES ALBIMANUS (NEW WORLD MALARIA MOSQUITO).//P41827
- F-HEMBA1000534//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/9.7e-32:96:78//HOMO SAPIENS (HUMAN).//P39193
- 10 F-HEMBA1000540//LANTIBIOTIC LACTICIN 481 PRECURSOR (LACTOCOCCIN DR).//1.0:12:75//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).//P36499
- F-HEMBA1000542//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.0089:79:31//MUS MUSCULUS (MOUSE).//P15265
- F-HEMBA1000545//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.0e-83:256:66//HOMO SAPIENS (HUMAN).//P08547
- 15 F-HEMBA1000555//TRANSLATION INITIATION FACTOR IF-2.//3.6e-06:252:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39730
- F-HEMBA1000557
- F-HEMBA1000561//ZINC FINGER PROTEIN 81 (FRAGMENT).//9.1e-18:200:28//HOMO SAPIENS (HUMAN).//P51508
- 20 F-HEMBA1000563
- F-HEMBA1000568
- F-HEMBA1000569//GPI-ANCHORED PROTEIN P137.//1.0e-40:137:54//HOMO SAPIENS (HUMAN).//Q14444
- F-HEMBA1000575
- F-HEMBA1000588
- 25 F-HEMBA1000591//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.1e-17:41:92//HOMO SAPIENS (HUMAN).//P39194
- F-HEMBA1000592//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//0.18:128:23//HOMO SAPIENS (HUMAN).//Q02224
- F-HEMBA1000594//HYPOTHETICAL 29.3 KD PROTEIN B0280.6 IN CHROMOSOME III.//0.93:24:54//CAENORHABDITIS ELEGANS.//P41997
- 30 F-HEMBA1000604//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00010:49:55//HOMO SAPIENS (HUMAN).//P39188
- F-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8e-55:179:61//HOMO SAPIENS (HUMAN).//Q43295
- 35 F-HEMBA1000622//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-21:94:62//HOMO SAPIENS (HUMAN).//P39188
- F-HEMBA1000638//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.34:73:36//VOLVOX CARTERI.//P21997
- F-HEMBA1000637//BASIC PROLINE-RICH PEPTIDE IB-1.//0.0057:76:38//HOMO SAPIENS (HUMAN).//P04281
- 40 F-HEMBA1000655
- F-HEMBA1000657//ZINC FINGER PROTEIN GCS1.//1.5e-07:66:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35197
- F-HEMBA1000662//METALLOTHIONEIN-II (MT-II).//0.79:33:39//CRICETULUS GRISEUS (CHINESE HAMSTER).//P02799
- 45 F-HEMBA1000673//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/3.1e-17:86:59//HOMO SAPIENS (HUMAN).//P39193
- F-HEMBA1000682//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//3.0e-13:45:44//MUS MUSCULUS (MOUSE).//P11369
- F-HEMBA1000686//HYPOTHETICAL 48.0 KD PROTEIN C1B3.08 IN CHROMOSOME I.//4.5e-07:79:34//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13873
- 50 F-HEMBA1000702
- F-HEMBA1000705//PROTEIN Q300.//0.80:25:44//MUS MUSCULUS (MOUSE).//Q02722
- F-HEMBA1000719//MYOSIN IC HEAVY CHAIN.//0.0026:115:44//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569
- 55 F-HEMBA1000722
- F-HEMBA1000726//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/7.4e-32:83:77//HOMO SAPIENS (HUMAN).//P39191
- F-HEMBA1000727//ZINC FINGER PROTEIN CTH2 (YTIS11 PROTEIN).//0.73:26:46//SACCHAROMYCES CER-

EVISIAE (BAKER'S YEAST) //P47977  
 F-HEMBA1000747  
 F-HEMBA1000749//HYPOTHETICAL PROTEIN HI1484.//1.0:42:35//HAEMOPHILUS INFLUENZAE.//P44211  
 F-HEMBA1000752//RETROVIRUS-RELATED ENV POLYPROTEIN.//1.0e-08:84:39//HOMO SAPIENS (HUMAN).//P10267  
 F-HEMBA1000769  
 F-HEMBA1000773//PAIRED BOX PROTEIN PAX-4.//1.0:107:33//HOMO SAPIENS (HUMAN).//O43316  
 F-HEMBA1000774//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.3e-23:92:63//HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBA1000791  
 F-HEMBA1000817//PROLACTIN RECEPTOR PRECURSOR (PRL-R).//0.079:87:29//CERVUS ELAPHUS (RED DEER).//Q28235  
 F-HEMBA1000822  
 F-HEMBA1000827//HYPOTHETICAL 8.4 KD PROTEIN.//0.98:48:39//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20546  
 F-HEMBA1000843//HYPOTHETICAL 7.3 KD PROTEIN D1044.5 IN CHROMOSOME III.//0.92:46:34//CAENORHABDITIS ELEGANS.//P41953  
 F-HEMBA1000851//HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEBOX PROTEIN 2).//0.048:39:51//HOMO SAPIENS (HUMAN).//P52951  
 F-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD).//4.0e-24:29:100//HOMO SAPIENS (HUMAN).//P51699  
 F-HEMBA1000867  
 F-HEMBA1000869//PROBABLE E5 PROTEIN.//0.99:70:27//HUMAN PAPILLOMAVIRUS TYPE 18.//P06792  
 F-HEMBA1000870//MYOTOXIN 3 PRECURSOR (CROTAMINE 3).//0.79:43:32//CROTALUS DURISSUS TERRIFICUS (SOUTH AMERICAN RATTLESNAKE).//P24333  
 F-HEMBA1000872//GAR2 PROTEIN.//0.89:70:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891  
 F-HEMBA1000876//DEFENSIN.//0.89:34:38//ALLOMYRINA DICHOTOMA.//Q10745  
 F-HEMBA1000908//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.69:43:37//HOMO SAPIENS (HUMAN).//P30808  
 F-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B3 (MAGE-B3 ANTIGEN).//5.1e-08:44:38//HOMO SAPIENS (HUMAN).//O15480  
 F-HEMBA1000918//60S RIBOSOMAL PROTEIN L37-A (YL35) (FRAGMENT).//1.0:19:52//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P22667  
 F-HEMBA1000919//69 KD PARAFLAGELLAR ROD PROTEIN (69 KD PFR PROTEIN) (PFR-A/PFR-B).//0.29:116:30//TRYPANOSOMA BRUCEI BRUCEI.//P22225  
 F-HEMBA1000934  
 F-HEMBA1000942//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.85:27:59//HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBA1000943  
 F-HEMBA1000946//STO-2 PROTEIN.//0.82:82:30//CAENORHABDITIS ELEGANS.//Q19958  
 F-HEMBA1000960//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/0.0097:29:72//HOMO SAPIENS (HUMAN).//P39192  
 F-HEMBA1000968//METALLOTHIONEIN 20-III ISOFORMS A AND B (MT-20-IIIa AND MT-20-IIIb).//0.047:45:37//MYTILUS EDULIS (BLUE MUSSEL).//P80253  
 F-HEMBA1000971//HYPOTHETICAL BHLF1 PROTEIN.//0.038:172:31//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181  
 F-HEMBA1000972  
 F-HEMBA1000974//HYPOTHETICAL PROTEIN MG441.//0.98:66:28//MYCOPLASMA GENITALIUM.//P47679  
 F-HEMBA1000975//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT).//0.028:57:36//HOMO SAPIENS (HUMAN).//P25067  
 F-HEMBA1000985  
 F-HEMBA1000986//SUBMANDIBULAR GLAND SECRETORY GLX-RICH PROTEIN CB PRECURSOR (GRP-CB) (CONTIGUOUS REPEAT POLYPEPTIDE) (CRP).//0.13:91:34//RATTUS NORVEGICUS (RAT).//P08462  
 F-HEMBA1000991//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II.//5.6e-05:37:45//CAENORHABDITIS ELEGANS.//Q18964  
 F-HEMBA1001007//HYPOTHETICAL PROTEIN KIAA0179.//0.27:72:41//HOMO SAPIENS (HUMAN).//Q14684  
 F-HEMBA1001008//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.4e-25:61:70//HOMO SAPIENS (HUMAN).//P39188

MAN).//P39194  
 F-HEMBA1001009//CUTICLE COLLAGEN 34.//0.044:214:29//CAENORHABDITIS ELEGANS.//P34687  
 F-HEMBA1001017//SYNDECAN-3 PRECURSOR (N-SYNDECAN) (NEUROGLYCAN).//5.0e-85:191:84//RAT-  
 TUS NORVEGICUS (RAT).//P33671  
 5 F-HEMBA1001019  
 F-HEMBA1001020//ALU SUBFAMILY J WARNING ENTRY !!!!!/6.7e-24:49:73//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-HEMBA1001022  
 10 F-HEMBA1001024//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.0e-11:61:59//HOMO SAPIENS (HU-  
 MAN).//P08547  
 F-HEMBA1001026//HYPOTHETICAL PROTEIN BB0073.//0.94:63:34//BORRELIA BURGDORFERI (LYME DIS-  
 EASE SPIROCHETE).//O51100  
 F-HEMBA1001043//INVOLUCRIN.//0.0036:238:25//SAGUINUS OEDIPUS (COTTON-TOP TAMARIN).//P24712  
 15 F-HEMBA1001051//ALU SUBFAMILY SB WARNING ENTRY !!!!!/3.3e-32:95:75//HOMO SAPIENS (HUMAN).//  
 P39189  
 F-HEMBA1001052//CURROMYCIN RESISTANCE PROTEIN.//1.0:31:38//STREPTOMYCES HYGROSCOPICUS.//P16961  
 F-HEMBA1001059//N-ACETYLGLACTOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.4) (N- ACETYLGA-  
 LACTOSAMINE-6-SULFATE SULFATASE) (GALACTOSE-6-SULFATE SULFATASE) (GALNAC6S SULFATASE)  
 20 (CHONDROITINSULFATASE) (CHONDROITINASE).//3.2e-132:249:94//HOMO SAPIENS (HUMAN).//P34059  
 F-HEMBA1001060  
 F-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//8.3e-23:51:96//HOMO SAPIENS (HU-  
 MAN).//P02461  
 F-HEMBA1001077//AUTOIMMUNE REGULATOR (APECED PROTEIN).//3.4e-06:37:56//HOMO SAPIENS (HU-  
 25 MAN).//O43918  
 F-HEMBA1001080//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP34.5).//0.0012:70:  
 38//HERPES SIMPLEX VIRUS (TYPE 1 / STRAW MGH-10).//P37319  
 F-HEMBA1001085//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PPS) (PROTEIN PHOS-  
 PHATASE T) (PPT) (FRAGMENT).//0.00018:76:32//MUS MUSCULUS (MOUSE).//Q60676  
 30 F-HEMBA1001088//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//3.5e-50:176:  
 57//HOMO SAPIENS (HUMAN).//P48059  
 F-HEMBA1001094  
 F-HEMBA1001099//LIGHT-HARVESTING PROTEIN B800/850/890, ALPHA-2 CHAIN (EHA-ALPHA-2) (ANTEN-  
 NA PIGMENT PROTEIN, ALPHA-2 CHAIN) (FRAGMENT).//1.0:15:60//ECTOTHIORHODOSPIRA HALOPHILA.//  
 35 P80101  
 F-HEMBA1001109//ALU SUBFAMILY SB WARNING ENTRY !!!!!/6.7e-37:102:82//HOMO SAPIENS (HU-  
 MAN).//P39189  
 F-HEMBA1001121//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.036:49:46//HOMO SAPIENS (HU-  
 40 MAN).//P08547  
 F-HEMBA1001122  
 F-HEMBA1001123  
 F-HEMBA1001133//HYPOTHETICAL 9.4 KD PROTEIN (ORF2).//0.86:29:41//FELINE IMMUNODEFICIENCY VI-  
 RUS (ISOLATE SAN DIEGO) (FIV), AND FELINE IMMUNODEFICIENCY VIRUS (ISOLATE PETALUMA) (FIV).//  
 45 P19033  
 F-HEMBA1001137//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.0e-22:103:52//HOMO SA-  
 PIENS (HUMAN).//P51523  
 F-HEMBA1001140//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.//0.032:94:36//HOMO SAPIENS (HUMAN).//  
 P53420  
 F-HEMBA1001172  
 50 F-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//2.9e-78:179:79//RATTUS NORVEGICUS  
 (RAT).//P51646  
 F-HEMBA1001197//MAJOR PRION PROTEIN PRECURSOR (PRP) (PRP27-30) (PRP33-35C) (FRAGMENT).//  
 0.051:96:32//CERCOCEBUS ATERRIMUS, AND MACACA SYLVANUS (BARBARY APE).//Q95145  
 F-HEMBA1001208  
 55 F-HEMBA1001213  
 F-HEMBA1001226//PROTEASOME COMPONENT C8 (EC 3.4.9.46) (MACROPAIN SUBUNIT C8) (MULTICAT-  
 ALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8).//1.5e-08:24:91//HOMO SAPIENS (HUMAN).//P25788  
 F-HEMBA1001235//FIBRONECTIN (FN) (FRAGMENT).//0.76:50:38//ORYCTOLAGUS CUNICULUS (RABBIT).//

Q28749

F-HEMBA1001247//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)//0.00052:16.81//VOLVOX CART-ERI//P21997

F-HEMBA1001257//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.)/1.6e-68:178.77//RATTUS NORVEGICUS (RAT)//P70473

F-HEMBA1001265//MANNAN ENDO-1,4-BETA-MANNOSIDASE A PRECURSOR (EC 3.2.1.78) (BETA-MANNANASE A) (1,4-BETA-D-MANNAN MANNANOHYDROLASE A)//0.67:23.60//PIROMYCES SP//P55296

F-HEMBA1001281//HYPOTHETICAL 8.9 KD PROTEIN YCF34 (ORF76)//0.83:48.35//PORPHYRA PURPUREA//P51229

F-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR//1.3e-07:185.29//CAVIA PORCELLUS (GUINEA PIG)//Q60401

F-HEMBA1001289//METABOTROPIC GLUTAMATE RECEPTOR 3 PRECURSOR//0.00018:159.30//RATTUS NORVEGICUS (RAT)//P31422

F-HEMBA1001294

F-HEMBA1001299//ALU SUBFAMILY SX WARNING ENTRY //5.3e-07:27.77//HOMO SAPIENS (HUMAN)//P39195

F-HEMBA1001302//45 KD CALCIUM-BINDING PROTEIN PRECURSOR (STROMAL CELL-DERIVED FACTOR 4) (SDF-4)//3.3e-61:150.76//MUS MUSCULUS (MOUSE)//Q61112

F-HEMBA1001303

F-HEMBA1001310//HYPOTHETICAL PROTEIN KIAA0161//2.7e-10:170.27//HOMO SAPIENS (HUMAN)//P50876

F-HEMBA1001319

F-HEMBA1001323

F-HEMBA1001326//HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION//1.1e-39:144.38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P43601

F-HEMBA1001327

F-HEMBA1001330

F-HEMBA1001351//VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPOBREVIN BINDING PROTEIN (VAP-33)//1.9e-37:155.46//APLYSIA CALIFORNICA (CALIFORNIA SEA HARE)//Q16943

F-HEMBA1001361//RUBREDOXIN (RD)//0.95:44.29//ALCALIGENES EUTROPHUS//P31912

F-HEMBA1001375//AEROLYSIN REGULATORY PROTEIN//0.013:45.33//AEROMONAS SOBRIA//P09165

F-HEMBA1001377//SPERM PROTAMINE P1//1.0:22.40//PLANIGALE MACULATA SINUALIS (COMMON PLANIGALE)//Q18746

F-HEMBA1001383//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN)//0.60:37.29//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z2/CDC-Z34 ISOLATE) (HIV-1)//P12508

F-HEMBA1001387//GTP-BINDING PROTEIN TC10//6.6e-43:83.92//HOMO SAPIENS (HUMAN)//P17081

F-HEMBA1001388//HYPOTHETICAL PROTEIN KIAA0136 (FRAGMENT)//0.00088:46.45//HOMO SAPIENS (HUMAN)//Q14149

F-HEMBA1001391

F-HEMBA1001398//CLOACIN (EC 3.1.-.-) (RIBONUCLEASE)//1.0:59.37//ESCHERICHIA COLI//P00645

F-HEMBA1001405//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.25:41.34//HOMO SAPIENS (HUMAN)//P22531

F-HEMBA1001407//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H]//4.0e-09:129.40//HOMO SAPIENS (HUMAN)//P04280

F-HEMBA1001411//HYPOTHETICAL 34.9 KD PROTEIN IN CYSJ-ENO INTERGENIC REGION (C0313)//0.95:88.31//ESCHERICHIA COLI//P55140

F-HEMBA1001413//SOX-12 PROTEIN (FRAGMENT)//0.95:46.32//MUS MUSCULUS (MOUSE)//Q04890

F-HEMBA1001415//HISTONE H5//0.43:95.29//GALLUS GALLUS (CHICKEN)//P02259

F-HEMBA1001432//LANTIBIOTIC NISIN A PRECURSOR//0.77:46.32//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS)//P13068

F-HEMBA1001433//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//4.8e-09:132.31//NYCTICEBUS COUCANG (SLOW LORIS)//P08548

F-HEMBA1001435//ALU SUBFAMILY SB WARNING ENTRY //1.2e-31:84.77//HOMO SAPIENS (HUMAN)//P39189

F-HEMBA1001442

F-HEMBA1001446//ANTIFREEZE PEPTIDE 4 PRECURSOR//0.71:41.39//PSEUDOPLEURONECTA AMERICANUS (WINTER FLOUNDER)//P02734

F-HEMBA1001450//PROLINE-RICH PROTEIN LAS17//0.13:127.27//SACCHAROMYCES CEREVISIAE (BAK-

ER'S YEAST).//Q12446  
 F-HEMBA1001454//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.57:38:47//HANSENULA WINGEI  
 (YEAST).//P48882  
 5 F-HEMBA1001455//CHEMOTAXIS PROTEIN CHEA (EC 2.7.3.-).//0.98:124:25//BORRELIA BURGDORFERI  
 (LYME DISEASE SPIROCHETE).//Q44737  
 F-HEMBA1001463//ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.8e-32:62:67//HOMO SAPIENS (HU-  
 MAN).//P39194  
 F-HEMBA1001476//NUCLEOPORIN NUP159 (NUCLEAR PORE PROTEIN NUP159).//6.8e-09:252:36//SAC-  
 CHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40477  
 10 F-HEMBA1001478  
 F-HEMBA1001497//ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-33:105:72//HOMO SAPIENS (HU-  
 MAN).//P39194  
 F-HEMBA1001510//ALU SUBFAMILY SB WARNING ENTRY !!!!!//8.3e-37:54:81//HOMO SAPIENS (HUMAN).//  
 P39189  
 15 F-HEMBA1001515//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.0e-63:223:57//HOMO SAPIENS (HU-  
 MAN).//P08547  
 F-HEMBA1001517  
 F-HEMBA1001522//TROPOMYOSIN ALPHA CHAIN, SMOOTH MUSCLE.//0.78:150:22//COTURNIX COTURNIX  
 JAPONICA (JAPANESE QUAIL).//P49437  
 20 F-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//1.6e-06:130:29//CLOSTRIDIUM  
 PASTEURIANUM.//P29166  
 F-HEMBA1001533//PROBABLE E5A PROTEIN.//0.73:35:37//HUMAN PAPILLOMAVIRUS TYPE 6A.//Q84296  
 F-HEMBA1001557//HYPOTHETICAL 17.1 KD PROTEIN IN PURS 3'REGION.//1.5e-07:99:36//SACCHAROMY-  
 CES CEREVISIAE (BAKER'S YEAST).//P38898  
 25 F-HEMBA1001566//HYPOTHETICAL PROTEIN BB0692.//0.91:27:44//BORRELIA BURGDORFERI (LYME DIS-  
 EASE SPIROCHETE).//O51635  
 F-HEMBA1001569//SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2).//2.2e-  
 50:110:95//HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE).//P19065  
 F-HEMBA1001570//ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.3e-33:107:72//HOMO SAPIENS (HU-  
 MAN).//P39195  
 30 F-HEMBA1001579//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-14:111:39//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY).//Q04652  
 F-HEMBA1001581  
 F-HEMBA1001585  
 35 F-HEMBA1001589//PROBABLE DNA-BINDING PROTEIN (AGNOPROTEIN).//0.98:51:33//HUMAN ADENOVIRUS  
 TYPE 2.//P03263  
 F-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//3.0e-124:274:85//HOMO SAPIENS (HUMAN).//  
 Q14141  
 40 F-HEMBA1001608//RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE  
 COTRANSPORTER).//0.99:28:39//ORYCTOLAGUS CUNICULUS (RABBIT).//Q28615  
 F-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//4.3e-45:222:46//  
 SPIRODELA POLYRRHIZA.//P42803  
 F-HEMBA1001635//FIBRILLARIN.//0.10:72:38//CAENORHABDITIS ELEGANS.//Q22053  
 F-HEMBA1001636//PAIRED BOX PROTEIN PAX-8, ISOFORMS 8C/8D.//0.75:38:47//HOMO SAPIENS (HU-  
 MAN).//Q09155  
 45 F-HEMBA1001640//ALU SUBFAMILY J WARNING ENTRY !!!!!//14.7e-08:80:41//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-HEMBA1001647//TRANSCRIPTION INITIATION FACTOR TFIIID 135 KD SUBUNIT (TAFII-135) (TAFII135)  
 (TAFII-130) (TAFII130).//0.075:165:32//HOMO SAPIENS (HUMAN).//Q00268  
 50 F-HEMBA1001651//GOLGIN-95.//6.8e-05:141:24//HOMO-SAPIENS (HUMAN).//Q08379  
 F-HEMBA1001655//PROLINE-RICH PROTEIN LAS17.//0.19:97:30//SACCHAROMYCES CEREVISIAE (BAK-  
 ER'S YEAST).//Q12446  
 F-HEMBA1001658//TETRAHYDROMETHANOPTERIN S-METHYLTRANSFERASE 12 KD SUBUNIT (EC  
 2.1.1.86) (N5-METHYLTETRAHYDROMETHANOPTERIN-COENZYME M METHYLTRANSFERASE 12 KD SUB-  
 55 UNIT).//1.0:29:44//METHANOBACTERIUM THERMOAUTOTROPHICUM (STRAIN MARBURG / DSM 2133).//  
 Q50773  
 F-HEMBA1001661//CELLULOSE COMPLEMENTING PROTEIN.//0.35:87:33//ACETOBACTER XYLINUM (AC-  
 ETOBACTER PASTEURIANUS).//P37697



F-HEMBA1001672//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//2.7e-10:216:35//PLASMODIUM CYNOMOLGI (STRAIN BEROK).//P08672

F-HEMBA1001675//NODULIN 20 PRECURSOR (N-20).//0.98:36:44//GLYCINE MAX (SOYBEAN).//P08960

5 F-HEMBA1001678//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.2e-13:62:64//HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1001681//HYPOTHETICAL 41.5 KD PROTEIN IN P6.5-VP48 INTERGENIC REGION (P40) (ORF3) (ORF102).//1.0:51:39//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//P24653

10 F-HEMBA1001702//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.017:54:37//TRYPANOSOMA BRUCEI BRUCEI.//P24499

F-HEMBA1001709//HYPOTHETICAL 21.2 KD PROTEIN IN TOR2-MNN4 INTERGENIC REGION.//0.59:109:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36042

F-HEMBA1001711

15 F-HEMBA1001712//HYPOTHETICAL 6.9 KD PROTEIN IN 100 KD PROTEIN REGION.//0.54:44:34//HUMAN ADENOVIRUS TYPE 41.//P23690

F-HEMBA1001714//ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR.//1.2e-19:60:75//RATTUS NORVEGICUS (RAT).//Q03344

F-HEMBA1001718//HYPOTHETICAL PROTEIN UL63.//1.0:54:37//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16820

20 F-HEMBA1001723//HYPOTHETICAL 34.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION.//5.1e-26:90:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41318

F-HEMBA1001731//HYPOTHETICAL 16.6 KD PROTEIN.//0.71:49:32//AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN 52/70) (IBDV).//P25221

F-HEMBA1001734

25 F-HEMBA1001744//ISCY1 PROTEIN.//2.1e-11:182:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53009

F-HEMBA1001745//HYPOTHETICAL 11.6 KD PROTEIN IN NUT1-ARO2 INTERGENIC REGION PRECURSOR.//1.0:36:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53116

F-HEMBA1001746//PROTEIN-EXPORT MEMBRANE PROTEIN SECG HOMOLOG.//0.94:48:35//MYCOBACTERIUM LEPRAE.//P38388

30 F-HEMBA1001761

F-HEMBA1001781//ZINC FINGER PROTEIN 19 (ZINC FINGER PROTEIN KOX12) (FRAGMENT).//0.028:47:40//HOMO SAPIENS (HUMAN).//P17023

F-HEMBA1001784//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X.//0.00068:32:46//CAENORHABDITIS ELEGANS.//Q11116

35 F-HEMBA1001791//METALLOTHIONEIN (MT).//1.0:34:35//PLEURONECTES PLATESSA (PLAICE).//P07216

F-HEMBA1001800//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//1.5e-14:60:48//MUS MUSCULUS (MOUSE).//P16372

F-HEMBA1001803

40 F-HEMBA1001804//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1 PRECURSOR.//9.3e-17:56:57//ORYZA SATIVA (RICE).//P25074

F-HEMBA1001808//PARANEOPlastic ENCEPHALOMYELITIS ANTIGEN HUD HOMOLOG (HU-ANTIGEN D).//0.75:97:31//RATTUS NORVEGICUS (RAT).//Q09032

F-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//4.5e-11:206:36//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675

45 F-HEMBA1001815//60S RIBOSOMAL PROTEIN L37-B (YL27) (FRAGMENT).//0.34:30:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P05733

F-HEMBA1001819//ZINC FINGER PROTEIN 135.//2.6e-102:262:66//HOMO SAPIENS (HUMAN).//P52742

F-HEMBA1001820

50 F-HEMBA1001822//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15).//1.2e-18:251:33//MUS MUSCULUS (MOUSE).//P42567

F-HEMBA1001824//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//4.7e-11:124:37//OVIS ARIES (SHEEP).//P26372

F-HEMBA1001835

55 F-HEMBA1001844//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.3e-14:36:63//HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//2.7e-36:135:51//MUS MUSCULUS (MOUSE).//Q07230

F-HEMBA1001861  
 F-HEMBA1001864//HEAT-STABLE ENTEROTOXIN A3/A4 PRECURSOR (STA3/STA4) (ST-IB) (ST-H).//1.0.31:  
 38//ESCHERICHIA COLI.//P07965  
 5 F-HEMBA1001866//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-)  
 (DUGT).//9.7e-42:234:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q09332  
 F-HEMBA1001869//HYPOTHETICAL 94.9 KD PROTEIN C22E12.11C IN CHROMOSOME 1.//5.3e-13:65.47//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10362  
 F-HEMBA1001888//HYPOTHETICAL 11.4 KD PROTEIN (ORF1).//0.85:62:37//STREPTOMYCES FRADIAE.//  
 P26800  
 10 F-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (ME2GLYDH).//9.8e-  
 20:250:29//RATTUS NORVEGICUS (RAT).//Q63342  
 F-HEMBA1001910//EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E) (MRNA CAP-  
 BINDING PROTEIN) (EIF-4F 25 KD SUBUNIT).//0.94:44:38//CAENORHABDITIS ELEGANS.//O61955  
 15 F-HEMBA1001912!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/8.7e-07:53.62//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-HEMBA1001913//GCN20 PROTEIN.//1.8e-21:68:60//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
 P43535  
 F-HEMBA1001915//KLEE PROTEIN (KCRB3 PROTEIN).//0.94:64:21//ESCHERICHIA COLI.//Q52280  
 F-HEMBA1001918  
 20 F-HEMBA1001921  
 F-HEMBA1001939//CHLOROPLAST 50S RIBOSOMAL PROTEIN L24.//1.0:47:31//ODONTELLA SINENSIS.//  
 P49560  
 F-HEMBA1001940!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.0017:31:77//HOMO SAPIENS (HUMAN).//  
 P39188  
 25 F-HEMBA1001942//HIBERNATION-ASSOCIATED PLASMA PROTEIN HP-27 PRECURSOR (HIBERNATOR-  
 SPECIFIC BLOOD COMPLEX, 27 KD SUBUNIT).//1.0:77:28//TAMIAS ASIATICUS (CHIPMUNK).//Q06577  
 F-HEMBA1001945//HYPOTHETICAL 4.6 KD PROTEIN IN GP47-AGT INTERGENIC REGION (ORF E).//1.0:35:  
 37//BACTERIOPHAGE T4.//P32269  
 F-HEMBA1001950//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.43:18:44//DROSOPHILA YAKUBA  
 30 (FRUIT FLY).//P03933  
 F-HEMBA1001960//HOMEOBOX PROTEIN HOX-C5 (HOX-3D) (CP11).//0.17:12:66//HOMO SAPIENS (HU-  
 MAN).//Q00444  
 F-HEMBA1001962//HYPOTHETICAL 9.0 KD PROTEIN IN ADH4 5'REGION.//1.0:30:36//SACCHAROMYCES  
 CEREVISIAE (BAKER'S YEAST).//P53056  
 35 F-HEMBA1001964  
 F-HEMBA1001967//HYPOTHETICAL PROTEIN UL61.//0.027:111:36//HUMAN CYTOMEGALOVIRUS (STRAIN  
 AD169).//P16818  
 F-HEMBA1001979  
 F-HEMBA1001987//HYPOTHETICAL 11.2 KD PROTEIN (ORF117).//1.0:83:32//ORGYIA PSEUDOTSUGATA  
 40 MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10356  
 F-HEMBA1001991//NEUROTOXIN 1 (TOXIN ATX-1).//0.99:31:45//ANEMONIA SULCATA (SNAKE-LOCKS SEA  
 ANEMONE).//P01533  
 F-HEMBA1002003//GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, TESTIS-SPECIFIC (EC  
 1.2.1.12) (GAPDH).//5.5e-07:109:32//MUS MUSCULUS (MOUSE).//Q64467  
 45 F-HEMBA1002008  
 F-HEMBA1002018//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.83:66:33//ARABIDOPSIS THALIANA  
 (MOUSE-EAR CRESS).//Q42377  
 F-HEMBA1002022//INSULIN.//1.0:59:32//SQUALUS ACANTHIAS (SPINY DOGFISH).//P12704  
 F-HEMBA1002035//MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN.//8.3e-15:64:40//HOMO SAPIENS (HU-  
 50 MAN).//Q92794  
 F-HEMBA1002039//HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269.//0.0070:70:40//HOMO SAPIENS  
 (HUMAN).//Q92558  
 F-HEMBA1002049!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.5e-07:37:75//HOMO SAPIENS (HUMAN).//  
 P39188  
 55 F-HEMBA1002084  
 F-HEMBA1002092//SPT23 PROTEIN.//0.12:208:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
 P35210  
 F-HEMBA1002100

F-HEMBA1002102//ANKYRIN.//1.4e-12:106:35//MUS MUSCULUS (MOUSE).//Q02357  
 F-HEMBA1002113//EARLY NODULIN 20 PRECURSOR (N-20).//0.073:155:32//MEDICAGO TRUNCATULA  
 (BARREL MEDIC).//P93329  
 5 F-HEMBA1002119//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.85:22:36//DROSOPHILA MELANO-  
 GASTER (FRUIT FLY).//Q01643  
 F-HEMBA1002125//GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30].//0.35:111:33//FELINE  
 SARCOMA VIRUS (STRAIN SNYDER-THEILEN).//P03338  
 F-HEMBA1002139//HYPOTHETICAL 12.4 KD PROTEIN IN SEC17-QCR1 INTERGENIC REGION.//0.88:72:25//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38192  
 10 F-HEMBA1002144  
 F-HEMBA1002150//THROMBOMODULIN (FETOMODULIN) (TM) (FRAGMENT).//4.8e-10:65:46//BOS TAURUS  
 (BOVINE).//P06579  
 F-HEMBA1002151//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.24:146:28//SACCHAROMY-  
 CES CEREVISIAE (BAKER'S YEAST).//P32323  
 15 F-HEMBA1002153//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.93:58:25//APIS MEL-  
 LIFERA (HONEYBEE).//P34859  
 F-HEMBA1002160//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/5.1e-21:94:65//HOMO SAPIENS (HUMAN).//  
 P39193  
 F-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.4e-51:180:56//SUS  
 SCROFA (PIG).//P79293  
 20 F-HEMBA1002162//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.1e-40:102:75//HOMO SAPIENS (HU-  
 MAN).//P39193  
 F-HEMBA1002166//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.8e-13:133:45//HOMO SAPIENS (HUMAN).//  
 P39188  
 25 F-HEMBA1002177//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//0.0014:153:26//HOMO SAPIENS (HU-  
 MAN).//P52746  
 F-HEMBA1002185  
 F-HEMBA1002189//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/0.86:46:45//HOMO SAPIENS (HUMAN).//  
 P39194  
 30 F-HEMBA1002191//MALE SPECIFIC SPERM PROTEIN MST84DC.//0.037:14:57//DROSOPHILA MELANO-  
 GASTER (FRUIT FLY).//Q01644  
 F-HEMBA1002199  
 F-HEMBA1002204  
 F-HEMBA1002212//DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE  
 35 KINASE OSOR1 (EC 2.7.1.-) (DOWNSTREAM OF RAF) (MAPKK).//3.2e-13:201:30//DROSOPHILA MELANO-  
 GASTER (FRUIT FLY).//Q24324  
 F-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//1.1e-62:147:84//MUS MUSCULUS  
 (MOUSE).//P47226  
 40 F-HEMBA1002226//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.6e-26:168:44//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-HEMBA1002229//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!/6.8e-18:68:72//HOMO SAPIENS (HU-  
 MAN).//P39190  
 F-HEMBA1002237//EAMZP30-47 PROTEIN (FRAGMENT).//0.96:21:61//EIMERIA ACERVULINA.//P21959  
 45 F-HEMBA1002241//METALLOTHIONEIN (MT).//0.95:25:48//PARACENTROTUS LIVIDUS (COMMON SEA UR-  
 CHIN).//P80367  
 F-HEMBA1002253//METALLOTHIONEIN-II (MT-II).//0.97:27:48//MESOCRICETUS AURATUS (GOLDEN HAM-  
 STER).//P17808  
 F-HEMBA1002257  
 F-HEMBA1002265//MALE SPECIFIC SPERM PROTEIN MST84DC.//0.95:24:50//DROSOPHILA MELANO-  
 50 GASTER (FRUIT FLY).//Q01644  
 F-HEMBA1002267//NEURONAL PROTEIN 3.1 (P311 PROTEIN).//0.94:33:33//GALLUS GALLUS (CHICKEN).//  
 Q90667  
 F-HEMBA1002270  
 F-HEMBA1002321//HYPOTHETICAL IMMUNITY REGION PROTEIN 14.//0.99:22:40//BACTERIOPHAGE PHI-  
 105.//P10437  
 55 F-HEMBA1002328  
 F-HEMBA1002337  
 F-HEMBA1002341//P53-BINDING PROTEIN 53BP2 (FRAGMENT).//3.7e-55:109:96//MUS MUSCULUS

(MOUSE).//Q62415  
 F-HEMBA1002348//PROBABLE E5 PROTEIN.//0.43:30:50//HUMAN PAPILLOMAVIRUS TYPE 35.//P27226  
 F-HEMBA1002349  
 F-HEMBA1002363//CHROMOSOME ASSEMBLY PROTEIN XCAP-E.//5.7e-105:278:71//XENOPUS LAEVIS  
 5 (AFRICAN CLAWED FROG).//P50533  
 F-HEMBA1002381//ALU SUBFAMILY J WARNING ENTRY !!!!!/3.3e-24:69:73//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-HEMBA1002389//EARLY NODULIN 20 PRECURSOR (N-20).//0.16:110:31//MEDICAGO TRUNCATULA (BAR-  
 10 REL MEDIC).//P93329  
 F-HEMBA1002417//TIGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1).//2.6e-51:187:56//MUS  
 MUSCULUS (MOUSE).//P39447  
 F-HEMBA1002419//PROLINE-RICH PEPTIDE P-B.//1.0:18:61//HOMO SAPIENS (HUMAN).//P02814  
 F-HEMBA1002430//HYPOTHETICAL 12.3 KD PROTEIN IN GAP1-NAP1 INTERGENIC REGION.//0.042:41:46//  
 15 SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36140  
 F-HEMBA1002439//CHLOROPLAST 50S RIBOSOMAL PROTEIN L27 (FRAGMENT).//0.99:47:29//CALYPTRO-  
 SPHAERA SPHAEROIDEA.//P41548  
 F-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.1e-24:109:55//HOMO SAPI-  
 ENS (HUMAN).//Q00994  
 F-HEMBA1002460  
 20 F-HEMBA1002462//SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).//0.00025:80:30//HOMO SAPIENS  
 (HUMAN).//P81489  
 F-HEMBA1002469//PUTATIVE TUMOR SUPPRESSOR LUCA15.//0.0012:110:33//HOMO SAPIENS (HUMAN).//  
 P52756  
 F-HEMBA1002475//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.37:106:33//MUS MUSCULUS  
 25 (MOUSE).//P05143  
 F-HEMBA1002477//ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.3e-34:96:71//HOMO SAPIENS (HU-  
 MAN).//P39194  
 F-HEMBA1002486  
 F-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.//2.9e-31:110:39//ARABIDOPSIS  
 30 THALIANA (MOUSE-EAR CRESS).//P48732  
 F-HEMBA1002498//SFT2 PROTEIN.//1.0:54:35//SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
 P38166  
 F-HEMBA1002503//ALU SUBFAMILY J WARNING ENTRY !!!!!/3.0e-06:49:63//HOMO SAPIENS (HUMAN).//  
 35 P39188  
 F-HEMBA1002508//ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.6e-22:169:44//HOMO SAPIENS (HU-  
 MAN).//P39195  
 F-HEMBA1002513//HYPOTHETICAL 89.8 KD PROTEIN F41H10.6 IN CHROMOSOME IV.//0.00017:79:35//  
 CAENORHABDITIS ELEGANS.//Q20296  
 F-HEMBA1002515  
 40 F-HEMBA1002538//ATP SYNTHASE E CHAIN, MITOCHONDRIAL (EC 3.6.1.34).//1.0:53:37//SACCCHAROMY-  
 CES CEREVISIAE (BAKER'S YEAST).//P81449  
 F-HEMBA1002542//ALU SUBFAMILY J WARNING ENTRY !!!!!/5.7e-32:96:75//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-HEMBA1002547//AGRIN PRECURSOR.//2.5e-100:218:80//RATTUS NORVEGICUS (RAT).//P25304  
 45 F-HEMBA1002552//HEP27 PROTEIN (PROTEIN D).//9.5e-12:29:82//HOMO SAPIENS (HUMAN).//Q13268  
 F-HEMBA1002555//COLLAGEN ALPHA 1(III) CHAIN.//2.4e-15:207:36//BOS TAURUS (BOVINE).//P04258  
 F-HEMBA1002558//ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.0:34:50//HOMO SAPIENS (HUMAN).//  
 P39193  
 F-HEMBA1002561//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-05:49:46//NYCTICEBUS COU-  
 50 CANG (SLOW LORIS).//P08548  
 F-HEMBA1002569//SINGLE-STRANDED DNA-BINDING PROTEIN P12.//0.97:60:33//BACTERIOPHAGE  
 PRD1.//P17637  
 F-HEMBA1002583  
 F-HEMBA1002590//ALU SUBFAMILY J WARNING ENTRY !!!!!/5.6e-15:54:55//HOMO SAPIENS (HUMAN).//  
 55 P39188  
 F-HEMBA1002592//HISTIDINE-RICH PROTEIN.//0.99:39:28//PLASMODIUM FALCIPARUM (ISOLATE FCM17 /  
 SENEGAL).//P14586  
 F-HEMBA1002609//SSM4 PROTEIN.//1.9e-12:135:29//SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).//

P40318  
 F-HEMBA1002621//CYTOCHROME B6-F COMPLEX 3.5 KD SUBUNIT (CYTOCHROME B6-F COMPLEX SUB-UNIT 6).//1.0:20:55//ZEA MAYS (MAIZE).//P19445  
 5 F-HEMBA1002624//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.0035:124:33//NICOTIANA TABACUM (COMMON TOBACCO).//P13983  
 F-HEMBA1002628  
 F-HEMBA1002629//IMMEDIATE-EARLY PROTEIN IE180.//0.84:80:36//PSEUDORABIES VIRUS (STRAIN KAP-LAN) (PRV).//P33479  
 10 F-HEMBA1002645//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!1.8e-16:57:68//HOMO SAPIENS (HUMAN).//P39193  
 F-HEMBA1002651  
 F-HEMBA1002659//CUTICLE COLLAGEN 2.//0.0077:77:38//CAENORHABDITIS ELEGANS.//P17656  
 F-HEMBA1002661//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.3e-89:116:72//HOMO SAPIENS (HU-MAN).//P08547  
 15 F-HEMBA1002666//BETA CRYSTALLIN A4.//0.18:58:44//GALLUS GALLUS (CHICKEN).//P49152  
 F-HEMBA1002678  
 F-HEMBA1002679//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//5.7e-06:219:27//PLASMODIUM FALCI-PARUM (ISOLATE FC27 / PAPUA NEW GUINEA).//P13816  
 F-HEMBA1002688//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//1.1e-07:198:32//NEPHILA CLA-VIPES (ORB SPIDER).//P46804  
 20 F-HEMBA1002696//COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLA-GEN).//0.16:158:33//HOMO SAPIENS (HUMAN).//Q02388  
 F-HEMBA1002703//HYPOTHETICAL BHLF1 PROTEIN.//0.78:147:29//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181  
 25 F-HEMBA1002712//I1.2 KD PROTEIN (ORF 103).//0.029:75:34//BACTERIOPHAGE PF1.//P25133  
 F-HEMBA1002716//50S RIBOSOMAL PROTEIN L28.//1.0:44:27//BACILLUS SUBTILIS.//P37807  
 F-HEMBA1002728//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!5.4e-18:56:75//HOMO SAPIENS (HUMAN).//P39195  
 30 F-HEMBA1002730//HYPOTHETICAL PROTEIN MJ0316.//0.097:84:35//METHANOCOCCUS JANNASCHII.//Q57764  
 F-HEMBA1002742//APOLOPOPROTEIN C-III PRECURSOR (APO-CIII).//0.97:26:50//SUS SCROFA (PIG).//P27917  
 F-HEMBA1002746//CALPHOTIN.//0.35:65:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q02910  
 35 F-HEMBA1002748//PLATELET GLYCOPROTEIN IB BETA CHAIN PRECURSOR (GP-IB BETA) (GPIIBB).//1.0:74:32//MUS MUSCULUS (MOUSE).//P56400  
 F-HEMBA1002750//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!7.0e-15:49:75//HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBA1002768//HYPOTHETICAL 72.2 KD PROTEIN C12C2.05C IN CHROMOSOME II.//0.00036:197:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09746  
 40 F-HEMBA1002770//UTEROGLOBIN PRECURSOR (BLASTOKININ).//0.023:88:27//ORYCTOLAGUS CUNICU-LUS (RABBIT).//P02779  
 F-HEMBA1002777//HOMEBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3).//0.00018:67:43//MUS MUSCULUS (MOUSE).//P06798  
 45 F-HEMBA1002779//HYPOTHETICAL 17.6 KD PROTEIN IN NPR1-RPS3 INTERGENIC REGION.//0.70:30:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53880  
 F-HEMBA1002780//OLFACTORY RECEPTOR 3 (K10) (FRAGMENT).//1.0:31:45//MUS MUSCULUS (MOUSE).//Q60879  
 F-HEMBA1002794//HMG-Y RELATED PROTEIN B (SB16B PROTEIN) (FRAGMENT).//0.0044:66:37//GLYCINE MAX (SOYBEAN).//Q10370  
 50 F-HEMBA1002801  
 F-HEMBA1002810//HYPOTHETICAL 25.9 KD PROTEIN AH6.3 IN CHROMOSOME II.//0.0033:116:31//CAENORHABDITIS ELEGANS.//Q09202  
 F-HEMBA1002816//HYPOTHETICAL 47.1 KD PROTEIN C9G1.13C IN CHROMOSOME I.//1.0e-17:68:48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14308  
 55 F-HEMBA1002818//FIBULIN-2 PRECURSOR.//2.1e-27:92:44//MUS MUSCULUS (MOUSE).//P37889  
 F-HEMBA1002826//DNA-BINDING PROTEIN 65 (PROTEIN GP65).//0.28:46:34//BACTERIOPHAGE T4.//P16012  
 F-HEMBA1002833

- F-HEMBA1002850//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:27:37//METRIDIDUM SENILE (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE)//O47493
- F-HEMBA1002863//PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV (PHOTOSYSTEM I 8.1 KD PROTEIN) (P30 PROTEIN) (PSI-E)//0.84:37:43//SYNECHOCYSTIS SP. (STRAIN PCC 6803)//P12975
- 5 F-HEMBA1002876//OCTAPEPTIDE-REPEAT PROTEIN T2//0.74:58:34//MUS MUSCULUS (MOUSE)//Q06666
- F-HEMBA1002886
- F-HEMBA1002896//HOMEBOX PROTEIN HOX-B3 (HOX-2G) (HOX-2.7)//4.7e-05:84:35//HOMO SAPIENS (HUMAN)//P14651
- 10 F-HEMBA1002921//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN)//0.21:42:42//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RF/HAT ISOLATE) (HIV-1)//P05908
- F-HEMBA1002924//EC PROTEIN HOMOLOG 2 (FRAGMENT)//0.85:75:22//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//Q42377
- F-HEMBA1002934//ALU SUBFAMILY J WARNING ENTRY !!!!!/3.4e-31:92:72//HOMO SAPIENS (HUMAN)//P39188
- 15 F-HEMBA1002935//GASTRULA ZINC FINGER PROTEIN XLCGF58.1 (FRAGMENT)//7.7e-06:187:29//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P18730
- F-HEMBA1002937//SUPPRESSOR PROTEIN SRP40//0.00031:150:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32583
- F-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)//5.2e-25:225:33//HOMO SAPIENS (HUMAN)//P16157
- 20 F-HEMBA1002944
- F-HEMBA1002951//TRICHOHYALIN//0.0011:220:24//HOMO SAPIENS (HUMAN)//Q07283
- F-HEMBA1002954//PROBABLE E8 PROTEIN//0.98:49:32//BOVINE PAPILLOMAVIRUS TYPE 4//P08352
- F-HEMBA1002968//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONIAL PEPTIDE B)//0.93:41:34//DROSOPHILA SECHELLIA (FRUIT FLY)//O18417
- 25 F-HEMBA1002970//ALU SUBFAMILY SP WARNING ENTRY !!!!!/0.00010:35:62//HOMO SAPIENS (HUMAN)//P39193
- F-HEMBA1002971//INSULIN//1.0:31:35//HYDROLAGUS COLLIEI (SPOTTED RATFISH) (PACIFIC RATFISH), AND CHIMAERA MONSTROSA (RABBIT FISH)//P09536
- 30 F-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPDE4)//3.0e-29:63:100//RATTUS NORVEGICUS (RAT)//P14646
- F-HEMBA1002997//HYPOTHETICAL 106.5 KD PROTEIN IN CTT1-PRP31 INTERGENIC REGION//1.0e-08:211:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53253
- F-HEMBA1002999//SUPPRESSOR PROTEIN SRP40//0.028:175:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32583
- 35 F-HEMBA1003021//ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.3e-36:102:70//HOMO SAPIENS (HUMAN)//P39194
- F-HEMBA1003033//HYPOTHETICAL 23.1 KD PROTEIN CY277.20C//0.029:75:29//MYCOBACTERIUM TUBERCULOSIS//P71779
- 40 F-HEMBA1003034//ALU SUBFAMILY SC WARNING ENTRY !!!!!/6.3e-23:144:46//HOMO SAPIENS (HUMAN)//P39192
- F-HEMBA1003035//HYPOTHETICAL 13.3 KD PROTEIN IN AROD-COMER INTERGENIC REGION//0.99:55:30//BACILLUS SUBTILIS//P54457
- F-HEMBA1003037//DNA-BINDING PROTEIN INHIBITOR ID-4//0.17:42:40//HOMO SAPIENS (HUMAN)//P47928
- 45 F-HEMBA1003041//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.69:28:46//HOMO SAPIENS (HUMAN)//P30808
- F-HEMBA1003046//MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRECURSOR (EC 3.4.24.64) (BETA-MPP) (P-52)//7.9e-124:253:96//HOMO SAPIENS (HUMAN)//O75439
- 50 F-HEMBA1003064//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3)//0.25:263:22//TRYPANOSOMA BRUCEI BRUCEI//P04540
- F-HEMBA1003067//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION//4.1e-05:189:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53214
- F-HEMBA1003071//CUTICLE COLLAGEN 40//6.0e-07:126:38//CAENORHABDITIS ELEGANS//P34804
- 55 F-HEMBA1003077//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN)//2.4e-12:139:34//HOMO SAPIENS (HUMAN)//Q06828
- F-HEMBA1003078//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE]//7.2e-05:60:40//MUS MUSCULUS (MOUSE)//P11369

F-HEMBA1003079//PROTEIN Q300.//0.0012:16:87//MUS MUSCULUS (MOUSE).//Q02722  
 F-HEMBA1003083//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/3.3e-32:95:75//HOMO SAPIENS (HUMAN).//  
 P39189  
 F-HEMBA1003086  
 5 F-HEMBA1003096//PROTAMINE IA (IRIDINE IA).//0.36:20:40//SALMO IRIDEUS (RAINBOW TROUT).//P02328  
 F-HEMBA1003098//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.4e-09:43:72//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-HEMBA1003117//PUTATIVE CUTICLE COLLAGEN C09G5.5.//1.0:88:38//CAENORHABDITIS ELEGANS.//  
 Q09456  
 10 F-HEMBA1003129//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.61:63:25//APIS MEL-  
 LIFERA (HONEYBEE).//P34859  
 F-HEMBA1003133//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT).//0.48:79:  
 37//HOMO SAPIENS (HUMAN).//P25067  
 15 F-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-  
 PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//3.6e-25:190:34//SAC-  
 CHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41940  
 F-HEMBA1003142  
 F-HEMBA1003148//HYPOTHETICAL 56.4 KD PROTEIN IN RPL30-CWH41 INTERGENIC REGION PRECUR-  
 SOR.//0.068:171:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53189  
 20 F-HEMBA1003166//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.8e-13:54:66//HOMO SAPIENS (HUMAN).//  
 P39192  
 F-HEMBA1003175//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.015:147:  
 31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214  
 F-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANS-  
 25 FERASE (EC 2.1.1.61).//2.6e-51:164:47//BACILLUS SUBTILIS.//O35020  
 F-HEMBA1003197  
 F-HEMBA1003199//HOMEBOX PROTEIN HOX-A4 (HOX-1D) (HOX-1.4).//0.00049:83:38//HOMO SAPIENS  
 (HUMAN).//Q00056  
 30 F-HEMBA1003202//SPERM PROTAMINE P1.//0.98:53:28//PLANIGALE GILESI (FLAT-SKULLED MARSUPIAL  
 MOUSE).//O18747  
 F-HEMBA1003204//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.2e-22:42:80//HOMO SAPIENS (HU-  
 MAN).//P39194  
 F-HEMBA1003212//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.6e-18:74:71//HOMO SAPIENS (HUMAN).//  
 P39193  
 35 F-HEMBA1003220//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.3e-18:56:78//HOMO SAPIENS (HU-  
 MAN).//P39194  
 F-HEMBA1003222//HYPOTHETICAL 37.5 KD PROTEIN IN GNTR-HTPG INTERGENIC REGION.//0.0018:159:  
 27//BACILLUS SUBTILIS.//P46327  
 40 F-HEMBA1003229//DIHYDRODIPICOLINATE SYNTHASE 1 PRECURSOR (EC 4.2.1.52) (DHDPs).//1.0:85:28//  
 TRITICUM AESTIVUM (WHEAT).//P24846  
 F-HEMBA1003235//TROPOMYOSIN.//8.3e-07:109:33//SCHIZOSACCHAROMYCES POMBE (FISSION  
 YEAST).//Q02088  
 F-HEMBA1003250  
 F-HEMBA1003257//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//1.5e-07:27:74//OWENIA FUSI-  
 45 FORMIS.//P21260  
 F-HEMBA1003273  
 F-HEMBA1003276  
 F-HEMBA1003278  
 F-HEMBA1003281//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4).//0.0053:116:36//GALLUS GALLUS (CHICK-  
 50 EN).//P17277  
 F-HEMBA1003286//DNA-DIRECTED RNA POLYMERASE SUBUNIT N (EC 2.7.7.6).//0.96:37:35//SULFOLOBUS  
 ACIDOCALDARIUS.//P39472  
 F-HEMBA1003291//5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-2 CHAIN (EC 2.7.1.-) (AMPK  
 ALPHA-2 CHAIN) (FRAGMENT).//3.3e-15:68:39//SUS SCROFA (PIG).//Q28948  
 55 F-HEMBA1003296//PULMONARY SURFACTANT-ASSOCIATED PROTEIN B (SP-B) (6 KD PROTEIN) (PULMO-  
 NARY SURFACTANT-ASSOCIATED PROTEOLIPID SPL(PHE)).//0.98:49:28//BOS TAURUS (BOVINE).//P15781  
 F-HEMBA1003304//MITOCHONDRIAL RIBOSOMAL PROTEIN S19.//0.99:36:30//PROTOTHECA WICKER-  
 HAMII.//P46750

F-HEMBA1003309//HYPOTHETICAL 7.9 KD PROTEIN//0.69:54:37//VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENHAGEN).//P04306

F-HEMBA1003314//MIXED LINEAGE KINASE 2 (EC 2.7.1.-) (FRAGMENT).//2.3e-06:143:22//HOMO SAPIENS (HUMAN).//Q02779

5 F-HEMBA1003322//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.5e-30:53:77//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1003327

F-HEMBA1003328//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).//0.53:21:42//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1).//P04612

10 F-HEMBA1003330//LONG NEUROTOXIN 3 (TOXIN VN2).//1.0:26:34//DENDROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA).//P25667

F-HEMBA1003348//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/6.5e-09:56:66//HOMO SAPIENS (HUMAN).//P39194

15 F-HEMBA1003369//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.//0.0042:97:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P40602

F-HEMBA1003370//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.0e-18:99:53//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1003373

20 F-HEMBA1003376//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/4.7e-16:60:75//HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1003380//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.8e-10:50:68//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1003384

25 F-HEMBA1003395//PROBABLE E5 PROTEIN.//0.62:64:29//HUMAN PAPILLOMAVIRUS TYPE 16.//P06927

F-HEMBA1003402//HYPOTHETICAL 12.0 KD PROTEIN IN TUB1-CPR3 INTERGENIC REGION PRECURSOR.//0.89:74:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04521

F-HEMBA1003403//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.0010:69:33//RATTUS NORVEGICUS (RAT).//P10164

30 F-HEMBA1003408//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//4.8e-06:93:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38968

F-HEMBA1003417//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].//0.0021:140:34//MUS MUSCULUS (MOUSE).//P28481

35 F-HEMBA1003418//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.7e-14:188:33//HOMO SAPIENS (HUMAN).//Q08170

F-HEMBA1003433//DNA REPAIR PROTEIN XRS2.//1.0:88:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33301

40 F-HEMBA1003447//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.0061:69:33//RATTUS NORVEGICUS (RAT).//P10164

F-HEMBA1003461//SPIRODRIN 1 (DRAGLINE SILK FIBROIN 1) (FRAGMENT).//2.3e-09:239:33//NEPHILA CLAVIPES (ORB SPIDER).//P19837

F-HEMBA1003463//METALLOTHIONEIN-A (MTA) (FRAGMENT).//1.0:40:35//SPHAERECHINUS GRANULARIS (PURPLE SEA URCHIN).//Q26497

45 F-HEMBA1003480//FUSARIC ACID RESISTANCE PROTEIN FUSB.//0.0043:96:32//BURKHOLDERIA CEPACIA (PSEUDOMONAS CEPACIA).//P24127

F-HEMBA1003528//36.4 KD PROLINE-RICH PROTEIN.//6.4e-15:167:33//LYCOPERSICON ESCULENTUM (TOMATO).//Q00451

50 F-HEMBA1003531//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.2e-18:56:78//HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1003538//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41).//2.5e-28:136:47//HOMO SAPIENS (HUMAN).//P00736

F-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (ISLET-2).//9.2e-105:217:85//RATTUS NORVEGICUS (RAT).//P50480

55 F-HEMBA1003548

F-HEMBA1003555//HYPOTHETICAL 31.9 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION.//8.7e-57:180:55//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40558

F-HEMBA1003556//HYPOTHETICAL 19.2 KD PROTEIN IN COX-REP INTERGENIC REGION (ORF5) (ORF21).//0.53:97:25//BACTERIOPHAGE HP1.//P51706

F-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAM-



- MA-1) //1.8e-32.71:100//BOS TAURUS (BOVINE) //P16874  
 F-HEMBA1003568//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN) //4.1e-19:126.31//HOMO SAPIENS (HUMAN) //P14373
- 5 F-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1 //3.9e-83:143.74//HOMO SAPIENS (HUMAN) //Q13330  
 F-HEMBA1003571//HYPOTHETICAL 8.7 KD PROTEIN (READING FRAME D) //1.0:64.25//STAPHYLOCOCCUS AUREUS //P03860  
 F-HEMBA1003579//CYTOTOXIN 1 (CYTOTOXIN V-II-1) (TOXIN V(II)1) //1.0:41.29//NAJA MELANOLEUCA (FOREST COBRA) (BLACK-LIPPED COBRA) //P01448
- 10 F-HEMBA1003581//TALIN //3.7e-36:52.98//MUS MUSCULUS (MOUSE) //P26039  
 F-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP) //1.6e-05:91.31//NICOTIANA SYLVESTRIS (WOOD TOBACCO) //P19682  
 F-HEMBA1003595//HYPOTHETICAL 12.0 KD PROTEIN IN DST1-HEM2 INTERGENIC REGION //1.0:55.32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P53182
- 15 F-HEMBA1003597  
 F-HEMBA1003598//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11) //4.9e-10:85.41//ORYCTOLAGUS CUNICULUS (RABBIT) //P06333  
 F-HEMBA1003615//PUTATIVE MINOR COAT PROTEIN (ORF43) //0.086:10.70//BACTERIOPHAGE PHI-LF //Q07482
- 20 F-HEMBA1003617//HYPOTHETICAL 36.8 KD PROTEIN C26A3.16 IN CHROMOSOME 1 //4.4e-13:58.48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //Q10169  
 F-HEMBA1003621//LONG NEUROTOXIN 1 (NEUROTOXIN A) //0.096:40.37//OPHIOPHAGUS HANNAH (KING COBRA) (NAJA HANNAH) //P01387  
 F-HEMBA1003622  
 F-HEMBA1003630
- 25 F-HEMBA1003637//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!! //2.4e-13:47.74//HOMO SAPIENS (HUMAN) //P39188  
 F-HEMBA1003640//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!! //0.87:25.64//HOMO SAPIENS (HUMAN) //P39193
- 30 F-HEMBA1003645//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHROMOSOME III //1.8e-10:157.26//CAENORHABDITIS ELEGANS //Q17963  
 F-HEMBA1003646//SERINE-ARGININE PROTEIN 55 (SRP55) (ENHANCER OF DEFORMED) (52-KD BRACKETING PROTEIN) (B52 PROTEIN) //4.9e-05:207.27//DROSOPHILA MELANOGASTER (FRUIT FLY) //P26686  
 F-HEMBA1003656
- 35 F-HEMBA1003662//PROLINE-RICH PEPTIDE P-B //0.57:17.52//HOMO SAPIENS (HUMAN) //P02814  
 F-HEMBA1003667//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! //6.0e-16:43.72//HOMO SAPIENS (HUMAN) //P39194  
 F-HEMBA1003679  
 F-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-) //3.9e-08:137.27//CAENORHABDITIS ELEGANS //P34629
- 40 F-HEMBA1003684//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13) //2.1e-20:127.40//MUS MUSCULUS (MOUSE) //Q60821  
 F-HEMBA1003690//HYPOTHETICAL PROTEIN KIAA0288 (HA6116) //3.0e-85:201.78//HOMO SAPIENS (HUMAN) //P56524
- 45 F-HEMBA1003692//CELL DIVISION CONTROL PROTEIN 1 //0.13:69.30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P40986  
 F-HEMBA1003711//CARCINOEMBRYONIC ANTIGEN PRECURSOR (CEA) (MECONIUM ANTIGEN 100) (CD66E ANTIGEN) //0.021:153.26//HOMO SAPIENS (HUMAN) //P06731  
 F-HEMBA1003714//ABAEIN //0.99:34.32//BOMBUS PASCUORUM //P81463
- 50 F-HEMBA1003715  
 F-HEMBA1003720//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //5.4e-34:155.56//HOMO SAPIENS (HUMAN) //P08547  
 F-HEMBA1003725//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //1.3e-27:181.41//HOMO SAPIENS (HUMAN) //P08547
- 55 F-HEMBA1003729//PTB-ASSOCIATED SPLICING FACTOR (PSF) //0.0037:103.33//HOMO SAPIENS (HUMAN) //P23246  
 F-HEMBA1003733//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //5.0e-54:210.58//HOMO SAPIENS (HUMAN) //P08547

- F-HEMBA1003742//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.066:72:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643  
F-HEMBA1003758  
F-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//1.5e-51:220:52//MUS MUSCULUS (MOUSE).//Q061221  
F-HEMBA1003773  
F-HEMBA1003783  
F-HEMBA1003784  
F-HEMBA1003799//SHORT NEUROTOXIN 1 (TOXIN AA C).//0.95:27:37//ACANTHOPHIS ANTARCTICUS (COMMON DEATH ADDER).//P01434  
F-HEMBA1003803//GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30].//0.46:96:34//FELINE SARCOMA VIRUS (STRAIN SNYDER-THEILEN).//P03338  
F-HEMBA1003804//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.019:30:50//HOMO SAPIENS (HUMAN).//P30808  
F-HEMBA1003805//HYPOTHETICAL 75.0 KD PROTEIN B0280.11 IN CHROMOSOME III.//1.8e-20:109:47//CAENORHABDITIS ELEGANS.//P42083  
F-HEMBA1003807  
F-HEMBA1003827//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//2.1e-09:23:78//OWENIA FUSIFORMIS.//P21260  
F-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).//2.0e-31:134:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40484  
F-HEMBA1003838//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.9e-22:39:76//HOMO SAPIENS (HUMAN).//P39192  
F-HEMBA1003856  
F-HEMBA1003864//HYPOTHETICAL 39.4 KD PROTEIN IN MET1-SIS2 INTERGENIC REGION.//1.5e-15:194:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36151  
F-HEMBA1003866//PROTEIN A39.//0.0027:72:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P21062  
F-HEMBA1003879//80 KD NUCLEAR CAP BINDING PROTEIN (NCBP 80 KD SUBUNIT) (CBP80).//2.9e-16:22:100//HOMO SAPIENS (HUMAN).//Q09161  
F-HEMBA1003880//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:39:38//FELIS SILVESTRIS CATUS (CAT).//P48896  
F-HEMBA1003885//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//3.5e-28:47:76//HOMO SAPIENS (HUMAN).//P39193  
F-HEMBA1003893//HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//1.7e-57:215:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53215  
F-HEMBA1003902  
F-HEMBA1003908  
F-HEMBA1003926//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.3e-10:60:63//HOMO SAPIENS (HUMAN).//P39188  
F-HEMBA1003937//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//8.1e-29:68:64//HOMO SAPIENS (HUMAN).//P39194  
F-HEMBA1003939//PROTEIN Q300.//0.0025:24:62//MUS MUSCULUS (MOUSE).//Q02722  
F-HEMBA1003942//EXCITATORY INSECT TOXIN BJXTR-IT PRECURSOR (BJ-XTRIT).//0.084:67:31//BUTHOTUS JUDAICUS (SCORPION) (HOTTENTOTTA JUDAICA).//P56637  
F-HEMBA1003950//HYPOTHETICAL 8.1 KD PROTEIN IN SPEA-METK INTERGENIC REGION (O71).//0.95:26:34//ESCHERICHIA COLI.//P46878  
F-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//2.5e-17:89:46//MUS MUSCULUS (MOUSE).//P16372  
F-HEMBA1003958//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.2e-23:43:76//HOMO SAPIENS (HUMAN).//P08547  
F-HEMBA1003959  
F-HEMBA1003976//HYPOTHETICAL PROTEIN KIAA0076 (HA0936).//0.99:88:28//HOMO SAPIENS (HUMAN).//Q14999  
F-HEMBA1003978//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.98:19:57//HOMO SAPIENS (HUMAN).//P22531  
F-HEMBA1003985//LYSYL-TRNA SYNTHETASE (EC 6.1.1.6) (LYSINE--TRNA LIGASE) (LYSRS) (FRAGMENT).//1.0:40:32//MYCOBACTERIUM LEPRAE.//P46861  
F-HEMBA1003987//HYPOTHETICAL PROTEIN UL66.//0.27:65:33//HUMAN CYTOMEGALOVIRUS (STRAIN

AD169) //P16822  
 F-HEMBA1003989//MALE SPECIFIC SPERM PROTEIN MST84DB.//5.2e-05:64.40//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643  
 5 F-HEMBA1004000//PROTEIN Q300.//0.00042:17:82//MUS MUSCULUS (MOUSE).//Q02722  
 F-HEMBA1004011//ALPHA-TYPE CALCITONIN GENE-RELATED PEPTIDE PRECURSOR (CGRP-1).//0.47:106:32//HOMO SAPIENS (HUMAN).//P06881  
 F-HEMBA1004012//ATP SYNTHASE PROTEIN 9, MITOCHONDRIAL (EC 3.6.1.34) (LIPID-BINDING PROTEIN).//0.96:36:33//PARAMECIUM TETRAURELIA.//P16001  
 10 F-HEMBA1004015//HYPOTHETICAL 29.3 KD PROTEIN B0280.6 IN CHROMOSOME III.//0.00018:90:34//CAENORHABDITIS ELEGANS.//P41997  
 F-HEMBA1004024//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.1e-34:75:80//HOMO SAPIENS (HUMAN).//P39194  
 F-HEMBA1004038  
 F-HEMBA1004042  
 15 F-HEMBA1004045//40S RIBOSOMAL PROTEIN S27A.//1.0:20:55//ASPARAGUS OFFICINALIS (GARDEN ASPARAGUS).//P31753  
 F-HEMBA1004048//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.3e-06:158:35//MUS MUSCULUS (MOUSE).//P05143  
 F-HEMBA1004049//32 KD HEAT SHOCK PROTEIN (4-1 PROTEIN).//0.098:106:32//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P54658  
 20 F-HEMBA1004055//HYPOTHETICAL PROTEIN H10258/259.//0.87:133:23//HAEMOPHILUS INFLUENZAE.//P43974  
 F-HEMBA1004056//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/3.3e-25:39:64//HOMO SAPIENS (HUMAN).//P39191  
 25 F-HEMBA1004074//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/9.9e-08:35:68//HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBA1004086  
 F-HEMBA1004097//IMMEDIATE-EARLY PROTEIN IE4 (IE68) (FRAGMENT).//0.71:95:35//HERPES SIMPLEX VIRUS (TYPE 2).//P14379  
 30 F-HEMBA1004111//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.7e-26:84:64//HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT).//2.8e-34:108:63//HOMO SAPIENS (HUMAN).//Q14141  
 F-HEMBA1004132//HYPOTHETICAL PROTEIN H11736.//1.0:44:34//HAEMOPHILUS INFLUENZAE.//P44300  
 35 F-HEMBA1004133//HYPOTHETICAL 8.5 KD PROTEIN CY274.40C.//0.89:21:57//MYCOBACTERIUM TUBERCULOSIS.//Q10826  
 F-HEMBA1004138//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT).//0.016:39:41//MEDICAGO SATIVA (ALFALFA).//P11728  
 F-HEMBA1004143//CYTOCHROME C OXIDASE POLYPEPTIDE VIII PRECURSOR (EC 1.9.3.1).//0.93:34:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P04039  
 40 F-HEMBA1004146//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.63:52:36//HOMO SAPIENS (HUMAN).//P02811  
 F-HEMBA1004150//METALLOTHIONEIN-II (MT-II).//1.0:20:45//MUS MUSCULUS (MOUSE).//P02798  
 45 F-HEMBA1004164//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/3.0e-13:57:71//HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBA1004168//V-TYPE SODIUM ATP SYNTHASE SUBUNIT F (EC 3.6.1.34) (NA(+)-TRANSLOCATING ATPASE SUBUNIT F).//0.00035:90:34//ENTEROCOCCUS HIRAE.//P43437  
 F-HEMBA1004199//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//5.1e-14:115:31//CAENORHABDITIS ELEGANS.//P34529  
 50 F-HEMBA1004200  
 F-HEMBA1004202//YPT1-RELATED PROTEIN 1.//2.5e-24:96:52//SCHIZOSACCHAROMYCES POMBE (FISION YEAST).//P11620  
 F-HEMBA1004203//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2 2e-09:48:64//HOMO SAPIENS (HUMAN).//P39193  
 55 F-HEMBA1004207//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70).//0.98:51:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779  
 F-HEMBA1004225//METALLOTHIONEIN-II.//1.0:30:33//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA).//P15114

- F-HEMBA1004227//PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015).//5.9e-06:109:33//HOMO SAPIENS (HUMAN).//P49593
- F-HEMBA1004238//VERY HYPOTHETICAL XYLX PROTEIN.//0.98:39:38//ESCHERICHIA COLI.//P05056
- 5 F-HEMBA1004241//SOX-13 PROTEIN (FRAGMENT).//0.66:36:38//MUS MUSCULUS (MOUSE).//Q04891
- F-HEMBA1004246
- F-HEMBA1004248//INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 (IMMEDIATE-EARLY PROTEIN CL-6).//1.0e-43:98:84//RATTUS NORVEGICUS (RAT).//Q08755
- F-HEMBA1004264//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.014:160:28//NEPHILA CLA-VIPES (ORB SPIDER).//P46804
- 10 F-HEMBA1004267//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.8e-52:56:83//HOMO SAPIENS (HUMAN).//P39189
- F-HEMBA1004272
- F-HEMBA1004274//HYPOTHETICAL 13.0 KD PROTEIN F59B2.10 IN CHROMOSOME III.//0.00084:33:54//CAENORHABDITIS ELEGANS.//P34485
- 15 F-HEMBA1004275//HYPOTHETICAL 56.5 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION//9.3e-06:125:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40034
- F-HEMBA1004276//BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A).//3.7e-30:239:32//HOMO SAPIENS (HUMAN).//Q10567
- 20 F-HEMBA1004286//CUTICLE COLLAGEN 34.//0.0027:71:38//CAENORHABDITIS ELEGANS.//P34687
- F-HEMBA1004289//PTR3 PROTEIN (SSY3 PROTEIN).//1.0:76:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43606
- F-HEMBA1004295//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.075:58:39//HOMO SAPIENS (HUMAN).//P30808
- 25 F-HEMBA1004306//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.020:132:30//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//Q10341
- F-HEMBA1004312//EARLY PROTEIN I73R.//0.99:65:32//AFRICAN SWINE FEVER VIRUS (STRAIN BA71V) (ASFV).//P27946
- F-HEMBA1004321//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).//4.3e-43:133:44//MUS MUSCULUS (MOUSE).//Q61967
- 30 F-HEMBA1004323
- F-HEMBA1004327//SMALL PROLINE-RICH PROTEIN 2-1.//0.027:48:43//HOMO SAPIENS (HUMAN).//P35326
- F-HEMBA1004330//HOMEOBOX PROTEIN ENGRAILED-1 (HU-EN-1).//0.46:70:34//HOMO SAPIENS (HUMAN).//Q05925
- 35 F-HEMBA1004334//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.7e-05:83:34//HOMO SAPIENS (HUMAN).//P08547
- F-HEMBA1004335//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.0e-24:41:80//HOMO SAPIENS (HUMAN).//P39195
- 40 F-HEMBA1004341//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//2.8e-06:148:35//MUS MUSCULUS (MOUSE).//P05143
- F-HEMBA1004353//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.2e-29:57:80//HOMO SAPIENS (HUMAN).//P39195
- F-HEMBA1004354//CHL1 PROTEIN.//0.017:40:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P22516
- 45 F-HEMBA1004356
- F-HEMBA1004366//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.00045:49:46//HOMO SAPIENS (HUMAN).//P08547
- F-HEMBA1004372//VERY HYPOTHETICAL 20.6 KD PROTEIN C56F8.15 IN CHROMOSOME I.//1.0:125:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10263
- 50 F-HEMBA1004389//HYPOTHETICAL 113.1 KD PROTEIN IN PRE5-FET4 INTERGENIC REGION.//0.76:170:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04893
- F-HEMBA1004394
- F-HEMBA1004396//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.2e-10:72:51//HOMO SAPIENS (HUMAN).//P08547
- 55 F-HEMBA1004405
- F-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN-10).//2.7e-29:146:48//CAENORHABDITIS ELEGANS.//P52017
- F-HEMBA1004429//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/0.0019:47:59//HOMO SAPIENS (HUMAN).

MAN).//P39191  
 F-HEMBA1004433//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.1e-20:47:68//HOMO SAPIENS (HUMAN).//P39192  
 5 F-HEMBA1004460//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/6.2e-64:134:69//HOMO SAPIENS (HUMAN).//P39193  
 F-HEMBA1004461//METALLOTHIONEIN-LIKE PROTEIN 1.//1.0:39:35//PISUM SATIVUM (GARDEN PEA).//P20830  
 F-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//9.7e-43:101:48//MUS MUSCULUS (MOUSE).//Q61221  
 10 F-HEMBA1004482//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34).//1.0:41:36//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA).//P05040  
 F-HEMBA1004499//TUBULIN BETA CHAIN.//0.00021:55:36//CAENORHABDITIS ELEGANS.//P52275  
 F-HEMBA1004502  
 15 F-HEMBA1004506//HYPOTHETICAL PROTEIN ORF-1137.//5.3-11:119:35//MUS MUSCULUS (MOUSE).//P11260  
 F-HEMBA1004507//SPLICESOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.00072:90:37//HOMO SAPIENS (HUMAN).//Q15428  
 F-HEMBA1004509//HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTERGENIC REGION.//6.3e-28:169:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43589  
 20 F-HEMBA1004534//ENDOTHELIAL ACTIN-BINDING PROTEIN (ABP-280) (NONMUSCLE FILAMIN) (FILAMIN 1).//1.3e-80:228:66//HOMO SAPIENS (HUMAN).//P21333  
 F-HEMBA1004538//HYPOTHETICAL PROTEIN MJ0764.//0.96:28:35//METHANOCOCCUS JANNASCHII.//Q58174  
 F-HEMBA1004542//METALLOTHIONEIN (MT).//0.78:36:41//GADUS MORHUA (ATLANTIC COD).//P51902  
 25 F-HEMBA1004554  
 F-HEMBA1004560//HYPOTHETICAL PROTEIN KIAA0281 (HA6725).//4.2e-15:56:69//HOMO SAPIENS (HUMAN).//Q92556  
 F-HEMBA1004573//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//0.65:31:58//PLASMODIUM BERGHEI.//P06915  
 30 F-HEMBA1004577//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/3.9e-08:35:80//HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBA1004586//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/6.6e-08:64:54//HOMO SAPIENS (HUMAN).//P39194  
 F-HEMBA1004596//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN C (HNRNP C) (HNRNP CORE PROTEIN C) (FRAGMENT).//0.00057:88:31//RATTUS NORVEGICUS (RAT).//P17132  
 35 F-HEMBA1004604//COLLAGEN ALPHA 2(XI) CHAIN PRECURSOR (FRAGMENT).//0.045:37:45//MUS MUSCULUS (MOUSE).//Q64739  
 F-HEMBA1004610//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.3e-11:73:54//HOMO SAPIENS (HUMAN).//P39188  
 40 F-HEMBA1004617  
 F-HEMBA1004629  
 F-HEMBA1004631//HYPOTHETICAL 7.8 KD PROTEIN IN WAPA-LICT INTERGENIC REGION.//1.0:36:38//BACILLUS SUBTILIS.//P42303  
 F-HEMBA1004632//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING 8.0 KD POLYPEPTIDE).//0.86:48:35//SYNECHOCOCCUS ELONGATUS NAEGELI.//P20453  
 45 F-HEMBA1004637//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III.//1.7e-32:159:42//CAENORHABDITIS ELEGANS.//P34535  
 F-HEMBA1004638//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//2.8e-06:50:46//OWENIA FUSIFORMIS.//P21260  
 50 F-HEMBA1004666//TOXIN S6C4.//1.0:36:30//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S MAMBA).//P25682  
 F-HEMBA1004669//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.6e-12:105:42//HOMO SAPIENS (HUMAN).//Q08170  
 F-HEMBA1004670//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//2.5e-06:62:45//HOMO SAPIENS (HUMAN).//P02452  
 55 F-HEMBA1004672//HYPOTHETICAL PROTEIN MJ0437.//0.95:37:29//METHANOCOCCUS JANNASCHII.//Q57879  
 F-HEMBA1004693//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN,

TYPE B) (NMMHC-B) //0.00035:217:23//HOMO SAPIENS (HUMAN) //P35580  
 F-HEMBA1004697//IMMUNOGLOBULIN G BINDING PROTEIN H PRECURSOR (PROTEIN H) //0.058:118:30//  
 STREPTOCOCCUS PYOGENES //P50470  
 5 F-HEMBA1004705//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//8.8e-09:43:72//HOMO SAPIENS (HUMAN) //P39188  
 F-HEMBA1004709//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//8.8e-18:50:84//HOMO SAPIENS (HUMAN) //P39189  
 F-HEMBA1004711//ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2) //0.0027:148:30//HOMO SAPIENS (HUMAN) //000321  
 10 F-HEMBA1004725//CUTICLE COLLAGEN 2 //0.0051:41:41//CAENORHABDITIS ELEGANS //P17656  
 F-HEMBA1004730//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //1.4e-22:210:37//HOMO SAPIENS (HUMAN) //P08547  
 F-HEMBA1004733//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.7e-07:50:62//HOMO SAPIENS (HUMAN) //P39188  
 15 F-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42) //9.9e-39:143:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS) //P42743  
 F-HEMBA1004736//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //4.1e-60:210:61//HOMO SAPIENS (HUMAN) //P08547  
 20 F-HEMBA1004748  
 F-HEMBA1004751//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.8e-20:88:63//HOMO SAPIENS (HUMAN) //P39188  
 F-HEMBA1004752//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN) //0.0043:126:34//  
 XENOPUS LAEVIS (AFRICAN CLAWED FROG) //P17437  
 25 F-HEMBA1004753//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//7.8e-28:47:78//HOMO SAPIENS (HUMAN) //P39193  
 F-HEMBA1004756//HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION //0.22:77:27//  
 SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P39981  
 F-HEMBA1004758  
 30 F-HEMBA1004763//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT) //1.1e-06:58:43//OWENIA FUSIFORMIS //P21260  
 F-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //4.7e-65:298:53//HOMO SAPIENS (HUMAN) //P08547  
 F-HEMBA1004770  
 35 F-HEMBA1004771  
 F-HEMBA1004776//GRANULIN 1 //0.78:28:42//CYPRINUS CARPIO (COMMON CARP) //P81013  
 F-HEMBA1004778  
 F-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT) //6.9e-20:74:63//HOMO SAPIENS (HUMAN) //P50851  
 40 F-HEMBA1004803//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //1.4e-22:58:86//HOMO SAPIENS (HUMAN) //P08547  
 F-HEMBA1004806//HYPOTHETICAL 24.3 KD PROTEIN IN PSBH-RPL11 INTERGENIC REGION (ORF182) //0.72:75:33//CYANOPHORA PARADOXA //P48324  
 F-HEMBA1004807  
 F-HEMBA1004816  
 45 F-HEMBA1004820//HEMOLYMPH TRYPSIN INHIBITOR A (BPI-TYPE) (FRAGMENT) //1.0:50:38//MANDUCA SEXTA (TOBACCO HAWKMOOTH) (TOBACCO HORNWORM) //P26226  
 F-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68) //3.0e-76:171:91//CANIS FAMILIARIS (DOG) //Q00004  
 F-HEMBA1004850//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS) //3.0e-05:64:43//BOS TAURUS (BOWTIE) //P25508  
 50 F-HEMBA1004863//TOXIN C13S1C1 PRECURSOR //0.38:52:30//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA) //P18329  
 F-HEMBA1004864//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT) //0.89:24:50//  
 HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1) //P04612  
 55 F-HEMBA1004865  
 F-HEMBA1004880  
 F-HEMBA1004889//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N) //0.66:23:47//HOMO SAPIENS (HUMAN) //P22532

- F-HEMBA1004900  
F-HEMBA1004909  
F-HEMBA1004918//CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 (FRAGMENT).//0.56:37:32//SPINACIA OL-  
ERACEA (SPINACH).//P09597
- 5 F-HEMBA1004923//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.5e-24:44:68//HOMO SAPIENS (HUMAN).//  
P39188  
F-HEMBA1004929//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.97:39:38//STRONGYLOCENTROTUS  
PURPURATUS (PURPLE SEA URCHIN).//P15997
- 10 F-HEMBA1004930//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.6e-15:64:59//HOMO SAPIENS (HU-  
MAN).//P08547  
F-HEMBA1004933//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.34:58:41//HOMO SAPIENS  
(HUMAN).//P50552  
F-HEMBA1004934  
F-HEMBA1004944
- 15 F-HEMBA1004954//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).//0.58:78:30//PARA-  
MECIUM TETRAURELIA.//P15579  
F-HEMBA1004956//HYPOTHETICAL 18.8 KD PROTEIN (ORF4).//0.98:57:31//PARAMECIUM TETRAURELIA.//  
P15805  
F-HEMBA1004960//HYPOTHETICAL 12.6 KD PROTEIN-(ORFJ) (RETRON EC67).//1.0:58:27//ESCHERICHIA  
COLI.//P21324
- 20 F-HEMBA1004972  
F-HEMBA1004973//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.90:55:30//HOMO SAPIENS  
(HUMAN).//P22531  
F-HEMBA1004977  
F-HEMBA1004978
- 25 F-HEMBA1004980//MOTILIN PRECURSOR.//0.088:79:31//MACACA MULATTA (RHESUS MACAQUE).//018811  
F-HEMBA1004983//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES).//0.87:51:31//BUCHNERA  
APHIDICOLA.//Q59176  
F-HEMBA1004995//MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACTOR-LIKE PRO-  
TEIN 2) (XMEF2) (RSRFR2).//0.17:52:40//HOMO SAPIENS (HUMAN).//Q02080
- 30 F-HEMBA1005008//METALLOTHIONEIN (MT).//1.0:52:32//CRASSOSTREA VIRGINICA (EASTERN OYS-  
TER).//P23038  
F-HEMBA1005009//ACTIN.//3.5e-27:171:38//CANDIDA ALBICANS (YEAST).//P14235  
F-HEMBA1005019//HYPOTHETICAL PROTEIN HI1222.//0.13:58:31//HAEMOPHILUS INFLUENZAE.//P44129
- 35 F-HEMBA1005029//P2Y PURINOCEPTOR 5 (P2Y5) (PURINERGIC RECEPTOR 5) (6H1).//0.76:72:31//GALLUS  
GALLUS (CHICKEN).//P32250  
F-HEMBA1005035//HOMEBOX PROTEIN HB9.//0.0086:60:40//HOMO SAPIENS (HUMAN).//P50219  
F-HEMBA1005039//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.47:49:32//HOMO SAPIENS  
(HUMAN).//P22532
- 40 F-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16).//1.5e-19:39:100//MUS MUSCULUS  
(MOUSE).//P35290  
F-HEMBA1005050//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.074:34:44//BOS TAURUS (BOVINE).//  
P25508  
F-HEMBA1005062
- 45 F-HEMBA1005066//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.1e-44:126:65//HOMO SAPIENS (HU-  
MAN).//P08547  
F-HEMBA1005075//SUPPRESSOR PROTEIN SRP40.//0.35:96:31//SACCHAROMYCES CEREVISIAE (BAK-  
ER'S YEAST).//P32583  
F-HEMBA1005079//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/3.6e-20:75:64//HOMO SAPIENS (HU-  
MAN).//P39191
- 50 F-HEMBA1005083//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.00015:72:34//BOS TAURUS (BO-  
VINE).//P25508  
F-HEMBA1005101//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP 48) (HRP48.1).//  
4.8e-10:176:25//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48809
- 55 F-HEMBA1005113  
F-HEMBA1005123//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.6e-24:99:60//HOMO SAPIENS (HU-  
MAN).//P39194  
F-HEMBA1005133//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION.//0.11:22:54//

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P40490

F-HEMBA1005149//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.7e-16:59:71//HOMO SAPIENS (HUMAN) //P39188

F-HEMBA1005152//GENOME POLYPROTEIN 2 [CONTAINS: HELPER COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); 70 KD PROTEIN] //1.0:77:27//BARLEY YELLOW MOSAIC VIRUS (JAPANESE STRAIN II-1) (BAYMV) //Q01207

F-HEMBA1005159//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3) //0.40:53:33//APIS MEL-LIFERA (HONEYBEE) //P34859

F-HEMBA1005185//MYOSIN IB HEAVY CHAIN //0.011:58:48//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD) //P34092

F-HEMBA1005201//HYPOTHETICAL 56.6 KD PROTEIN C16C9.03 IN CHROMOSOME I //1.3:9e-67:241:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //Q09817

F-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68) //3.8e-124:257:95//CANIS FAMILIARIS (DOG) //Q00004

F-HEMBA1005206//CUTICLE COLLAGEN 1 //0.010:118:33//CAENORHABDITIS ELEGANS //P08124

F-HEMBA1005219//PTB-ASSOCIATED SPLICING FACTOR (PSF) //0.99:85:40//HOMO SAPIENS (HUMAN) //P23246

F-HEMBA1005223//HYPOTHETICAL GENE 1.05 PROTEIN //0.31:75:28//BACTERIOPHAGE T3 //P07715

F-HEMBA1005232//HYPOTHETICAL 7.8 KD PROTEIN //0.99:48:29//VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENHAGEN) //P20544

F-HEMBA1005241//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-28:138:55//HOMO SAPIENS (HUMAN) //P39193

F-HEMBA1005244//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930) //0.014:39:41//HOMO SAPIENS (HUMAN) //P22531

F-HEMBA1005251//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L) //0.55:15:46//DICENTRARCHUS LABRAX (EUROPEAN SEA BASS) //Q36362

F-HEMBA1005252//EC PROTEIN HOMOLOG (ZINC-METALLOTHIONEIN CLASS II) //0.088:33:42//ZEA MAYS (MAIZE) //P43401

F-HEMBA1005274

F-HEMBA1005275//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.96:42:45//HOMO SAPIENS (HUMAN) //P39188

F-HEMBA1005293//PROBABLE COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP) //0.55:98:30//CAENORHABDITIS ELEGANS //Q20168

F-HEMBA1005296//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2) //0.095:75:34//HOMO SAPIENS (HUMAN) //Q02817

F-HEMBA1005304//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/5.4e-33:103:74//HOMO SAPIENS (HUMAN) //P39189

F-HEMBA1005311//PERIOD CLOCK PROTEIN (FRAGMENT) //0.99:45:31//DROSOPHILA SALTANS (FRUIT FLY) //Q04536

F-HEMBA1005314//HYPOTHETICAL 6.3 KD PROTEIN T19C3.3 IN CHROMOSOME III //0.98:30:30//CAENORHABDITIS ELEGANS //Q10009

F-HEMBA1005315//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //1.1e-05:35:51//HOMO SAPIENS (HUMAN) //P08547

F-HEMBA1005318//OLFACATORY RECEPTOR-LIKE PROTEIN COR8 (FRAGMENT) //0.57:44:38//GALLUS GALLUS (CHICKEN) //Q98913

F-HEMBA1005331//IMMEDIATE-EARLY PROTEIN IE180 //0.57:106:33//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV) //P11675

F-HEMBA1005338//CARTIAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1) //1.8e-55:199:59//GALLUS GALLUS (CHICKEN) //P05099

F-HEMBA1005353//CHLOROPLAST 30S RIBOSOMAL PROTEIN S17 //0.88:33:36//PORPHYRA PURPUREA //P51305

F-HEMBA1005359//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1) //1.1e-68:255:48//HOMO SAPIENS (HUMAN) //P51522

F-HEMBA1005367//ALPHA-AMYLASE INHIBITOR AAI //1.0:25:40//AMARANTHUS HYPOCHONDRIACUS (PRINCE'S FEATHER) //P80403

F-HEMBA1005372

F-HEMBA1005374//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.0e-34:92:75//HOMO SAPIENS (HUMAN) //P39194



F-HEMBA1005382//APOLOPOPROTEIN C-II (APO-CII)//0.99:39:33//BOS TAURUS (BOVINE)//P19034  
 F-HEMBA1005389//HYPOTHETICAL 70.0 KD PROTEIN IN DNAX 3'REGION (ORF4)//0.82:164:31//LACTO-  
 COCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS)//P42377  
 5 F-HEMBA1005394//HYPOTHETICAL 8.9 KD PROTEIN IN IE0-IE1 INTERGENIC REGION//0.98:44:38//  
 AUTOGRAPH CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV)//P41703  
 F-HEMBA1005403//SPERM HISTONE P2 PRECURSOR (PROTAMINE MP2)//0.066:64:29//MUS MUSCULUS  
 (MOUSE)//P07978  
 F-HEMBA1005408//50S RIBOSOMAL PROTEIN L33//0.77:32:25//BACILLUS SUBTILIS//Q06798  
 10 F-HEMBA1005410//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE  
 (EC 2.7.7.49); ENDONUCLEASE//0.0065:38:52//MUS MUSCULUS (MOUSE)//P11369  
 F-HEMBA1005411//TOXIN S4C8//0.16:46:28//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMES-  
 ON'S MAMBA)//P25683  
 F-HEMBA1005423//CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT KINASE  
 4 INHIBITOR C) (P18-INK4C)//4.3e-09:29:96//HOMO SAPIENS (HUMAN)//P42773  
 15 F-HEMBA1005426//TOXIN C10S2C2//0.99:49:34//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAM-  
 BA)//P25684  
 F-HEMBA1005443//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.9e-16:78:60//HOMO SAPIENS (HUMAN)//  
 P39188  
 F-HEMBA1005447//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.99:57:31//DASYPS NOVEMCINCTUS  
 20 (NINE-BANDED ARMADILLO)//O21329  
 F-HEMBA1005468//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRAGMENTS)//0.68:41:  
 31//ARTEMIA SALINA (BRINE SHRIMP)//P19040  
 F-HEMBA1005469  
 25 F-HEMBA1005472//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.5e-39:142:70//HOMO SAPIENS (HU-  
 MAN)//P08547  
 F-HEMBA1005474//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.8e-10:44:68//HOMO SAPIENS (HU-  
 MAN)//P39194  
 F-HEMBA1005475//U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD (U1 SNRNP 70 KD) (SNRP70)//9.2e-  
 14:179:33//HOMO SAPIENS (HUMAN)//P08621  
 30 F-HEMBA1005497  
 F-HEMBA1005500//60S RIBOSOMAL PROTEIN L37//0.11:53:33//SCHISTOSOMA MANSONI (BLOOD  
 FLUKE)//044125  
 F-HEMBA1005506  
 F-HEMBA1005508  
 35 F-HEMBA1005511//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.5e-30:92:73//HOMO SAPIENS (HUMAN)//  
 P39194  
 F-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-)//2.0e-39:95:61//DROSOPHILA  
 MELANOGASTER (FRUIT FLY)//O02193  
 40 F-HEMBA1005517//PROLINE-RICH PROTEIN MP-2 PRECURSOR//2.1e-06:56:44//MUS MUSCULUS  
 (MOUSE)//P05142  
 F-HEMBA1005518//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//5.8e-05:192:33//BOS TAURUS (BO-  
 VINE)//P02453  
 F-HEMBA1005520//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.0e-18:87:57//HOMO SAPIENS (HUMAN)//  
 P39188  
 45 F-HEMBA1005526//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/5.1e-22:77:54//HOMO SAPIENS (HU-  
 MAN)//P39191  
 F-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1)//1.2e-81:157:98//MUS MUSCULUS (MOUSE)//  
 Q60809  
 F-HEMBA1005530//POLLEN ALLERGEN AMB P 5-A PRECURSOR (AMB P V-A)//0.98:19:47//AMBROSIA PSI-  
 50 LOSTACHYA (WESTERN RAGWEED)//P43174  
 F-HEMBA1005548//TRANSCRIPTION FACTOR MAF1//1.4e-72:137:97//RATTUS NORVEGICUS (RAT)//  
 P54842  
 F-HEMBA1005552//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.7e-29:47:78//HOMO SAPIENS (HUMAN)//  
 P39193  
 55 F-HEMBA1005558//HYPOTHETICAL 25.6 KD PROTEIN IN ABF2-CHL12 INTERGENIC REGION//1.6e-20:202:  
 30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q04272  
 F-HEMBA1005568  
 F-HEMBA1005570//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6 (EC 1.6.5.3)//1.0:80:31//

CAENORHABDITIS ELEGANS //P24885

F-HEMBA1005576//TRANSMEMBRANE PROTEIN SEX PRECURSOR //8.5e-58:152:75//HOMO SAPIENS (HUMAN).//P51805

F-HEMBA1005577//KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A //0.98:57:36//OVIS ARIES (SHEEP).//P02438

F-HEMBA1005581//SLIT PROTEIN PRECURSOR //1.1e-62:254:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//P24014

F-HEMBA1005582//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP-150) (DAP-150) (P150-GLUED).//0.0091:189:29//RATTUS NORVEGICUS (RAT).//P28023

F-HEMBA1005583//HYPOTHETICAL 41.2 KD PROTEIN IN CPS REGION (ORF7).//0.83:119:23//KLEBSIELLA PNEUMONIAE.//Q48453

F-HEMBA1005588//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.9e-17:108:53//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1005593//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.23:24:54//HOMO SAPIENS (HUMAN).//P22532

F-HEMBA1005595//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).//2.7e-39:257:39//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34036

F-HEMBA1005606

F-HEMBA1005609//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.2e-20:27:96//HOMO SAPIENS (HUMAN).//P39192

F-HEMBA1005616//LATE CONTROL GENE B PROTEIN (GPB).//0.48:51:33//BACTERIOPHAGE 186.//P08711

F-HEMBA1005621//MITOTIC MAD2 PROTEIN.//1.2e-06:137:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40958

F-HEMBA1005627//HYPOTHETICAL 17.1 KD PROTEIN IN PUBS 3'REGION.//0.18:100:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898

F-HEMBA1005631

F-HEMBA1005632//HYPOTHETICAL 7.4 KD PROTEIN.//0.32:59:32//VACCINIA VIRUS (STRAIN WR).//P04309

F-HEMBA1005634//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.6e-14:93:58//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1005666//HYPOTHETICAL PROTEIN KIAA0129.//2.1e-05:126:25//HOMO SAPIENS (HUMAN).//Q14142

F-HEMBA1005670

F-HEMBA1005679//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.2e-08:40:72//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1005680//SMALL PROLINE-RICH PROTEIN 2-1.//0.015:19:47//HOMO SAPIENS (HUMAN).//P35326

F-HEMBA1005685

F-HEMBA1005699//EPHRIIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 8) (LERK-8) (EPH-RELATED RECEPTOR TRANSMEMBRANE LIGAND ELK-L3).//4.2e-38:98:81//HOMO SAPIENS (HUMAN).//Q15768

F-HEMBA1005705//PROTEIN Q300.//0.11:23:56//MUS MUSCULUS (MOUSE).//Q02722

F-HEMBA1005717

F-HEMBA1005732//BACTENECIN 7 PRECURSOR (BACT7).//0.22:55:41//OVIS ARIES (SHEEP).//P50415

F-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT).//4.5e-18:167:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25296

F-HEMBA1005746

F-HEMBA1005755//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.4e-30:69:65//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1005765//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.8e-19:60:63//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1005780//METALLOTHIONEIN-I (MT-1).//1.0:31:38//COLUMBA LIVIA (DOMESTIC PIGEON).//P15786

F-HEMBA1005813

F-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU/M-TYPE).//1.0e-23:200:31//GALLUS GALLUS (CHICKEN).//P00789

F-HEMBA1005822//PROTEIN Q300.//0.0016:21:80//MUS MUSCULUS (MOUSE).//Q02722

F-HEMBA1005829//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.6e-33:96:73//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1005834//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.6e-22:103:46//NYCTICEBUS COU-

CANG (SLOW LORIS).//P08548  
 F-HEMBA1005852//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//8.8e-06:95.35//MUS MUSCULUS (MOUSE).//P05143  
 5 F-HEMBA1005853//HYPOTHETICAL PROTEIN MJ0647.//0.39:28:39//METHANOCOCCUS JANNASCHII.//Q58063  
 F-HEMBA1005884  
 F-HEMBA1005891//HYPOTHETICAL PROTEIN MTH137.//0.95:51:27//METHANOBACTERIUM THERMOAUTOTROPHICUM.//O26240  
 10 F-HEMBA1005894//ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.6e-29:81:71//HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBA1005909//HYPOTHETICAL 8.2 KD PROTEIN B0353.1 IN CHROMOSOME III.//0.98:19:52//CAENORHABDITIS ELEGANS.//Q10958  
 F-HEMBA1005911//ALU SUBFAMILY J WARNING ENTRY !!!!!/1.9e-27:86:70//HOMO SAPIENS (HUMAN).//P39188  
 15 F-HEMBA1005921//ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.3e-38:99:81//HOMO SAPIENS (HUMAN).//P39194  
 F-HEMBA1005931//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//2.3e-17:76:51//HOMO SAPIENS (HUMAN).//P51522  
 F-HEMBA1005934//ALU SUBFAMILY SB WARNING ENTRY !!!!!/0.024:54:40//HOMO SAPIENS (HUMAN).//P39189  
 20 F-HEMBA1005962  
 F-HEMBA1005963//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.7e-32:89:79//BOS TAURUS (BOVINE).//P53620  
 F-HEMBA1005990//HYPOTHETICAL BHLF1 PROTEIN.//3.0e-09:180:36//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181  
 25 F-HEMBA1005991//HYPOTHETICAL PROTEIN KIAA0032.//3.0e-17:107:43//HOMO SAPIENS (HUMAN).//Q15034  
 F-HEMBA1005999  
 F-HEMBA1006002  
 30 F-HEMBA1006005//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).//0.0017:45:44//MUS MUSCULUS (MOUSE).//Q62267  
 F-HEMBA1006031//BASIC PROLINE-RICH PEPTIDE IB-1.//0.00016:84:39//HOMO SAPIENS (HUMAN).//P04281  
 35 F-HEMBA1006035//DNAK PROTEIN 1 (HEAT SHOCK PROTEIN 70) (HSP70).//0.43:100:27//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q55154  
 F-HEMBA1006036//ALU SUBFAMILY SQ WARNING ENTRY !!!!!/6.2e-64:150:74//HOMO SAPIENS (HUMAN).//P39194  
 F-HEMBA1006042  
 40 F-HEMBA1006067//METALLOTHIONEIN A (MT-A).//0.86:34:41//THERMARCUS CERBERUS.//P52721  
 F-HEMBA1006081  
 F-HEMBA1006090//SODIUM/GLUCOSE COTRANSPORTER 3 (NA(+)/GLUCOSE COTRANSPORTER 3) (LOW AFFINITY SODIUM-GLUCOSE COTRANSPORTER).//0.87:35:54//SUS SCROFA (PIG).//P31636  
 F-HEMBA1006091//EARLY NODULIN 20 PRECURSOR (N-20).//0.027:87:32//MEDICAGO TRUNCATULA (BARREL MEDIC).//P93329  
 45 F-HEMBA1006100//ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.1e-09:58:60//HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBA1006108//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//5.6e-16:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867  
 F-HEMBA1006121//HOMEBOX PROTEIN CDX-1 (CAUDAL-TYPE HOMEBOX PROTEIN 1).//3.4e-05:106:37//HOMO SAPIENS (HUMAN).//P47902  
 50 F-HEMBA1006124//50S RIBOSOMAL PROTEIN L33.//1.0:12:83//BACILLUS STEAROTHERMOPHILUS.//P23375  
 F-HEMBA1006130//SEL-10 PROTEIN.//7.7e-05:129:28//CAENORHABDITIS ELEGANS.//Q93794  
 F-HEMBA1006138//ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.8e-13:41:73//HOMO SAPIENS (HUMAN).//P39194  
 55 F-HEMBA1006142//ALU SUBFAMILY SC WARNING ENTRY !!!!!/2.3e-39:101:77//HOMO SAPIENS (HUMAN).//P39192  
 F-HEMBA1006155//GENE 33 POLYPEPTIDE.//0.21:70:31//RATTUS NORVEGICUS (RAT).//P05432

- F-HEMBA1006158  
F-HEMBA1006173//PROTEIN-TYROSINE PHOSPHATASE STRIATUM-ENRICHED (EC 3.1.3.48) (STEP) (NEURAL-SPECIFIC PROTEIN-TYROSINE PHOSPHATASE) (FRAGMENT)//0.017:20:95//HOMO SAPIENS (HUMAN)//P54829
- 5 F-HEMBA1006182!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.37:31:61//HOMO SAPIENS (HUMAN)//P39188  
F-HEMBA1006198//HOMEBOX PROTEIN HOX-B3 (HOX-2.7) (MH-23)//0.85:61:29//MUS MUSCULUS (MOUSE)//P09026  
F-HEMBA1006235//50S RIBOSOMAL PROTEIN L33//1.0:26:38//AQUIFEX AEOLICUS//O67756
- 10 F-HEMBA1006248//MALE SPECIFIC SPERM PROTEIN MST84DB//0.0041:64:37//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01643  
F-HEMBA1006252//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR DE-3//1.0:22:40//DOLICHOS AXILLARIS (MACROTYLOMA AXILLARE)//P01057  
F-HEMBA1006253//DISINTEGRIN ERISTICOPHIN (PLATELET AGGREGATION ACTIVATION INHIBITOR)//0.95:19:47//ERISTOCOPHIS MACMAHONI (LEAF-NOSED VIPER)//P22826
- 15 F-HEMBA1006259  
F-HEMBA1006268!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/7.0e-05:32:65//HOMO SAPIENS (HUMAN)//P39192  
F-HEMBA1006272//RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 2)//4.8e-112:248:78//HOMO SAPIENS (HUMAN)//P10264
- 20 F-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) (FRAGMENT)//2.5e-71:164:75//HOMO SAPIENS (HUMAN)//P51003  
F-HEMBA1006283//50S RIBOSOMAL PROTEIN L32//0.01:27:44//THERMUS AQUATICUS (SUBSP. THERMOPHILUS)//P80339
- 25 F-HEMBA1006284//CUTICLE COLLAGEN 2//0.36:42:40//CAENORHABDITIS ELEGANS//P17656  
F-HEMBA1006291//HYPOTHETICAL 43.3 KD PROTEIN IN EVGS-GLK INTERGENIC REGION//2.4e-37:143:31//ESCHERICHIA COLI//P76518  
F-HEMBA1006293//MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR//0.20:134:29//RATTUS NORVEGICUS (RAT)//Q63345
- 30 F-HEMBA1006309//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION//2.1e-43:187:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38821  
F-HEMBA1006310//SIGNAL TRANSDUCER CD24 PRECURSOR (HEAT STABLE ANTIGEN) (HSA) (NECTADRIN)//0.71:46:39//RATTUS NORVEGICUS (RAT)//Q07490  
F-HEMBA1006328//RNA POLYMERASE ALPHA SUBUNIT (EC 2.7.7.48) (NUCLEOCAPSID PHOSPHOPROTEIN)//0.44:141:24//HUMAN PARAINFLUENZA 1 VIRUS (STRAIN CI-5/73)//P32531
- 35 F-HEMBA1006334//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR AF1627//0.98:26:46//ARCHAEOGLOBUS FULGIDUS//O28646  
F-HEMBA1006344//EZRN (P81) (CYTOVILLIN) (VILLIN-2)//8.8e-08:91:36//MUS MUSCULUS (MOUSE)//P26040  
F-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-)//9.1e-48:149:50//DROSOPHILA MELANOGASTER (FRUIT FLY)//O2193
- 40 F-HEMBA1006349//METALLOTHIONEIN-LIKE PROTEIN 1//0.015:59:33//CASUARINA GLAUCA (SWAMP OAK)//Q39511  
F-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)//6.8e-96:261:66//HOMO SAPIENS (HUMAN)//P28160
- 45 F-HEMBA1006364//PUTATIVE ENDONUCLEASE C1F12.06C (EC 3.1.-)//0.97:60:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10348  
F-HEMBA1006377//EARLY NODULIN 20 PRECURSOR (N-20)//0.00023:110:35//MEDICAGO TRUNCATULA (BARREL MEDIC)//P93329  
F-HEMBA1006380
- 50 F-HEMBA1006381//METALLOTHIONEIN-II//1.0:26:38//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA)//P15114  
F-HEMBA1006398//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//3.3e-26:123:52//HOMO SAPIENS (HUMAN)//P08547  
F-HEMBA1006416
- 55 F-HEMBA1006419!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.2e-24:102:50//HOMO SAPIENS (HUMAN)//P39189  
F-HEMBA1006421!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.1e-21:101:57//HOMO SAPIENS (HUMAN)//P39188

- F-HEMBA1006424//HYPOTHETICAL PROTEIN IORF1.//0.85:55:30//BOVINE CORONAVIRUS (STRAIN ME-BUS), AND BOVINE CORONAVIRUS (STRAIN QUEBEC).//P22053
- F-HEMBA1006425//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.8e-36:78:74//HOMO SAPIENS (HUMAN).//P39195
- 5 F-HEMBA1006438//HYPOTHETICAL 8.1 KD PROTEIN (ORF65).//1.0:38:36//GUILLARDIA THETA (CRYPTO-MONAS PHI).//O78421
- F-HEMBA1006445//RAS-LIKE PROTEIN 3.//1.9e-06:40:47//RHIZOMUCOR RACEMOSUS (MUCOR CIRCINEL-LOIDES F. LUSITANICUS).//P22280
- F-HEMBA1006446
- 10 F-HEMBA1006461//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.4e-18:68:67//HOMO SAPIENS (HUMAN).//P39192
- F-HEMBA1006467
- F-HEMBA1006471
- F-HEMBA1006474//40 KD PROTEIN.//1.1e-37:231:38//BORNA DISEASE VIRUS (BDV).//Q01552
- 15 F-HEMBA1006483//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/6.1e-38:77:74//HOMO SAPIENS (HUMAN).//P39192
- F-HEMBA1006485//HYPOTHETICAL 9.3 KD PROTEIN IN NAD3-NAD7 INTERGENIC REGION (ORF 79).//0.91:30:40//MARCHANTIA POLYMORPHA (LIVERWORT).//P38465
- F-HEMBA1006486//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.1e-12:78:51//HOMO SAPIENS (HU-MAN).//P08547
- 20 F-HEMBA1006489//FUN34 PROTEIN.//0.94:58:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32907
- F-HEMBA1006492//NADH-UBIQUINONE OXIDOREDUCTASE MWFE SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-MWFE) (CI-MWFE).//0.87:44:36//HOMO SAPIENS (HUMAN).//O15239
- 25 F-HEMBA1006494//FERREDOXIN-LIKE PROTEIN IN NIF REGION.//0.11:46:26//RHIZOBIUM LEGUMINOSA-RUM (BIOVAR TRIFOLI).//P42711
- F-HEMBA1006497
- F-HEMBA1006502//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.15:26:73//HOMO SAPIENS (HUMAN).//P39188
- 30 F-HEMBA1006507//DIAPHANOUS PROTEIN.//0.0055:129:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48608
- F-HEMBA1006521//3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE).//1.1e-32:177:41//ESCHERICHIA COLI.//P25716
- F-HEMBA1006530//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.052:84:26//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//P15583
- 35 F-HEMBA1006535//INHIBITOR OF APOPTOSIS PROTEIN 1 (MIAP1) (MIAP-1).//6.6e-05:53:39//MUS MUSCU-LUS (MOUSE).//O08863
- F-HEMBA1006540//PRESYNAPTIC PROTEIN SAP97 (SYNAPSE-ASSOCIATED PROTEIN 97) (DISCS, LARGE HOMOLOG 1).//2.1e-07:206:23//RATTUS NORVEGICUS (RAT).//Q62696
- 40 F-HEMBA1006546//PROBABLE E5 PROTEIN.//0.11:70:32//HUMAN PAPILLOMAVIRUS TYPE 51.//P26553
- F-HEMBA1006559//SUPPRESSOR PROTEIN SRP40.//0.015:221:20//SACCHAROMYCES CEREVISIAE (BAK-ER'S YEAST).//P32583
- F-HEMBA1006562//SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).//1.5e-07:122:33//HO-MO SAPIENS (HUMAN).//P10163
- 45 F-HEMBA1006568//CELL DIVISION PROTEIN KINASE 2 (EC 2.7.1.-) (CDC2 HOMOLOG EG1 PROTEIN KI-NASE).//0.63:53:37//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P23437
- F-HEMBA1006569//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//4.4e-06:88:39//BOS TAURUS (BOVINE).//P02465
- F-HEMBA1006579
- 50 F-HEMBA1006583//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.011:61:40//MUS MUSCULUS (MOUSE).//P05142
- F-HEMBA1006595//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.6e-34:93:77//HOMO SAPIENS (HU-MAN).//P39194
- F-HEMBA1006597//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.9e-26:75:74//HOMO SAPIENS (HUMAN).//P39195
- 55 F-HEMBA1006612//SUPPRESSOR PROTEIN SRP40.//0.026:221:22//SACCHAROMYCES CEREVISIAE (BAK-ER'S YEAST).//P32583
- F-HEMBA1006617//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.6e-20:73:63//HOMO SAPIENS (HUMAN).//

- P39188  
F-HEMBA1006624//HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION.//2.6e-31.209:  
44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40506
- 5 F-HEMBA1006631//HYPOTHETICAL 62.8 KD PROTEIN IN TAF145-YOR1 INTERGENIC REGION.//1.5e-15:  
131:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53331  
F-HEMBA1006635  
F-HEMBA1006639//POLYADENYLATE-BINDING PROTEIN 1 (POLY(A) BINDING PROTEIN 1) (PABP 1).//2.2e-  
11:48:75//MUS MUSCULUS (MOUSE).//P29341
- 10 F-HEMBA1006643//LONG NEUROTOXIN CR1 PRECURSOR (KAPPA NEUROTOXIN).//0.28:48:27//BUNGA-  
RUS MULTICINCTUS (MANY-BANDED KRAIT).//P15817  
F-HEMBA1006648//ZINC FINGER PROTEIN 12 (ZINC FINGER PROTEIN KOX3) (FRAGMENT).//0.26:17:47//  
HOMO SAPIENS (HUMAN).//P17014  
F-HEMBA1006652//60S RIBOSOMAL PROTEIN L7.//2.4e-44:206:47//MUS MUSCULUS (MOUSE).//P14148  
F-HEMBA1006653  
15 F-HEMBA1006659  
F-HEMBA1006665//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.018:43:58//HOMO SAPIENS (HU-  
MAN).//P08547  
F-HEMBA1006674//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135)  
(TAFII-130) (TAFII130).//2.9e-05:154:33//HOMO SAPIENS (HUMAN).//O00268
- 20 F-HEMBA1006676//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//3.6e-09:52:51//OWENIA FUSI-  
FORMIS.//P21260  
F-HEMBA1006682  
F-HEMBA1006695//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.1e-06:35:65//HOMO SAPIENS (HUMAN).//  
P39188
- 25 F-HEMBA1006696  
F-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMC1-TFG2  
INTERGENIC REGION.//3.4e-19:104:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53196  
F-HEMBA1006709//RETINOIC ACID RECEPTOR RXR-BETA.//0.24:111:36//HOMO SAPIENS (HUMAN).//  
P28702
- 30 F-HEMBA1006717  
F-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//  
5.8e-09:111:40//HOMO SAPIENS (HUMAN).//Q01485  
F-HEMBA1006744//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//1.8e-32:84:78//HOMO SAPIENS (HU-  
MAN).//P39191
- 35 F-HEMBA1006754//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.3e-75:220:62//HOMO SAPIENS (HU-  
MAN).//P08547  
F-HEMBA1006758//VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VECADHERIN) (CADHERIN-5)  
(7B4 ANTIGEN) (CD144 ANTIGEN).//0.024:110:29//HOMO SAPIENS (HUMAN).//P33151  
F-HEMBA1006767
- 40 F-HEMBA1006779//MITOCHONDRIAL RIBOSOMAL PROTEIN S12.//0.67:19:42//LEISHMANIA TARENTOLAE  
(SAUROLEISHMANIA TARENTOLAE).//Q34940  
F-HEMBA1006780  
F-HEMBA1006789//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.056:98:30//MUS MUSCULUS  
(MOUSE).//P05143
- 45 F-HEMBA1006795//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.9e-11:143:30//NYCTICEBUS COU-  
CANG (SLOW LORIS).//P08548  
F-HEMBA1006796//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).//0.16:38:42//MUS MUS-  
CULUS (MOUSE).//P70315
- 50 F-HEMBA1006807//HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME III.//4.4e-75:184:77//  
CAENORHABDITIS ELEGANS.//P34568  
F-HEMBA1006821//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.011:20:85//HOMO SAPIENS (HUMAN).//  
P39194  
F-HEMBA1006824//PROTEIN B11.//0.44:27:44//VACCINIA VIRUS (STRAIN WR).//Q01229  
F-HEMBA1006832//HYPOTHETICAL 34.6 KD PROTEIN C1G5.2 IN CHROMOSOME III.//1.0:46:36//  
CAENORHABDITIS ELEGANS.//P34327
- 55 F-HEMBA1006849  
F-HEMBA1006865//ACROSIN INHIBITORS IIA AND IIB (BUSI-I).//1.0:41:31//BOS TAURUS (BOVINE).//P01001  
F-HEMBA1006877//OXYSTEROL-BINDING PROTEIN.//3.7e-26:239:36//ORYZOLAGUS CUNICULUS (RAB-

- BIT).//P16258  
F-HEMBA1006885//HYPOTHETICAL 27.2 KD PROTEIN F09E5.8 IN CHROMOSOME II.//4.5e-38:185.43//  
CAENORHABDITIS ELEGANS.//P52057  
F-HEMBA1006900
- 5 F-HEMBA1006914//UBIQUITIN-ACTIVATING ENZYME E1-LIKE (POLYMERASE-INTERACTING PROTEIN 2).//  
5.2e-27:269:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P52488  
F-HEMBA1006921//CYTOTOXIN 3 (COMPONENT 3.20).//0.99:32:37//NAJA MELANOLEUCA (FOREST CO-  
BRA) (BLACK-LIPPED COBRA).//P01473  
F-HEMBA1006926//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//0.0024:148:  
10 33//RATTUS NORVEGICUS (RAT).//P54258  
F-HEMBA1006929//HYPOTHETICAL PROTEIN MJ0525.//0.95:35:20//METHANOCOCCUS JANNASCHII.//  
Q57945  
F-HEMBA1006936//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1 / PRP-  
3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C) [CONTAINS: PEPTIDE P-C].//0.074:116:31//HOMO  
15 SAPIENS (HUMAN).//P02810  
F-HEMBA1006938  
F-HEMBA1006941//THIOREDOXIN H-TYPE 1 (TRX-H1).//2.1e-13:90:33//NICOTIANA TABACUM (COMMON  
TOBACCO).//P29449  
F-HEMBA1006949  
F-HEMBA1006973//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.75:29:55//BOS TAURUS (BOVINE).//  
20 P25508  
F-HEMBA1006976//CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANS-  
FERASE (EC 2.4.99.-) (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALIII) (ALPHA 2,3-ST)  
(GAL-NAC6S) (STZ) (SIAT4-C) (SAT-3) (ST-4).//3.9e-108:117:95//HOMO SAPIENS (HUMAN).//Q11206  
25 F-HEMBA1006993  
F-HEMBA1006996//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70).//  
0.12:51:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779  
F-HEMBA1007002//PLATELET GLYCOPROTEIN IX PRECURSOR (GPIX) (CD42A).//0.00096:60:33//HOMO SA-  
PIENS (HUMAN).//P14770  
30 F-HEMBA1007017//HYPOTHETICAL 7.2 KD PROTEIN IN CYAY-DAPF INTERGENIC REGION.//1.0:25:56//ES-  
CHERICHIA COLI.//P39166  
F-HEMBA1007018//DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (LIC57/59) (DYNEIN LIGHT CHAIN  
A) (DLC-A).//8.5e-120:278:80//GALLUS GALLUS (CHICKEN).//Q90828  
F-HEMBA1007045//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//2.1e-12:158:29//  
35 XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437  
F-HEMBA1007051  
F-HEMBA1007052//60S RIBOSOMAL PROTEIN L37-B (L35) (YP55).//0.94:37:35//SACCHAROMYCES CERE-  
VISIAE (BAKER'S YEAST).//P51402  
F-HEMBA1007062//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.93:55:29//RHINOCEROS UNICORNIS  
40 (GREATER INDIAN RHINOCEROS).//Q96063  
F-HEMBA1007066//ECLOSION HORMONE PRECURSOR (ECDYSIS ACTIVATOR) (EH).//0.58:49:38//BOM-  
BYX MORI (SILK MOTH).//P25331  
F-HEMBA1007073//PUTATIVE SMALL MEMBRANE PROTEIN (ORF 4).//0.86:46:34//CANINE ENTERIC  
CORONAVIRUS (STRAIN INSVC-1) (CCV).//P36696  
45 F-HEMBA1007078//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//8.6e-29:56:67//HOMO SAPIENS (HUMAN).//  
P39193  
F-HEMBA1007080//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.028:122:30//XENO-  
PUS LAEVIS (AFRICAN CLAWED FROG).//P17437  
F-HEMBA1007085//RTOA PROTEIN (RATIO-A).//7.4e-11:221:31//DICTYOSTELIUM DISCOIDEUM (SLIME  
50 MOLD).//P54681  
F-HEMBA1007087//HYPOTHETICAL PROTEIN MJ0162.//3.3e-29:173:36//METHANOCOCCUS JANNASCHII.//  
Q57626  
F-HEMBA1007112  
F-HEMBA1007113  
55 F-HEMBA1007121//INOSITOL POLYPHOSPHATE 1-PHOSPHATASE (EC 3.1.3.57) (IPP).//5.4e-07:90:28//HO-  
MO SAPIENS (HUMAN).//P49441  
F-HEMBA1007129//HIRUSTASIN.//0.88:37:32//HIRUDO MEDICINALIS (MEDICINAL LEECH).//P80302  
F-HEMBA1007147//HYPOTHETICAL 12.0 KD PROTEIN IN DST1-HEM2 INTERGENIC REGION.//0.92:23:34//

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53182  
 F-HEMBA1007149//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17)//0.0078:17:70//ESCHERICHIA COLI//P05834  
 5 F-HEMBA1007151//WDNM1 PROTEIN PRECURSOR//0.25:45:37//MUS MUSCULUS (MOUSE)//Q62477  
 F-HEMBA1007174//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REGION//6.9e-18:97:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47160  
 F-HEMBA1007178//ALU SUBFAMILY SX WARNING ENTRY //9.8e-06:38:65//HOMO SAPIENS (HUMAN)//P39195  
 10 F-HEMBA1007194//GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST ISOFORM PRECURSOR (EC 1.1.1.49) (G6PD)//1.0:80:32//NICOTIANA TABACUM (COMMON TOBACCO)//Q43793  
 F-HEMBA1007203//PROTEIN A22//1.0:115:26//VARIOLE VIRUS//P33845  
 F-HEMBA1007206  
 F-HEMBA1007224//HYPOTHETICAL 35.7 KD PROTEIN C41C4.6 IN CHROMOSOME II//2.4e-05:92:30//CAENORHABDITIS ELEGANS//Q09275  
 15 F-HEMBA1007243//HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) (HGPRT) (HGPRTASE) (HPRT B)//3.1e-74:205:67//MUS MUSCULUS (MOUSE)//P00493  
 F-HEMBA1007251//VITELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-4) (PROTEIN SV23)//0.52:108:30//DROSOPHILA MELANOGASTER (FRUIT FLY)//P13238  
 F-HEMBA1007256  
 20 F-HEMBA1007267//ICALICIN (FRAGMENT)//0.060:88:31//HOMO SAPIENS (HUMAN)//Q13939  
 F-HEMBA1007273//HYPOTHETICAL 8.1 KD PROTEIN (ORF65)//0.95:40:37//GUILLARDIA THETA (CRYPTOMONAS PHI)//O78421  
 F-HEMBA1007279//ALU SUBFAMILY J WARNING ENTRY //4.6e-24:98:64//HOMO SAPIENS (HUMAN)//P39188  
 25 F-HEMBA1007281  
 F-HEMBA1007288//HYPOTHETICAL 13.5 KD PROTEIN IN ZMS1-MNS1 INTERGENIC REGION//0.88:11:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47162  
 F-HEMBA1007300//CGMP-SPECIFIC 3'-5'-CYCLIC PHOSPHODIESTERASE (EC 3.1.4.17) (CGB-PDE)//2.7e-43:220:41//BOS TAURUS (BOVINE)//Q28156  
 30 F-HEMBA1007301//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR//3.3e-22:115:33//HOMO SAPIENS (HUMAN)//P02461  
 F-HEMBA1007319  
 F-HEMBA1007320//HYPOTHETICAL 28.0 KD PROTEIN IN GLOB-RNHA INTERGENIC REGION//1.0:48:37//ESCHERICHIA COLI//P75672  
 35 F-HEMBA1007322//THREONINE DEHYDRATASE OPERON ACTIVATOR PROTEIN//1.0:59:33//ESCHERICHIA COLI//P11866  
 F-HEMBA1007327  
 F-HEMBA1007374//ALU SUBFAMILY J WARNING ENTRY //9.1e-12:37:62//HOMO SAPIENS (HUMAN)//P39188  
 40 F-HEMBA1007342//PROBABLE E5 PROTEIN//0.89:96:29//PYGMY CHIMPANZEE PAPILLOMAVIRUS TYPE 1//Q02268  
 F-HEMBA1007347//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2)//0.92:62:43//OVIS ARIES (SHEEP)//Q29400  
 F-HEMBA1000005//WEAK NEUROTOXIN 5//0.98:30:33//NAJA NAJA (INDIAN COBRA)//P29179  
 45 F-HEMBA1000008//ALU SUBFAMILY SX WARNING ENTRY //2.7e-35:73:84//HOMO SAPIENS (HUMAN)//P39195  
 F-HEMBA1000018//HYPOTHETICAL BHLF1 PROTEIN//0.39:90:37//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)//P03181  
 F-HEMBA1000024//VIRE LOCUS 9 KD VIRULENCE PROTEIN//0.66:36:41//AGROBACTERIUM TUMEFACIENS//P08061  
 50 F-HEMBA1000025//MUSCARINIC TOXIN ALPHA (MT-ALPHA)//0.46:32:40//DENDROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA)//P80494  
 F-HEMBA1000030//SUPPRESSOR PROTEIN SRP40//6.7e-07:50:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32583  
 55 F-HEMBA1000036//HYPOTHETICAL 43.2 KD PROTEIN C34E10.1 IN CHROMOSOME III//2.5e-07:120:29//CAENORHABDITIS ELEGANS//P46576  
 F-HEMBA1000037//HYPOTHETICAL 59.9 KD PROTEIN-IN SGA1-KTR7 INTERGENIC REGION//1.7e-05:71:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40492



- F-HEMBB1000039//VERY HYPOTHETICAL 11.9 KD PROTEIN C4H3.12C IN CHROMOSOME I.//1.0.61.21//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10219  
F-HEMBB1000044
- 5 F-HEMBB1000048//HYPOTHETICAL 15.7 KD PROTEIN IN IDH-DEOR INTERGENIC REGION.//1.0.63.31//BACILLUS SUBTILIS.//P54942  
F-HEMBB1000050//ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.0e-14:34:79//HOMO SAPIENS (HUMAN).//P39194  
F-HEMBB1000054//ALU SUBFAMILY SP WARNING ENTRY !!!!!/5.9e-31:45:73//HOMO SAPIENS (HUMAN).//P39193
- 10 F-HEMBB1000055//MUSCARINIC TOXIN ALPHA (MT-ALPHA).//1.0.14:57//DENDROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA).//P80494  
F-HEMBB1000059//ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.0e-21:82:59//HOMO SAPIENS (HUMAN).//P39195  
F-HEMBB1000083//CHROMOGRANIN A PRECURSOR (CGA) [CONTAINS: PANCREASTATIN; BETA-GRANIN; WE-14].//0.87:172:28//RATTUS NORVEGICUS (RAT).//P10354
- 15 F-HEMBB1000089//HYPOTHETICAL 9.5 KD PROTEIN IN SPEA-METK INTERGENIC REGION (F83).//1.0.42:33//ESCHERICHIA COLI.//P46879  
F-HEMBB1000099//ALU SUBFAMILY SB WARNING ENTRY !!!!!/7.7e-08:31:87//HOMO SAPIENS (HUMAN).//P39189
- 20 F-HEMBB1000103//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-38:136:58//HOMO SAPIENS (HUMAN).//P08547  
F-HEMBB1000113//ALU SUBFAMILY J WARNING ENTRY !!!!!/3.9e-13:57:64//HOMO SAPIENS (HUMAN).//P39188  
F-HEMBB1000119//MAF PROTEIN.//3.6e-32:195:43//BACILLUS SUBTILIS.//Q02169
- 25 F-HEMBB1000136//HYPOTHETICAL 12.7 KD PROTEIN IN PCS60-ABD1 INTERGENIC REGION.//0.65:71:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38327  
F-HEMBB1000141//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.00014:34:64//HOMO SAPIENS (HUMAN).//P20931  
F-HEMBB1000144//ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/2.0e-26:81:69//HOMO SAPIENS (HUMAN).//P39191
- 30 F-HEMBB1000173//ALU SUBFAMILY J WARNING ENTRY !!!!!/9.2e-29:91:71//HOMO SAPIENS (HUMAN).//P39188  
F-HEMBB1000175//ANTIMICROBIAL PEPTIDE ENAP-1 (FRAGMENT).//0.97:41:36//EQUUS CABALLUS (HORSE).//P80930
- 35 F-HEMBB1000198//HYPOTHETICAL 7.7 KD PROTEIN YCF33 (ORF67).//0.91:21:52//PORPHYRA PURPUREA.//P51329  
F-HEMBB1000215//ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.4e-08:39:76//HOMO SAPIENS (HUMAN).//P39192  
F-HEMBB1000217//DNA DAMAGE TOLERANCE PROTEIN RHC31 (RAD31 HOMOLOG).//2.9e-32:174:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06624
- 40 F-HEMBB1000218//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.73:31:38//MICROTUS PENNSYLVANICUS (MEADOW VOLE).//P24949  
F-HEMBB1000226//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//6.5e-26:191:34//CAENORHABDITIS ELEGANS.//Q09217
- 45 F-HEMBB1000240  
F-HEMBB1000244//ALU SUBFAMILY J WARNING ENTRY !!!!!/1.9e-05:44:61//HOMO SAPIENS (HUMAN).//P39188  
F-HEMBB1000250  
F-HEMBB1000258
- 50 F-HEMBB1000264//CUTICLE COLLAGEN SQT-1.//0.15:89:33//CAENORHABDITIS ELEGANS.//P12114  
F-HEMBB1000266//TRANSLATION INITIATION FACTOR IF-2.//2.7e-06:167:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39730  
F-HEMBB1000272//CYTOCHROME C OXIDASE POLYPEPTIDE VIB (EC 1.9.3.1) (AED).//0.75:30:43//BOS TAURUS (BOVINE).//P00429
- 55 F-HEMBB1000274//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).//1.0:38:36//SUS SCROFA (PIG).//P35323  
F-HEMBB1000284//CALTRIN (CALCIUM TRANSPORT INHIBITOR).//1.0:56:30//MUS MUSCULUS (MOUSE).//Q09098

F-HEMBB1000307  
 F-HEMBB1000312  
 F-HEMBB1000317//THROMBOSPONDIN 1 PRECURSOR.//3.2e-32:135:43//HOMO SAPIENS (HUMAN).//  
 P07996  
 5 F-HEMBB1000318//PUTATIVE SMALL MEMBRANE PROTEIN (NONSTRUCTURAL PROTEIN NS3) (NON-  
 STRUCTURAL 9.5 KD PROTEIN).//0.41:51:31//HUMAN CORONAVIRUS (STRAIN OC43).//Q04854  
 F-HEMBB1000335//ZINC FINGER PROTEIN 13 (ZFP-13) (KROX-8 PROTEIN) (FRAGMENT).//0.82:33:45//MUS  
 MUSCULUS (MOUSE).//P10754  
 10 F-HEMBB1000336//ALDEHYDE OXIDASE (EC 1.2.3.1) (FRAGMENTS).//0.80:44:40//ORYZOTOLAGUS CUNIC-  
 ULUS (RABBIT).//P80456  
 F-HEMBB1000337//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR  
 SRP75).//0.94:118:22//HOMO SAPIENS (HUMAN).//Q08170  
 F-HEMBB1000338//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.042:33:39//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY).//Q01842  
 15 F-HEMBB1000339//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.2e-14:54:55//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-HEMBB1000341//GENE 74 PROTEIN (GP74).//1.0:39:33//MYCOBACTERIOPHAGE L5.//Q05289  
 F-HEMBB1000343  
 F-HEMBB1000354//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-15:83:56//HOMO SAPIENS (HUMAN).//  
 20 P39188  
 F-HEMBB1000369//PROTEIN Q300.//0.99:27:40//MUS MUSCULUS (MOUSE).//Q02722  
 F-HEMBB1000374//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/4.7e-34:56:78//HOMO SAPIENS (HUMAN).//  
 P39189  
 F-HEMBB1000376  
 25 F-HEMBB1000391//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.0013:79:35//BOS TAURUS (BO-  
 VINE).//P25508  
 F-HEMBB1000399//CHECKPOINT PROTEIN RAD17.//2.8e-15:187:31//SCHIZOSACCHAROMYCES POMBE  
 (FISSION YEAST).//P50531  
 F-HEMBB1000402//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.027:60:  
 38//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//P15583  
 30 F-HEMBB1000404//CYANELLE 50S RIBOSOMAL PROTEIN L28.//0.94:29:27//CYANOPHORA PARADOXA.//  
 P48129  
 F-HEMBB1000420//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.023:97:35//HOMO SA-  
 PIENS (HUMAN).//Q15427  
 35 F-HEMBB1000434//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.8e-20:111:54//HOMO SAPIENS (HU-  
 MAN).//P39194  
 F-HEMBB1000438//HYPOTHETICAL 7.9 KD PROTEIN IN GP55-NRDG INTERGENIC REGION.//0.93:24:50//  
 BACTERIOPHAGE T4.//P07076  
 40 F-HEMBB1000441//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.4e-23:85:70//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-HEMBB1000449//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.88:27:51//HOMO SAPIENS (HUMAN).//  
 P39195  
 F-HEMBB1000455  
 F-HEMBB1000472  
 45 F-HEMBB1000480//PROTEIN STBC.//1.0:52:30//ESCHERICHIA COLI.//P11905  
 F-HEMBB1000487//SHORT NEUROTOXIN 1 (NEUROTOXIN ALPHA) (NEUROTOXIN II).//0.93:29:34//NAJA  
 OXIANA (CENTRAL ASIAN COBRA) (OXUS COBRA).//P01427  
 F-HEMBB1000490//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.3e-16:50:80//HOMO SAPIENS (HUMAN).//  
 P39195  
 50 F-HEMBB1000491  
 F-HEMBB1000493//3A PROTEIN.//1.0:51:35//AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN BEAU-  
 DETTE) (IBV).//P30237  
 F-HEMBB1000510//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.7e-27:132:45//HOMO SAPIENS (HU-  
 MAN).//P08547  
 55 F-HEMBB1000518//CYTOCHROME C OXIDASE POLYPEPTIDE III (EC 1.9.3.1).//0.021:47:40//LEISHMANIA  
 TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//P14546  
 F-HEMBB1000523  
 F-HEMBB1000530//COLLAGEN ALPHA 1(XIV) CHAIN PRECURSOR (UNDULIN).//9.8e-14:43:83//GALLUS

GALLUS (CHICKEN).//P32018  
 F-HEMBB1000550//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3).//0.19:97:30//TRYPA-  
 SOMA BRUCEI BRUCEI.//P04540  
 5 F-HEMBB1000554//MATERNAL B9.10 PROTEIN (P30 B9.10).//0.94:82:25//XENOPUS LAEVIS (AFRICAN  
 CLAWED FROG).//P40744  
 F-HEMBB1000556//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135)  
 (TAFII-130) (TAFII130).//0.043:201:29//HOMO SAPIENS (HUMAN).//000268  
 F-HEMBB1000564//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:5:2:34//METRIDIVM SENILE  
 (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE).//O47493  
 10 F-HEMBB1000573//ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/2.3e-10:52:73//HOMO SAPIENS (HU-  
 MAN).//P39191  
 F-HEMBB1000575//ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.8e-26:76:76//HOMO SAPIENS (HUMAN).//  
 P39192  
 15 F-HEMBB1000586//NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3)  
 (COMPLEX I-MLRQ) (CI-MLRQ).//0.74:23:52//HOMO SAPIENS (HUMAN).//O00483  
 F-HEMBB1000589//ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.9e-25:61:75//HOMO SAPIENS (HUMAN).//  
 P39193  
 F-HEMBB1000591//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:34:35//PETROMYZON MARINUS  
 (SEA LAMPREY).//Q35537  
 20 F-HEMBB1000592//SMALL PROLINE-RICH PROTEIN 2-1.//0.0016:49:42//HOMO SAPIENS (HUMAN).//P35326  
 F-HEMBB1000593//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENTS).//0.0070:189:32//GALLUS GALLUS  
 (CHICKEN).//P12105  
 F-HEMBB1000598//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.7e-10:110:41//NYCTICEBUS COU-  
 CANG (SLOW LORIS).//P08548  
 25 F-HEMBB1000623//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III.//0.0022:98:28//  
 CAENORHABDITIS ELEGANS.//P34284  
 F-HEMBB1000630  
 F-HEMBB1000631//ALPHA-2C-1 ADRENERGIC RECEPTOR (ALPHA-2C-1 ADRENOCEPTOR) (SUBTYPE  
 C4).//8.8e-06:59:40//HOMO SAPIENS (HUMAN).//P18825  
 30 F-HEMBB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//7.3e-13:173:28//MUS MUSCU-  
 LUS (MOUSE).//P27671  
 F-HEMBB1000637//ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.6e-41:94:82//HOMO SAPIENS (HUMAN).//  
 P39193  
 F-HEMBB1000638//INVOLUCRIN.//1.9e-06:144:29//HOMO SAPIENS (HUMAN).//P07476  
 35 F-HEMBB1000643//ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.3e-30:77:76//HOMO SAPIENS (HUMAN).//  
 P39195  
 F-HEMBB1000649//ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.5e-37:58:81//HOMO SAPIENS (HUMAN).//  
 P39189  
 40 F-HEMBB1000652//ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.2e-37:61:77//HOMO SAPIENS (HUMAN).//  
 P39193  
 F-HEMBB1000665//HYPOTHETICAL PROTEIN BBD24.//0.83:38:36//BORRELIA BURGDORFERI (LYME DIS-  
 EASE SPIROCHETE).//P70845  
 F-HEMBB1000671//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.8e-51:74:71//HOMO SAPIENS (HU-  
 MAN).//P08547  
 45 F-HEMBB1000673//HEAT-STABLE ENTEROTOXIN A3/A4 PRECURSOR (STA3/STA4) (ST-IB) (ST-H).//0.012:  
 37:37//ESCHERICHIA COLI.//P07965  
 F-HEMBB1000684//ALU SUBFAMILY SP WARNING ENTRY !!!!!/3.1e-21:66:72//HOMO SAPIENS (HUMAN).//  
 P39193  
 F-HEMBB1000693//HUNTINGTIN ASSOCIATED PROTEIN 1 (HAP1).//5.2e-26:121:49//RATTUS NORVEGICUS  
 (RAT).//P54256  
 50 F-HEMBB1000705  
 F-HEMBB1000706  
 F-HEMBB1000709//HYPOTHETICAL 5.8 KD PROTEIN.//1.0:29:44//CLOVER YELLOW MOSAIC VIRUS  
 (CYMV).//P16485  
 55 F-HEMBB1000725//RAS-RELATED PROTEIN RAB-8B.//7.4e-105:205:98//RATTUS NORVEGICUS (RAT).//  
 P70550  
 F-HEMBB1000726//ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.4e-25:85:70//HOMO SAPIENS (HU-  
 MAN).//P39194

F-HEMBB1000738//50S RIBOSOMAL PROTEIN L33.//1.0:41:31//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P35871  
 F-HEMBB1000749//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.3e-29:42:85//HOMO SAPIENS (HUMAN).//P39194  
 5 F-HEMBB1000763//NIFU PROTEIN.//0.089:63:36//FRANKIA ALNI.//P46045  
 F-HEMBB1000770//CALTRIN-LIKE PROTEIN II.//0.98:13:69//CAVIA PORCELLUS (GUINEA PIG).//P22075  
 F-HEMBB1000774//HIGH MOBILITY GROUP PROTEIN HMG-Y.//0.029:53:32//MUS MUSCULUS (MOUSE).//P17095  
 10 F-HEMBB1000781//MAPK/ERK KINASE KINASE 2 (EC 2.7.1.-) (MEK KINASE 2) (MEKK 2).//3.5e-75:144:98//MUS MUSCULUS (MOUSE).//Q61083  
 F-HEMBB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//2.6e-49:232:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39956  
 F-HEMBB1000790//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.9e-16:93:51//HOMO SAPIENS (HUMAN).//P39188  
 15 F-HEMBB1000794  
 F-HEMBB1000807//MUSCARINIC ACETYLCHOLINE RECEPTOR M3.//0.54:111:27//GALLUS GALLUS (CHICKEN).//P49578  
 F-HEMBB1000810  
 F-HEMBB1000821  
 20 F-HEMBB1000822//HYPOTHETICAL 10 KD PROTEIN (ORF 6).//0.10:50:34//NARCISSUS MOSAIC VIRUS (NMV).//P15099  
 F-HEMBB1000826//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.00025:73:39//HOMO SAPIENS (HUMAN).//P20931  
 F-HEMBB1000827//HYPOTHETICAL 7.4 KD PROTEIN.//0.89:23:52//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19302  
 25 F-HEMBB1000831//MALE SPECIFIC SPERM PROTEIN MST87F.//0.98:35:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175  
 F-HEMBB1000835//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.8e-31:96:46//HOMO SAPIENS (HUMAN).//P08547  
 30 F-HEMBB1000840//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.00012:102:36//NYCTICEBUS COUCANG (SLOW LORIS).//P08548  
 F-HEMBB1000848//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.3e-97:239:70//HOMO SAPIENS (HUMAN).//P08547  
 F-HEMBB1000852  
 35 F-HEMBB1000870  
 F-HEMBB1000876//METALLOTHIONEIN (MT).//0.99:14:64//PERCA FLUVIATILIS (PERCH).//P52725  
 F-HEMBB1000883//HYPOTHETICAL 7.8 KD PROTEIN (ORF62).//0.34:60:33//GUILLARDIA THETA (CRYPTOMONAS PHI).//Q78459  
 40 F-HEMBB1000887//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//1.0:26:42//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251  
 F-HEMBB1000888  
 F-HEMBB1000890  
 F-HEMBB1000893  
 45 F-HEMBB1000908//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.0074:45:51//HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBB1000910//PROBABLE E5 PROTEIN.//1.0:49:36//HUMAN PAPILLOMAVIRUS TYPE 58.//P26552  
 F-HEMBB1000913//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.29:56:46//HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBB1000915//CYTOCHROME B (EC 1.10.2.2).//2.5e-24:62:90//HOMO SAPIENS (HUMAN).//P00156  
 50 F-HEMBB1000917//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/5.9e-26:53:66//HOMO SAPIENS (HUMAN).//P39193  
 F-HEMBB1000927//NEURONAL CALCIUM SENSOR 1 (NCS-1) (FREQUENIN).//3.9e-44:182:45//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q91614  
 F-HEMBB1000947//SMALL PROLINE-RICH PROTEIN 2-1.//0.24:69:27//HOMO SAPIENS (HUMAN).//P35326  
 55 F-HEMBB1000959//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/3.0e-31:89:68//HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBB1000973//CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.//0.96:66:36//BOS TAURUS (BOWTIE).//I018739

F-HEMBB1000975//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (HISTIDINE-PROLINE RICH GLYCOPROTEIN) (HPRG).//0.0042:77-41//HOMO SAPIENS (HUMAN).//P04196  
 F-HEMBB1000981  
 5 F-HEMBB1000985//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//1.0e-18:178:30//MUS MUSCULUS (MOUSE).//P28575  
 F-HEMBB1000991  
 F-HEMBB1000996//HYPOTHETICAL 10.1 KD PROTEIN IN RHSD-GCL INTERGENIC REGION (ORFD3).//0.58:34:35//ESCHERICHIA COLI.//P33669  
 10 F-HEMBB1001004//PROBABLE E4 PROTEIN.//0.24:110:35//HUMAN PAPILLOMAVIRUS TYPE 5B.//P26550  
 F-HEMBB1001008  
 F-HEMBB1001011//ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4) (ZINC FINGER PROTEIN HF.16).//3.2e-17:104:47//HOMO SAPIENS (HUMAN).//P17097  
 F-HEMBB1001014//EOTAXIN PRECURSOR (EOSINOPHIL CHEMOTACTIC PROTEIN).//1.0e-58:39//RATTUS NORVEGICUS (RAT).//P97545  
 15 F-HEMBB1001020//ALU SUBFAMILY SB WARNING ENTRY !!!!!1.4e-07:36:75//HOMO SAPIENS (HUMAN).//P39189  
 F-HEMBB1001024  
 F-HEMBB1001037//FERREDOXIN.//1.0:52:25//MOORELLA THERMOACETICA (CLOSTRIDIUM THERMOACETICUM).//P00203  
 20 F-HEMBB1001047  
 F-HEMBB1001051//PROTEIN FAN (FACTOR ASSOCIATED WITH N-SMASE ACTIVATION).//3.4e-21:50:100//HOMO SAPIENS (HUMAN).//Q92636  
 F-HEMBB1001056//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0099:115:35//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341  
 25 F-HEMBB1001058//ALU SUBFAMILY SC WARNING ENTRY !!!!!1.1e-33:95:76//HOMO SAPIENS (HUMAN).//P39192  
 F-HEMBB1001060//HYPOTHETICAL 8.2 KD PROTEIN ZC21.7 IN CHROMOSOME III.//1.0:38:36//CAENORHABDITIS ELEGANS.//P34591  
 F-HEMBB1001063  
 30 F-HEMBB1001068  
 F-HEMBB1001096//NOXIUSTOXIN (NTX) (TOXIN II.11).//0.99:36:38//CENTRUROIDES NOXIUS (MEXICAN SCORPION).//P08815  
 F-HEMBB1001102//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//1.1e-27:115:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701  
 35 F-HEMBB1001105//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR.//0.80:70:40//HOMO SAPIENS (HUMAN).//P28067  
 F-HEMBB1001112//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.1e-126:287:85//RATTUS NORVEGICUS (RAT).//P38378  
 40 F-HEMBB1001114//HYPOTHETICAL 9.6 KD PROTEIN (ORF2).//0.84:62:27//BACTERIOPHAGE L2.//P42537  
 F-HEMBB1001117  
 F-HEMBB1001119//COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR.//1.6e-21:50:98//HOMO SAPIENS (HUMAN).//Q99715  
 F-HEMBB1001126//HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME II.//1.7e-50:184:53//CAENORHABDITIS ELEGANS.//Q09296  
 45 F-HEMBB1001133//ALU SUBFAMILY SC WARNING ENTRY !!!!!1.4e-09:53:62//HOMO SAPIENS (HUMAN).//P39192  
 F-HEMBB1001137//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//2.0e-05:206:27//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414  
 50 F-HEMBB1001142//ALU SUBFAMILY SP WARNING ENTRY !!!!!4.1e-05:46:56//HOMO SAPIENS (HUMAN).//P39193  
 F-HEMBB1001151//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I.//2.3e-23:109:44//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149  
 F-HEMBB1001153//PROCOLLAGEN ALPHA 2(IV) CHAIN PRECURSOR.//0.75:76:34//ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P27393  
 55 F-HEMBB1001169//ALU SUBFAMILY SX WARNING ENTRY !!!!!1.4e-16:71:59//HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBB1001175//ANKYRIN.//3.2e-12:169:31//MUS MUSCULUS (MOUSE).//Q02357  
 F-HEMBB1001177//PERIODIC TRYPTOPHAN PROTEIN 2 HOMOLOG.//9.4e-07:148:27//HOMO SAPIENS (HUMAN).

MAN).//Q15269  
 F-HEMBB1001182//HYPOTHETICAL 36.0 KD PROTEIN.//1.3e-09:110:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P54858  
 F-HEMBB1001199  
 5 F-HEMBB1001208//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.053:23:47//MUS MUSCULUS (MOUSE).//P15974  
 F-HEMBB1001209  
 F-HEMBB1001210//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.14:40:37//MUS MUSCULUS (MOUSE).//P15974  
 10 F-HEMBB1001218//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.4e-19:49:67//HOMO SAPIENS (HUMAN).//P39194  
 F-HEMBB1001221//CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-LIVER PRECURSOR (EC 1.9.3.1).//0.11:44:38//HOMO SAPIENS (HUMAN).//P14406  
 F-HEMBB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).//2.0e-45:192:53//MUS MUSCULUS (MOUSE).//P46938  
 15 F-HEMBB1001242//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN CHROMOSOME I.//5.5e-37:226:41//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09876  
 F-HEMBB1001249//OXALOACETATE DECARBOXYLASE GAMMA CHAIN (EC 4.1.1.3).//1.0:23:43//KLEBSIELLA PNEUMONIAE.//P13155  
 20 F-HEMBB1001253//METALLOTHIONEIN-IH (MT-1H) (METALLOTHIONEIN-O) (MT-O).//0.14:16:43//HOMO SAPIENS (HUMAN).//P80294  
 F-HEMBB1001254//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.4e-12:40:75//HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBB1001267//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.0e-12:33:78//HOMO SAPIENS (HUMAN).//P39193  
 25 F-HEMBB1001271//HYPOTHETICAL 25.1 KD PROTEIN B0302.5 IN CHROMOSOME X.//1.0:58:37//CAENORHABDITIS ELEGANS.//Q10928  
 F-HEMBB1001282//ANKYRIN HOMOLOG PRECURSOR.//9.5e-13:206:31//CHROMATIUM VINOSUM.//Q06527  
 F-HEMBB1001288//COPPER HOMEOSTASIS PROTEIN CUTC.//4.6e-42:163:51//ESCHERICHIA COLI.//P46719  
 30 F-HEMBB1001289//HYPOTHETICAL PROTEIN ORF-1137.//1.0e-05:106:26//MUS MUSCULUS (MOUSE).//P11260  
 F-HEMBB1001294//GTP-BINDING PROTEIN TC10.//1.3e-34:58:94//HOMO SAPIENS (HUMAN).//P17081  
 F-HEMBB1001302//HOMEBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEBOX PROTEIN 2) (CDX-3).//0.24:49:46//HOMO SAPIENS (HUMAN).//Q99626  
 35 F-HEMBB1001304//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).//1.0:17:70//LYCOPERSICON ESCULENTUM (TOMATO).//Q01157  
 F-HEMBB1001314//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.21:104:27//DROSOPHILA ERECTA (FRUIT FLY).//P13730  
 40 F-HEMBB1001315//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.3e-24:53:71//HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBB1001317//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//0.24:90:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09782  
 F-HEMBB1001326//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.36:26:50//MUS MUSCULUS (MOUSE).//P15974  
 45 F-HEMBB1001331//HYPOTHETICAL BHLF1 PROTEIN.//1.0:127:33//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181  
 F-HEMBB1001335//ESCARGOT/SLAIL PROTEIN HOMOLOG (FRAGMENT).//0.85:44:29//SCIARA COPROPHILA (FUNGUS GNAT).//Q01799  
 50 F-HEMBB1001337//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.2e-20:62:62//HOMO SAPIENS (HUMAN).//P39194  
 F-HEMBB1001339//HYPOTHETICAL 17.3 KD PROTEIN CY1A11.16C.//8.2e-07:123:34//MYCOBACTERIUM TUBERCULOSIS.//Q05066  
 F-HEMBB1001346//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.2e-14:60:45//HOMO SAPIENS (HUMAN).//P08547  
 55 F-HEMBB1001348//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.6e-14:61:62//HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBB1001356

F-HEMBB1001364  
 F-HEMBB1001366/HISTIDINE-RICH PROTEIN.//0.87:26:42//PLASMODIUM FALCIPARUM (ISOLATE FCM17 /  
 SENEGAL).//P14586  
 5 F-HEMBB1001367//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/8.6e-40:146:61//HOMO SAPIENS (HU-  
 MAN).//P39192  
 F-HEMBB1001369  
 F-HEMBB1001380//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.9e-25:49:83//HOMO SAPIENS (HUMAN).//  
 P39193  
 10 F-HEMBB1001384//BH3 INTERACTING DOMAIN DEATH AGONIST (BID).//0.80:95:29//MUS MUSCULUS  
 (MOUSE).//P70444  
 F-HEMBB1001387//PEA2 PROTEIN (PPF2 PROTEIN).//0.022:117:34//SACCHAROMYCES CEREVISIAE (BAK-  
 ER'S YEAST).//P40091  
 F-HEMBB1001394//ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE  
 CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA  
 15 A SUBUNIT).//0.38:85:31//MUS MUSCULUS (MOUSE).//P17426  
 F-HEMBB1001410  
 F-HEMBB1001424//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR.//0.99:37:21//  
 ORYZA SATIVA (RICE).//P12162  
 F-HEMBB1001426//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.0035:40:60//HOMO SAPIENS (HUMAN).//  
 20 P39195  
 F-HEMBB1001429//CYTOSOL AMINOPEPTIDASE (EC 3.4.11.1) (LEUCINE AMINOPEPTIDASE) (LAP) (LEU-  
 CYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (EC 3.4.11.5) (PROLYL AMINOPEPTIDASE).//1.1e-  
 99:21:86//BOS TAURUS (BOVINE).//P00727  
 F-HEMBB1001436//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/3.4e-30:57:78//HOMO SAPIENS (HUMAN).//  
 25 P39195  
 F-HEMBB1001443//[PYRUVATE DEHYDROGENASE (LIPOAMIDE)]-PHOSPHATASE PRECURSOR (PDP) (EC  
 3.1.3.43) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SUBUNIT (PDPC)).//2.5e-79:155:97//  
 BOS TAURUS (BOVINE).//P35816  
 F-HEMBB1001449  
 30 F-HEMBB1001454//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAG-  
 MENT).//1.1e-05:196:31//HOMO SAPIENS (HUMAN).//P10161  
 F-HEMBB1001458//24 KD ANTIGEN (FRAGMENT).//0.94:18:50//PLASMODIUM CHABAUDI.//P14592  
 F-HEMBB1001463  
 F-HEMBB1001464//PPF2L ANTIGEN (FRAGMENT).//1.0:45:28//PLASMODIUM FALCIPARUM (ISOLATE PALO  
 35 ALTO / UGANDA).//P07765  
 F-HEMBB1001482//GASTRULA ZINC FINGER PROTEIN XLGCF16.1 (FRAGMENT).//4.2e-10:37:43//XENO-  
 PUS LAEVIS (AFRICAN CLAWED FROG).//P18712 F-HEMBB1001500  
 F-HEMBB1001521//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.4e-39:59:72//HOMO SAPIENS (HUMAN).//  
 P39188  
 40 F-HEMBB1001527//HOMEBOX PROTEIN HOX-B5 (XLHBOX-4) (XHBOX-1B) (FRAGMENT).//0.21:131:25//  
 XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P09019  
 F-HEMBB1001531//GENE 32 PROTEIN (GP32).//0.88:95:30//MYCOBACTERIOPHAGE L5.//Q05241  
 F-HEMBB1001535//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:31:38//LUMBRICUS TERRESTRIS  
 (COMMON EARTHWORM).//Q34942  
 45 F-HEMBB1001536  
 F-HEMBB1001537//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/0.0063:52:50//HOMO SAPIENS (HU-  
 MAN).//P39191  
 F-HEMBB1001555//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.9e-23:69:63//HOMO SAPIENS (HUMAN).//  
 P39188  
 50 F-HEMBB1001562//RABPHILIN-3A.//0.087:147:27//RATTUS NORVEGICUS (RAT).//P47709  
 F-HEMBB1001564//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.9e-27:107:54//HOMO SAPIENS (HU-  
 MAN).//P08547  
 F-HEMBB1001565//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.9e-12:51:54//HOMO SAPIENS (HU-  
 MAN).//P39194  
 55 F-HEMBB1001585  
 F-HEMBB1001586  
 F-HEMBB1001588//HYPOTHETICAL 12.3 KD PROTEIN IN GAP1-NAP1 INTERGENIC REGION.//0.0031:31:48//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36140

F-HEMBB1001603  
 F-HEMBB1001618//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE  
 (EC 2.7.7.49); ENDONUCLEASE]//0.00076:47:44//MUS MUSCULUS (MOUSE)//P11369  
 5 F-HEMBB1001619//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//1.0:52:32//HOMO SAPIENS  
 (HUMAN)//P22531  
 F-HEMBB1001630  
 F-HEMBB1001635//METALLOTHIONEIN-LIKE PROTEIN TYPE 2 A//1.0:27:44//LYCOPERSICON ESCULEN-  
 TUM (TOMATO)//Q40157  
 10 F-HEMBB1001637//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.0042:26:73//HOMO SAPIENS (HUMAN)//  
 P39188  
 F-HEMBB1001641  
 F-HEMBB1001653//SURVIVAL MOTOR NEURON PROTEIN 1//0.51:36:47//CANIS FAMILIARIS (DOG)//  
 Q02771  
 15 F-HEMBB1001665//HOMEBOX PROTEIN ENGRAILED-1 (HU-EN-1)//0.0030:135:34//HOMO SAPIENS (HU-  
 MAN)//Q05925  
 F-HEMBB1001668//PROBABLE 60S RIBOSOMAL PROTEIN L39//0.99:25:44//CAENORHABDITIS ELEGANS//  
 P52814  
 F-HEMBB1001673//HYPOTHETICAL 46.1 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION//0.0054:128:  
 34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38823.  
 20 F-HEMBB1001684//SUPPRESSOR PROTEIN SRP40//0.56:81:34//SACCHAROMYCES CEREVISIAE (BAK-  
 ER'S YEAST)//P32583  
 F-HEMBB1001685//CYTOCHROME C OXIDASE POLYPEPTIDE VIII-HEART PRECURSOR (EC 1.9.3.1) (VIIIb)  
 (IX)//1.0:21:47//BOS TAURUS (BOVINE)//P10175  
 F-HEMBB1001695//MYOSIN IC HEAVY CHAIN//8.9e-05:86:40//ACANTHAMOEBA CASTELLANII (AMOEBA)//  
 25 P10569  
 F-HEMBB1001704//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/9.0e-08:35:71//HOMO SAPIENS (HUMAN)//  
 P39195  
 F-HEMBB1001706//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUA-  
 MOUS CELL MARKER) (SPRP)//0.91:39:41//SUS SCROFA (PIG)//P35323  
 30 F-HEMBB1001707//FERREDOXIN-LIKE PROTEIN IN NIF REGION//1.0:43:23//BRADYRHIZOBIUM JAPONI-  
 CUM//P27394  
 F-HEMBB1001717//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3) (FRAGMENT)//1.0:71:25//  
 LEMUR CATTA (RING-TAILED LEMUR)//Q34878  
 35 F-HEMBB1001735//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.0e-35:97:74//HOMO SAPIENS (HU-  
 MAN)//P39194  
 F-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 BETA SUBUNIT (EIF-3 BETA) (EIF3  
 P116) (EIF3 P116)//0.00069:180:28//HOMO SAPIENS (HUMAN)//P55884  
 F-HEMBB1001747  
 40 F-HEMBB1001749//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.8e-43:75:70//HOMO SAPIENS (HUMAN)//  
 P39195  
 F-HEMBB1001753//PROTEIN Q300//0.00091:16:81//MUS MUSCULUS (MOUSE)//Q02722  
 F-HEMBB1001756//CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 2 (XE-P9)//0.94:35:42//XENO-  
 PUS LAEVIS (AFRICAN CLAWED FROG)//Q91879  
 45 F-HEMBB1001760  
 F-HEMBB1001762//GENE 35 PROTEIN (GP35)//0.76:21:47//MYCOBACTERIOPHAGE L5//Q05245  
 F-HEMBB1001785  
 F-HEMBB1001797//CHLOROPLAST 50S RIBOSOMAL PROTEIN L35//0.99:41:31//PORPHYRA PURPUREA//  
 P51270  
 50 F-HEMBB1001802  
 F-HEMBB1001812//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.2e-39:54:77//HOMO SAPIENS (HUMAN)//  
 P39193  
 F-HEMBB1001816//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.1e-19:97:57//HOMO SAPIENS (HU-  
 MAN)//P39194  
 F-HEMBB1001831//HYPOTHETICAL 45.6 KD PROTEIN IN COX5A-ALG11 INTERGENIC REGION//0.62:204:  
 23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53951  
 55 F-HEMBB1001834//GLYCINE-RICH RNA-BINDING PROTEIN 1 (FRAGMENT)//0.0014:40:45//SORGHUM VUL-  
 GARE (SORGHUM)//Q99069  
 F-HEMBB1001836//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/7.1e-14:85:61//HOMO SAPIENS (HU-



MAN).//P39191  
 F-HEMBB1001839//PROBABLE E4 PROTEIN.//0.61:49:34//HUMAN PAPILLOMAVIRUS TYPE 6C.//P20969  
 F-HEMBB1001850  
 5 F-HEMBB1001863//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.7e-30:57:68//HOMO SAPIENS (HUMAN).//P39194  
 F-HEMBB1001867  
 F-HEMBB1001868//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.00036:47:53//NICOTIANA TABACUM (COMMON TOBACCO).//P13983  
 10 F-HEMBB1001869//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.0e-11:95:45//HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBB1001872//HYPOTHETICAL 8.2 KD PROTEIN IN LEF8-FP INTERGENIC REGION.//1.0:34:38//AUTOGRAPH CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41459  
 F-HEMBB1001874  
 F-HEMBB1001875  
 15 F-HEMBB1001880  
 F-HEMBB1001899//GENE 11 PROTEIN.//1.0:45:31//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15902  
 F-HEMBB1001905//HYPOTHETICAL 81.7 KD PROTEIN IN MOL1-NAT2 INTERGENIC REGION.//8.8e-54:216:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48234  
 F-HEMBB1001906  
 20 F-HEMBB1001908//MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN.//6.3e-51:138:80//HOMO SAPIENS (HUMAN).//Q92794  
 F-HEMBB1001910  
 F-HEMBB1001911  
 F-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E).//2.3e-27:71:70//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24574  
 25 F-HEMBB1001921//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.8e-13:75:53//HOMO SAPIENS (HUMAN).//P08547  
 F-HEMBB1001922  
 30 F-HEMBB1001925//EPITHELIAL MEMBRANE PROTEIN-1 (EMP-1) (TUMOR-ASSOCIATED MEMBRANE PROTEIN).//1.0:55:30//MUS MUSCULUS (MOUSE).//P47801  
 F-HEMBB1001930//HYPOTHETICAL 9.6 KD PROTEIN K10D2.7 IN CHROMOSOME III.//0.43:49:26//CAENORHABDITIS ELEGANS.//Q09412  
 F-HEMBB1001944//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//5.1e-34:63:85//HOMO SAPIENS (HUMAN).//P39189  
 35 F-HEMBB1001945//NONSPECIFIC LIPID-TRANSFER PROTEIN (LTP) (PHOSPHOLIPID TRANSFER PROTEIN) (PLTP).//0.28:45:40//AMARANTHUS CAUDATUS (LOVE-LIES-BLEEDING) (INCA-WHEAT).//P80450  
 F-HEMBB1001947//PROTEIN UL24.//0.48:42:47//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).//P10208  
 40 F-HEMBB1001950//HYPOTHETICAL 42.6 KD PROTEIN IN GSHB-ANSB INTERGENIC REGION (O378).//1.6e-24:162:36//ESCHERICHIA COLI.//P52062  
 F-HEMBB1001952  
 F-HEMBB1001953  
 F-HEMBB1001957//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.7e-11:51:60//HOMO SAPIENS (HUMAN).//P39188  
 45 F-HEMBB1001962//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.6e-24:163:42//HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBB1001967//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.1e-35:55:80//HOMO SAPIENS (HUMAN).//P39189  
 F-HEMBB1001973//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.1e-37:108:75//HOMO SAPIENS (HUMAN).//P39192  
 50 F-HEMBB1001983//LYSIS PROTEIN (E PROTEIN) (GPE).//0.84:45:37//BACTERIOPHAGE ALPHA-3.//P31280  
 F-HEMBB1001988  
 F-HEMBB1001990  
 F-HEMBB1001996//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-14:98:40//HOMO SAPIENS (HUMAN).//P08547  
 55 F-HEMBB1001997//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.1e-19:38:73//HOMO SAPIENS (HUMAN).//P39188  
 F-HEMBB1002002//CYTOCHROME C BIOGENESIS PROTEIN CCSA.//1.0:150:25//PORPHYRA PURPUREA.//

- P51369  
F-HEMBB1002005//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/7.6e-12:94.40//HOMO SAPIENS (HUMAN).//P39195
- 5 F-HEMBB1002009  
F-HEMBB1002015//HYPOTHETICAL 7.7 KD PROTEIN IN MRR-TSR INTERGENIC REGION (F67).//1.0:17:47//ESCHERICHIA COLI.//P39395  
F-HEMBB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYP1VC1).//2.4e-50:139.55//BLABERUS DISCOIDALIS (TROPICAL COCKROACH).//P29981
- 10 F-HEMBB1002043//HYPOTHETICAL 9.5 KD PROTEIN IN DHFR 3'REGION (ORF3).//0.052:40.42//HERPESVIRUS SAIMIRI (SUBGROUP C / STRAIN 488).//P22577  
F-HEMBB1002044//CELLULOSE COMPLEMENTING PROTEIN.//0.45:87:33//ACETOBACTER XYLINUM (ACETOBACTER PASTEURIANUS).//P37697  
F-HEMBB1002045//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.78:18:55//HOMO SAPIENS (HUMAN).//P03928
- 15 F-HEMBB1002049  
F-HEMBB1002050//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT).//1.0e-06:188:27//HOMO SAPIENS (HUMAN).//P02812  
F-HEMBB1002068//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4).//0.0023:56.44//GALLUS GALLUS (CHICKEN).//P17277
- 20 F-HEMBB1002069//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.0074:134:33//NICOTIANA TABACUM (COMMON TOBACCO).//P13983  
F-HEMBB1002092//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEMBRANE PROTEIN GP70; TRANSMEMBRANE PROTEIN P20E].//2.4e-07:75:40//BABOON ENDOGENOUS VIRUS (STRAIN M7).//P10269
- 25 F-HEMBB1002094//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/1.9e-24:63:82//HOMO SAPIENS (HUMAN).//P39191  
F-HEMBB1002115//EC PROTEIN HOMOLOG (ZINC-METALLOTHIONEIN CLASS II).//0.94:26:42//ZEA MAYS (MAIZE).//P43401  
F-HEMBB1002134//ZINC-FINGER PROTEIN NEURO-D4.//4.6e-57:176:67//RATTUS NORVEGICUS (RAT).//P56163
- 30 F-HEMBB1002139//CHLOROPLAST 50S RIBOSOMAL PROTEIN L35.//1.0:17:52//PORPHYRA PURPUREA.//P51270  
F-HEMBB1002142//EARLY NODULIN 20 PRECURSOR (N-20).//0.087:52:36//MEDICAGO TRUNCATULA (BARREL MEDIC).//P93329
- 35 F-HEMBB1002152//HYPOTHETICAL 12.3 KD PROTEIN IN RPL3-RPL33 INTERGENIC REGION (ORF102).//5.8e-05:61:37//CYANOPHORA PARADOXA.//P15811  
F-HEMBB1002189//HYPOTHETICAL PROTEIN UL125.//1.0:77:32//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16835  
F-HEMBB1002190
- 40 F-HEMBB1002193//TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN KINASE DTK).//1.2e-27:59:100//HOMO SAPIENS (HUMAN).//Q06418  
F-HEMBB1002217//ZINC FINGER PROTEIN 184 (FRAGMENT).//6.6e-22:106:50//HOMO SAPIENS (HUMAN).//Q99676
- 45 F-HEMBB1002218//PROTEIN Q300.//0.85:19:52//MUS MUSCULUS (MOUSE).//Q02722  
F-HEMBB1002232//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/9.6e-21:56:71//HOMO SAPIENS (HUMAN).//P39195  
F-HEMBB1002247  
F-HEMBB1002249//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.2e-29:93:69//HOMO SAPIENS (HUMAN).//P39194
- 50 F-HEMBB002254//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.0e-29:101:67//HOMO SAPIENS (HUMAN).//P39194  
F-HEMBB1002255//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).//1.0:73:28//PARAMECIUM TETRAURELIA.//P15579
- 55 F-HEMBB1002266//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//0.0079:151:26//PLASMODIUM FALCIPARUM (ISOLATE FC27 / PAPUA NEW GUINEA).//P13816  
F-HEMBB1002280//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.2e-15:182:36//NYCTICEBUS COUCANG (SLOW LORIS).//P08548

F-HEMBB1002300  
 F-HEMBB1002306//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.00011:26:84//HOMO SAPIENS (HUMAN).//P39195  
 5 F-HEMBB1002327//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/4.1e-11:41:85//HOMO SAPIENS (HUMAN).//P39189  
 F-HEMBB1002329//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION.//9.9e-17:232:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032  
 F-HEMBB1002340  
 10 F-HEMBB1002342//HYPOTHETICAL 32.5 KD PROTEIN IN MSH6-BMH2 INTERGENIC REGION.//3.6e-40:102:57//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03835  
 F-HEMBB1002358//THYMIDYLATE KINASE (EC 2.7.4.9) (DTMP KINASE).//6.1e-30:63:96//HOMO SAPIENS (HUMAN).//P23919  
 F-HEMBB1002359//HYPOTHETICAL 7.1 KD PROTEIN C6G9.01C IN CHROMOSOME I.//0.97:28:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q92346  
 15 F-HEMBB1002364//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT).//0.47:119:25//HOMO SAPIENS (HUMAN).//P12895  
 F-HEMBB1002371//HYPOTHETICAL 15.5 KD PROTEIN C2F7.12 IN CHROMOSOME I PRECURSOR.//3.0e-05:111:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09703  
 F-HEMBB1002381//PUTATIVE CUTICLE COLLAGEN C09G5.4.//0.34:105:34//CAENORHABDITIS ELEGANS.//Q09455  
 20 F-HEMBB1002383//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.049:103:32//AQUIFEX AEOLICUS.//O66566  
 F-HEMBB1002387//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (HEAT SHOCK PROTEIN 11).//0.18:75:28//RICKETTSIA TSUTSUGAMUSHI.//P16626  
 25 F-HEMBB1002409//HIGH MOBILITY GROUP PROTEIN HMG-Y.//0.014:61:36//MUS MUSCULUS (MOUSE).//P17095  
 F-HEMBB1002415  
 F-HEMBB1002425//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.8e-18:55:70//HOMO SAPIENS (HUMAN).//P39194  
 30 F-HEMBB1002442//LIN-10 PROTEIN.//5.1e-15:121:31//CAENORHABDITIS ELEGANS.//P34692  
 F-HEMBB1002453//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.2e-32:54:75//HOMO SAPIENS (HUMAN).//P39189  
 F-HEMBB1002457//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.5e-07:31:64//HOMO SAPIENS (HUMAN).//P39188  
 35 F-HEMBB1002458//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.92:28:53//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01642  
 F-HEMBB1002477//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//0.0066:198:27//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414  
 40 F-HEMBB1002489//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B5).//0.030:182:28//HOMO SAPIENS (HUMAN).//Q15427  
 F-HEMBB1002492  
 F-HEMBB1002495//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/2.1e-08:41:75//HOMO SAPIENS (HUMAN).//P39192  
 45 F-HEMBB1002502//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT).//0.00030:31:77//HOMO SAPIENS (HUMAN).//P12895  
 F-HEMBB1002509  
 F-HEMBB1002510  
 F-HEMBB1002520//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.8e-36:162:50//NYCTICEBUS COUCANG (SLOW LORIS).//P08548  
 50 F-HEMBB1002522//7 KD PROTEIN (ORF 4).//0.77:32:40//CHRYSANTHEMUM VIRUS B (CVB).//P37990  
 F-HEMBB1002531  
 F-HEMBB1002534//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/3.1e-36:80:73//HOMO SAPIENS (HUMAN).//P39195  
 F-HEMBB1002545  
 55 F-HEMBB1002550//HOMEODOMAIN PROTEIN HOX-D11 (HOX-4.6) (HOX-5.5).//3.8e-05:83:34//MUS MUSCULUS (MOUSE).//P23813  
 F-HEMBB1002556  
 F-HEMBB1002579//SPLICING FACTOR U2AF 35 KD SUBUNIT (U2 AUXILIARY FACTOR 35 KD SUBUNIT) (U2

SNRNP AUXILIARY FACTOR SMALL SUBUNIT) (FRAGMENT) //5.0e-06:27:77//SUS SCROFA (PIG) //Q29350  
 F-HEMBB1002582//PROTEINASE INHIBITOR //1.0:27:40//SOLANUM MELONGENA (EGGPLANT) (AUBER-  
 GINE) //P01078  
 5 F-HEMBB1002590//HYPOTHETICAL PROTEIN IN MMSB 3'REGION (ORF1) (FRAGMENT) //1.9e-20:90:54//  
 PSEUDOMONAS AERUGINOSA //P28812  
 F-HEMBB1002596  
 F-HEMBB1002600//NOVEL ANTIGEN 2 (NAG-2) //1.9e-60:187:59//HOMO SAPIENS (HUMAN) //O14817  
 F-HEMBB1002601//M PROTEIN, SEROTYPE 6 PRECURSOR //1.0:71:35//STREPTOCOCCUS PYOGENES //  
 P08089  
 10 F-HEMBB1002603  
 F-HEMBB1002607//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-  
 MENT) //0.0032:142:33//HOMO SAPIENS (HUMAN) //P10162  
 F-HEMBB1002610//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //2.0e-11:79:49//HOMO SAPIENS (HU-  
 MAN) //P08547  
 15 F-HEMBB1002613//ALU SUBFAMILY J WARNING ENTRY //3.9e-08:41:60//HOMO SAPIENS (HUMAN) //  
 P39188  
 F-HEMBB1002614//HYPOTHETICAL 9.5 KD PROTEIN //1.0:40:35//VACCINIA VIRUS (STRAIN COPENHA-  
 GEN) //P20553  
 F-HEMBB1002617//INSECT TOXIN 1 (BOT IT1) //1.0:44:29//BUTHUS OCCITANUS TUNETANUS (COMMON  
 20 EUROPEAN SCORPION) //P55902  
 F-HEMBB1002623//HYPOTHETICAL 9.7 KD PROTEIN (ORF88) (PUTATIVE DNA-BINDING PROTEIN) //0.42:  
 31:54//BACTERIOPHAGE P4 //P12552  
 F-HEMBB1002635//STRESS-ACTIVATED PROTEIN KINASE JNK3 (EC 2.7.1.-) (C-JUN N-TERMINAL KINASE  
 3) (MAP KINASE P49 3F12) //6.2e-17:44:95//HOMO SAPIENS (HUMAN) //P53779  
 25 F-HEMBB1002664//SMALL NUCLEAR RIBONUCLEOPROTEIN ASSOCIATED PROTEIN B (SM-B) (SNRNP-B)  
 (SM11) (FRAGMENT) //1.0:57:36//RATTUS NORVEGICUS (RAT) //P17136  
 F-HEMBB1002677//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //1.9e-06:194:34//NYCTICEBUS COU-  
 CANG (SLOW LORIS) //P08548  
 F-HEMBB1002683//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT) //0.96:56:  
 35//LEMUR CATTI (RING-TAILED LEMUR) //Q34879  
 30 F-HEMBB1002684//SILLUCIN //1.0:16:50//RHIZOMUCOR PUSILLUS //P02885  
 F-HEMBB1002686  
 F-HEMBB1002692  
 F-HEMBB1002697//HELIX-DESTABILIZING PROTEIN (SINGLE-STRANDED DNA BINDING PROTEIN) (GPV) //  
 0.57:36:38//BACTERIOPHAGE FD, BACTERIOPHAGE F1, AND BACTERIOPHAGE M13 //P03669  
 35 F-HEMBB1002699  
 F-HEMBB1002702  
 F-HEMBB1002705//HYPOTHETICAL 34.8 KD PROTEIN C4H3.04C IN CHROMOSOME I //3.6e-40:180:37//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //Q10212  
 40 F-HEMBB1002712  
 F-MAMMA1000009//ALU SUBFAMILY SB WARNING ENTRY //1.2e-32:95:75//HOMO SAPIENS (HU-  
 MAN) //P39189  
 F-MAMMA1000019  
 F-MAMMA1000020//DIMETHYLANILINE MONOOXYGENASE [N-OXIDE FORMING] 5 (EC 1.14.13.8) (HEPATIC  
 45 FLAVIN-CONTAINING MONOOXYGENASE 5) (FMO 5) (DIMETHYLANILINE OXIDASE 5) //5.2e-12:24:100//HO-  
 MO SAPIENS (HUMAN) //P49326  
 F-MAMMA1000025//BETA-2-MICROGLOBULIN PRECURSOR //1.0:73:26//BRACHYDANIO RERIO (ZE-  
 BRAFISH) (ZEBRA DANIO) //Q04475  
 F-MAMMA1000043//HYPOTHETICAL PXBL-1 PROTEIN (FRAGMENT) //0.057:130:31//BOVINE LEUKEMIA VI-  
 50 RUS (JAPANESE ISOLATE BLV-1) (BLV) //P03412  
 F-MAMMA1000045  
 F-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)] //7.5e-44:138:55//MUS MUSCULUS  
 (MOUSE) //P47226  
 F-MAMMA1000057//ALU SUBFAMILY SQ WARNING ENTRY //1.2e-39:92:69//HOMO SAPIENS (HU-  
 55 MAN) //P39194  
 F-MAMMA1000069//HYPOTHETICAL 29.3 KD PROTEIN (ORF92) //0.0044:96:34//ORGYIA PSEUDOTSUGATA  
 MULTICAPSID POLYHEDROSIS VIRUS (OPMPNV) //O10341  
 F-MAMMA1000084//ALU SUBFAMILY SX WARNING ENTRY //5.4e-28:94:73//HOMO SAPIENS (HU-

- MAN).//P39195  
F-MAMMA1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.16) (CYSTEINE--TRNA LIGASE) (CYRSR).//6.6e-38:90:51//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09860
- 5 F-MAMMA1000092//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/6.4e-30:43:86//HOMO SAPIENS (HUMAN).//P39192  
F-MAMMA1000103//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.038:17:52//HOMO SAPIENS (HUMAN).//P22531  
F-MAMMA1000117//50S RIBOSOMAL PROTEIN L24E (HL21/HL22).//0.90:25:48//HALOARcula MARISMORTUI (HALOBACTERIUM MARISMORTUI).//P14116
- 10 F-MAMMA1000129//HYPOTHETICAL BHLF1 PROTEIN.//0.0016:75:40//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181  
F-MAMMA1000133  
F-MAMMA1000134//HYPOTHETICAL PROTEIN MJ0647.//1.0:41:41//METHANOCOCCUS JANNASCHII.//Q58063
- 15 F-MAMMA1000139//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-3 SUBUNIT.//0.99:69:28//BOS TAURUS (BOVINE), AND MUS MUSCULUS (MOUSE).//P29798  
F-MAMMA1000143//CALPAIN INHIBITOR (CALPASTATIN) (FRAGMENT).//0.023:11:27//MUS MUSCULUS (MOUSE).//P51125  
F-MAMMA1000155//PUTATIVE CUTICLE COLLAGEN C09G5.5.//0.018:125:34//CAENORHABDITIS ELEGANS.//Q09456
- 20 F-MAMMA1000163//MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR (PERIPLASMIC MERCURY ION BINDING PROTEIN) (MERCURY SCAVENGER PROTEIN).//0.11:88:25//SHEWANELLA PUTREFACIENS (PSEUDOMONAS PUTREFACIENS).//Q54463  
F-MAMMA1000171
- 25 F-MAMMA1000173//DREBRIN E.//7.6e-41:197:43//HOMO SAPIENS (HUMAN).//Q16643  
F-MAMMA1000175//GAMMA-THIONIN HOMOLOG PPT PRECURSOR.//0.92:39:38//PETUNIA INTEGRIFOLIA (VIOLET-FLOWERED PETUNIA) (PETUNIA INFLATA).//Q40901  
F-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.4e-106:249:61//HOMO SAPIENS (HUMAN).//P51523
- 30 F-MAMMA1000198//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.0014:35:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645  
F-MAMMA1000221  
F-MAMMA1000227//6.8 KD MITOCHONDRIAL PROTEOLIPID.//1.0:30:40//MUS MUSCULUS (MOUSE).//P56379
- 35 F-MAMMA1000241//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X (PSI-K).//1.0:40:37//PORPHYRA PURPUREA.//P51370  
F-MAMMA1000251//HYPOTHETICAL 6.8 KD PROTEIN IN FIC-PPIA INTERGENIC REGION.//0.99:29:48//SALMONELLA TYPHIMURIUM.//P37771
- 40 F-MAMMA1000254//HYPOTHETICAL 6.0 KD PROTEIN IN TH12 5'REGION.//1.0:20:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53820  
F-MAMMA1000257//HYPOTHETICAL 50.0 KD PROTEIN IN HEML 3'REGION (ORF2).//0.22:50:44//PSEUDOMONAS AERUGINOSA.//Q51470  
F-MAMMA1000284//GASTRIN-RELEASING PEPTIDE RECEPTOR (GRP-R) (GRP-PREFERRING BOMBESIN RECEPTOR).//0.80:39:43//HOMO SAPIENS (HUMAN).//P30550
- 45 F-MAMMA1000266  
F-MAMMA1000270//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/9.5e-42:95:84//HOMO SAPIENS (HUMAN).//P39189  
F-MAMMA1000277//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].//0.0062:90:34//MUS MUSCULUS (MOUSE).//P28461
- 50 F-MAMMA1000278//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.00096:59:33//HORDEUM VULGARE (BARLEY).//P17991  
F-MAMMA1000279//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.4e-17:56:76//HOMO SAPIENS (HUMAN).//P39195
- 55 F-MAMMA1000284//ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2).//0.017:146:30//MUS MUSCULUS (MOUSE).//Q61324  
F-MAMMA1000287//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.5e-32:84:58//HOMO SAPIENS (HUMAN).//P39189  
F-MAMMA1000302//C-HORDEIN (CLONE PC-919) (FRAGMENT).//1.0:42:33//HORDEUM VULGARE (BAR-

- LEY).//P17992  
 F-MAMMA1000307//PROBABLE E4 PROTEIN.//0.21:71:30//RHESUS PAPILLOMAVIRUS TYPE 1 (RHPV 1).//P24832
- 5 F-MAMMA1000309//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN).//0.0026:141:36//HOMO SAPIENS (HUMAN).//P27658  
 F-MAMMA1000312  
 F-MAMMA1000313//DNA REPAIR PROTEIN RAD51 HOMOLOG (25 KD PROTEIN) (FRAGMENT).//0.76:52:32//STAPHYLOCOCCUS AUREUS.//P31337  
 F-MAMMA1000331
- 10 F-MAMMA1000339//50S RIBOSOMAL PROTEIN L29P.//0.78:32:46//METHANOBACTERIUM THERMAUTOTROPHICUM.//O26117  
 F-MAMMA1000340//HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION.//1.0:29:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36039  
 F-MAMMA1000348//ALU SUBFAMILY J WARNING ENTRY !!!/7.5e-09:63:60//HOMO SAPIENS (HUMAN).//P39188
- 15 F-MAMMA1000356//ALU SUBFAMILY J WARNING ENTRY !!!/3.3e-05:42:52//HOMO SAPIENS (HUMAN).//P39188  
 F-MAMMA1000360  
 F-MAMMA1000361//ALU SUBFAMILY SB WARNING ENTRY !!!/4.4e-33:84:72//HOMO SAPIENS (HUMAN).//P39189
- 20 F-MAMMA1000372//ALU SUBFAMILY SP WARNING ENTRY !!!/6.6e-21:53:71//HOMO SAPIENS (HUMAN).//P39193  
 F-MAMMA1000385  
 F-MAMMA1000388//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//0.40:72:36//HOMO SAPIENS (HUMAN).//P43489  
 F-MAMMA1000395//RABPHILIN-3A (FRAGMENT).//0.032:125:25//MUS MUSCULUS (MOUSE).//P47708  
 F-MAMMA1000402//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.1e-28:266:40//HOMO SAPIENS (HUMAN).//P08547
- 30 F-MAMMA1000410//NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-B SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-13KD-B) (CI-13KD-B) (B13).//5.9e-06:32:68//HOMO SAPIENS (HUMAN).//Q16718  
 F-MAMMA1000413//RETROVIRUS-RELATED POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE).//6.7e-05:93:31//MUS MUSCULUS (MOUSE).//P11369  
 F-MAMMA1000414
- 35 F-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//4.1e-28:119:53//CAENORHABDITIS ELEGANS.//Q09232  
 F-MAMMA1000421//ALU SUBFAMILY SQ WARNING ENTRY !!!/2.7e-23:68:76//HOMO SAPIENS (HUMAN).//P39194  
 F-MAMMA1000422//METALLOTHIONEIN (MT).//0.037:42:42//GADUS MORHUA (ATLANTIC COD).//P51902  
 F-MAMMA1000423
- 40 F-MAMMA1000424//ALU SUBFAMILY SB WARNING ENTRY !!!/0.048:23:73//HOMO SAPIENS (HUMAN).//P39189  
 F-MAMMA1000429//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5.//2.7e-05:110:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q09231  
 F-MAMMA1000431//ALU SUBFAMILY SQ WARNING ENTRY !!!/9.4e-15:85:58//HOMO SAPIENS (HUMAN).//P39194
- 45 F-MAMMA1000444//ALU SUBFAMILY SQ WARNING ENTRY !!!/4.3e-25:65:76//HOMO SAPIENS (HUMAN).//P39194  
 F-MAMMA1000446//ZYXIN.//0.79:155:29//GALLUS GALLUS (CHICKEN).//Q04584  
 F-MAMMA1000458//HYPOTHETICAL 37.7 KD PROTEIN C18B11.06 IN CHROMOSOME I.//0.0048:46:43//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09713
- 50 F-MAMMA1000468//PERIOD CLOCK PROTEIN (FRAGMENT).//0.50:20:55//DROSOPHILA ROBUSTA (FRUIT FLY).//Q03296  
 F-MAMMA1000472//ALU SUBFAMILY J WARNING ENTRY !!!/1.5e-17:106:55//HOMO SAPIENS (HUMAN).//P39188
- 55 F-MAMMA1000478//ALU SUBFAMILY SX WARNING ENTRY !!!/3.9e-35:80:68//HOMO SAPIENS (HUMAN).//P39195  
 F-MAMMA1000483//ALU SUBFAMILY SP WARNING ENTRY !!!/2.8e-24:74:77//HOMO SAPIENS (HUMAN).//P39193

- F-MAMMA1000490//TYROSINE-PROTEIN KINASE TXK (EC 2.7.1.112) (PTK-RL-18) (RESTING LYMPHOCYTE KINASE).//0.43:21:57//MUS MUSCULUS (MOUSE).//P42682
- F-MAMMA1000500//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.61:33:54//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z2/CDC-Z34 ISOLATE) (HIV-1).//P12506
- 5 F-MAMMA1000501//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.1e-32:43:83//HOMO SAPIENS (HUMAN).//P39194
- F-MAMMA1000516
- F-MAMMA1000522//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.0015:113:32//HOMO SAPIENS (HUMAN).//P08547
- 10 F-MAMMA1000524//HYPOTHETICAL HOST RANGE 8.5 KD PROTEIN.//1.0:63:31//VACCINIA VIRUS (STRAIN WR).//P17359
- F-MAMMA1000559//METALLOTHIONEIN-I (MT-I) (MT-IB/MT-IA).//0.31:16:50//CALLINECTES SAPIDUS (BLUE CRAB).//P55949
- F-MAMMA1000565//FERREDOXIN-TYPE PROTEIN NAF.//0.98:37:35//ESCHERICHIA COLI.//P33939
- 15 F-MAMMA1000567//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.5e-37:95:76//HOMO SAPIENS (HUMAN).//P39195
- F-MAMMA1000576//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/4.1e-07:34:64//HOMO SAPIENS (HUMAN).//P39191
- F-MAMMA1000583
- 20 F-MAMMA1000585//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.5e-28:89:75//HOMO SAPIENS (HUMAN).//P39194
- F-MAMMA1000594//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.8e-24:38:71//HOMO SAPIENS (HUMAN).//P39195
- F-MAMMA1000597//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.1e-25:74:77//HOMO SAPIENS (HUMAN).//P39195
- 25 F-MAMMA1000605//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.1e-18:83:50//HOMO SAPIENS (HUMAN).//P39195
- F-MAMMA1000612//HYPOTHETICAL 34.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION.//4.0e-42:166:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41318
- 30 F-MAMMA1000616
- F-MAMMA1000621
- F-MAMMA1000623//METALLOTHIONEIN-IK (MT-1K).//0.0045:25:48//HOMO SAPIENS (HUMAN).//P80296
- F-MAMMA1000625//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.00078:79:35//MUS MUSCULUS (MOUSE).//P05143
- 35 F-MAMMA1000643//HYPOTHETICAL 9.3 KD PROTEIN.//1.0:25:28//MAGUARI VIRUS.//P16607
- F-MAMMA1000664
- F-MAMMA1000669//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.2e-05:186:30//HOMO SAPIENS (HUMAN).//P08547
- 40 F-MAMMA1000670//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.6e-06:195:30//MUS MUSCULUS (MOUSE).//P05143
- F-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.-).//3.8e-28:184:35//AEDES AEGYPTI (YELLOW FEVER MOSQUITO).//P42660
- F-MAMMA1000684//DNA-BINDING PROTEIN (VMW21).//1.1e-07:55:56//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).//P04487
- 45 F-MAMMA1000696//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.2e-31:97:74//HOMO SAPIENS (HUMAN).//P39194
- F-MAMMA1000707//METALLOTHIONEIN-II (MT-II) (MT-IB/MT-IA).//0.31:19:42//CALLINECTES SAPIDUS (BLUE CRAB).//P55950
- F-MAMMA1000713//XYLULOSE KINASE (EC 2.7.1.17) (XYLULOKINASE).//1.6e-05:88:35//LACTOBACILLUS PENTOSUS.//P21939
- 50 F-MAMMA1000714//PROTEIN-LYSINE 6-OXIDASE PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE).//0.44:126:30//RATTUS NORVEGICUS (RAT).//P16636
- F-MAMMA1000718//METALLOTHIONEIN-II (MT-2E).//1.0:51:31//ORYZOLAGUS CUNICULUS (RABBIT).//P80292
- 55 F-MAMMA1000720//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/3.3e-28:60:71//HOMO SAPIENS (HUMAN).//P39193
- F-MAMMA1000723//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.7e-14:63:53//HOMO SAPIENS (HUMAN).//P08547

F-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2).//1.8e-43:258:43//HOMO SAPIENS (HUMAN).//O14647

F-MAMMA1000732//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/9.9e-12:76:55//HOMO SAPIENS (HUMAN).//P39188

5 F-MAMMA1000733

F-MAMMA1000734//NPL1 PROTEIN (SEC63 PROTEIN).//2.5e-18:181:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P14906

F-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//5.4e-52:196:58//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87115

10 F-MAMMA1000744//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!/6.3e-36:144:47//HOMO SAPIENS (HUMAN).//P39190

F-MAMMA1000746

F-MAMMA1000752

15 F-MAMMA1000760//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/6.6e-29:75:72//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1000761//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.6e-09:59:64//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1000775

F-MAMMA1000776//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/3.3e-35:99:74//HOMO SAPIENS (HUMAN).//P39193

20 F-MAMMA1000778//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.1e-19:65:70//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1000782

F-MAMMA1000798//HYPOTHETICAL PROTEIN ORF-1137.//0.015:59:37//MUS MUSCULUS (MOUSE).//P11260

25 F-MAMMA1000802//MYOSIN IC HEAVY CHAIN.//0.35:94:41//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569

F-MAMMA1000824//ACTIN 1.//0.046:60:31//ZEA MAYS (MAIZE).//P02582

F-MAMMA1000831//PROBABLE NI/FE-HYDROGENASE 1 B-TYPE CYTOCHROME SUBUNIT.//1.0:30:46//ESCHERICHIA COLI.//P19929

30 F-MAMMA1000839//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-28:80:58//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4).//1.5e-39:130:36//METHANOBACTERIUM THERMAUTOTROPHICUM.//O27540

35 F-MAMMA1000842//C-HORDEIN (CLONE PC-919) (FRAGMENT).//0.064:43:41//HORDEUM VULGARE (BARLEY).//P17992

F-MAMMA1000843

F-MAMMA1000845//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).//0.43:58:34//DROSOPHILA YAKUBA (FRUIT FLY).//P03895

40 F-MAMMA1000851//CUTICLE COLLAGEN 34.//0.019:107:29//CAENORHABDITIS ELEGANS.//P34687

F-MAMMA1000855//SPliceosome ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.00098:149:32//HOMO SAPIENS (HUMAN).//Q15428

F-MAMMA1000856//METALLOTHIONEIN (MT).//0.63:39:41//POTAMON POTAMIOS.//P55952

45 F-MAMMA1000859//GLYCOPROTEIN X PRECURSOR.//0.014:192:28//EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).//P28968

F-MAMMA1000862//DISINTEGRIN KISTRIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).//1.0:66:27//AGKISTRODON RHODOSTOMA (MALAYAN PIT VIPER) (CALLOSELASMA RHODOSTOMA).//P17494

F-MAMMA1000863//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.4e-16:41:68//HOMO SAPIENS (HUMAN).//P39188

50 F-MAMMA1000865//SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).//0.030:100:32//HOMO SAPIENS (HUMAN).//P81489

F-MAMMA1000867//APTOTOXIN IX (PARALYTIC PEPTIDE IX) (PP IX).//0.98:43:32//APTOSTICHUS SCHLINGERI (TRAP-DOOR SPIDER).//P49272

F-MAMMA1000875//PROLINE-RICH PEPTIDE P-B.//0.18:21:47//HOMO SAPIENS (HUMAN).//P02814

55 F-MAMMA1000876//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.5e-22:85:71//HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1000877//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.2e-38:62:74//HOMO SAPIENS (HUMAN).//P39188



- F-MAMMA1000880//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.49:79:32//BOS TAURUS (BOVINE).//P25508
- F-MAMMA1000883//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X.//0.87:15:60//CAENORHABDITIS ELEGANS.//Q11116
- 5 F-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR (ITI HEAVY CHAIN H4) (INTER-ALPHA-TRYPSIN INHIBITOR FAMILY HEAVY CHAIN-RELATED PROTEIN) (PLASMA KALLIKREIN SENSITIVE GLYCOPROTEIN 120) (PK-120).//5.3e-17:130:40//HOMO SAPIENS (HUMAN).//Q14624
- F-MAMMA1000905
- F-MAMMA1000906
- 10 F-MAMMA1000908//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//8.0e-17:70:62//HOMO SAPIENS (HUMAN).//P08547
- F-MAMMA1000914//HYPOTHETICAL 6.2 KD PROTEIN.//0.97:36:36//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19299
- F-MAMMA1000921
- 15 F-MAMMA1000931//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.6e-10:49:65//HOMO SAPIENS (HUMAN).//P39188
- F-MAMMA1000940//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L32.//0.42:22:54//RECLINOMONAS AMERICANA.//Q21281
- F-MAMMA1000941//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.3e-25:55:69//HOMO SAPIENS (HUMAN).//P39188
- 20 F-MAMMA1000942//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.3e-08:36:75//HOMO SAPIENS (HUMAN).//P39194
- F-MAMMA1000943
- F-MAMMA1000956//SMALL HISTIDINE-ALANINE-RICH PROTEIN PRECURSOR (SHARP) (ANTIGEN 57).//0.041:122:25//PLASMODIUM FALCIPARUM (ISOLATE FC27 / PAPUA NEW GUINEA).//P04930
- 25 F-MAMMA1000957//HEAT-STABLE ENTEROTOXIN A2 PRECURSOR (STA2).//0.024:37:37//ESCHERICHIA COLI.//Q47185
- F-MAMMA1000962//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/6.0e-39:61:78//HOMO SAPIENS (HUMAN).//P39189
- 30 F-MAMMA1000968//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/0.0054:29:72//HOMO SAPIENS (HUMAN).//P39194
- F-MAMMA1000975//CUTICLE COLLAGEN DPY-2 PRECURSOR.//1.0:93:30//CAENORHABDITIS ELEGANS.//P35799
- F-MAMMA1000979//PROLINE-RICH PEPTIDE P-B.//0.012:12:66//HOMO SAPIENS (HUMAN).//P02814
- 35 F-MAMMA1000987//HYPOTHETICAL PROTEIN LAMBDA-SP34.//1.0:47:40//MUS MUSCULUS (MOUSE).//P15973
- F-MAMMA1000996
- F-MAMMA1001003//PROBABLE E5 PROTEIN.//1.0:52:42//HUMAN PAPILLOMAVIRUS TYPE 33.//P06426
- 40 F-MAMMA1001008//PROGASTRINSIN PRECURSOR (EC 3.4.23.3) (PEPSINOGEN C) (FRAGMENT).//3.2e-14:131:35//MACACA FUSCATA FUSCATA (JAPANESE MACAQUE).//P03955
- F-MAMMA1001021//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.016:61:42//STREPTOMYCES FRADIAE.//P20186
- F-MAMMA1001024
- 45 F-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (LSH-R) (LUTEINIZING HORMONE RECEPTOR) (FRAGMENT).//2.4e-20:234:29//GALLUS GALLUS (CHICKEN).//Q90674
- F-MAMMA1001035//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.7e-15:52:78//HOMO SAPIENS (HUMAN).//P39193
- 50 F-MAMMA1001038//NEUROTOXIN II (TOXIN RP-II) (SODIUM CHANNEL TOXIN II).//0.53:25:48//RADIANTHUS PAUMOTENSIS (SEA ANEMONE) (HETERACTIS PAUMOTENSIS).//P01534
- F-MAMMA1001041//SPECTRIN BETA CHAIN, ERYTHROCYTE.//6.3e-18:112:43//MUS MUSCULUS (MOUSE).//P15508
- F-MAMMA1001050
- F-MAMMA1001059//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//1.3e-34:187:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09747
- 55 F-MAMMA1001067//PROTEIN Q300.//0.36:12:75//MUS MUSCULUS (MOUSE).//Q02722
- F-MAMMA1001073//HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 1 (HFH-1).//1.0:70:37//RATTUS NORVEGICUS (RAT).//Q63244

- F-MAMMA1001074//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.00067:163:32//HOMO SAPIENS (HUMAN).//P08547
- F-MAMMA1001075//RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1).//0.53:72:34//HOMO SAPIENS (HUMAN).//P29374
- 5 F-MAMMA1001078//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.0e-79:184:73//HOMO SAPIENS (HUMAN).//P08547
- F-MAMMA1001080//G HEAVY CHAIN PRECURSOR V-III REGION (VH26).//1.7e-27:82:71//HOMO SAPIENS (HUMAN).//P01764
- F-MAMMA1001082
- 10 F-MAMMA1001091//HYPOTHETICAL BHLF1 PROTEIN.//3.1e-05:198:32//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
- F-MAMMA1001092//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.1e-21:65:72//HOMO SAPIENS (HUMAN).//P08547
- 15 F-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN).//1.0e-18:68:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P51521
- F-MAMMA1001110//PROCOLLAGEN ALPHA 1(IV) CHAIN PRECURSOR.//0.080:108:37//MUS MUSCULUS (MOUSE).//P02463
- F-MAMMA1001126/////ALU SUBFAMILY SB WARNING ENTRY /////2.3e-07:66:45//HOMO SAPIENS (HUMAN).//P39189
- 20 F-MAMMA1001133//HYPOTHETICAL 13.2 KD PROTEIN IN RPS4A-BAT2 INTERGENIC REGION.//0.96:43:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47174
- F-MAMMA1001139//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.//5.4e-42:81:62//CAENORHABDITIS ELEGANS.//Q09201
- F-MAMMA1001143/////ALU SUBFAMILY J WARNING ENTRY /////0.00014:36:66//HOMO SAPIENS (HUMAN).//P39188
- 25 F-MAMMA1001145
- F-MAMMA1001154//CSBA PROTEIN.//1.0:39:38//BACILLUS SUBTILIS.//P37953
- F-MAMMA1001161/////ALU SUBFAMILY J WARNING ENTRY /////5.2e-23:53:64//HOMO SAPIENS (HUMAN).//P39188
- 30 F-MAMMA1001162//CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27).//0.69:86:31//MUS MUSCULUS (MOUSE).//P41272
- F-MAMMA1001181//HYPOTHETICAL 81.0 KD PROTEIN C35D10.4 IN CHROMOSOME III.//0.00010:74:47//CAENORHABDITIS ELEGANS.//Q18486
- F-MAMMA1001186/////ALU SUBFAMILY SQ WARNING ENTRY /////9.0e-32:44:86//HOMO SAPIENS (HUMAN).//P39194
- 35 F-MAMMA1001191//OCTAMER-BINDING TRANSCRIPTION FACTOR 1 (OTF-1) (NF-A1) (FRAGMENT).//0.096:40:40//MACROPUS EUGENII (TAMMAR WALLABY).//Q28466
- F-MAMMA1001198//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN).//2.5e-75:204:70//HOMO SAPIENS (HUMAN).//P42566
- 40 F-MAMMA1001202//METALLOTHIONEIN-II (MT-II) (MT-IIB/MT-IA).//0.52:46:32//CALLINECTES SAPIDUS (BLUE CRAB).//P55950
- F-MAMMA1001203/////ALU SUBFAMILY SC WARNING ENTRY /////7.3e-11:82:58//HOMO SAPIENS (HUMAN).//P39192
- F-MAMMA1001206/////ALU SUBFAMILY J WARNING ENTRY /////1.9e-17:67:71//HOMO SAPIENS (HUMAN).//P39188
- 45 F-MAMMA1001215//9 KD PROTEIN.//1.0:51:33//HOMO SAPIENS (HUMAN).//P13994
- F-MAMMA1001220/////ALU SUBFAMILY SB WARNING ENTRY /////3.4e-37:55:87//HOMO SAPIENS (HUMAN).//P39189
- F-MAMMA1001222//HYPOTHETICAL 73.6 KD PROTEIN CY49.21.//3.7e-06:168:38//MYCOBACTERIUM TUBERCULOSIS.//Q10690
- 50 F-MAMMA1001243
- F-MAMMA1001244//TRP OPERON LEADER PEPTIDE.//1.0:18:55//SERRATIA MARCESCENS.//P03055
- F-MAMMA1001249//HYPOTHETICAL 7.2 KD PROTEIN IN RPS2 3'REGION (ORF57).//0.57:23:34//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34774
- 55 F-MAMMA1001256/////ALU SUBFAMILY J WARNING ENTRY /////2.3e-07:79:44//HOMO SAPIENS (HUMAN).//P39188
- F-MAMMA1001259//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//0.046:86:32//MYCOPLASMA GENITALIUM.//P47486

- F-MAMMA1001260//MYOSIN HEAVY CHAIN, PERINATAL SKELETAL MUSCLE.//2.7e-05:219.27//HOMO SAPIENS (HUMAN).//P13535
- F-MAMMA1001268//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.7e-27:89.67//HOMO SAPIENS (HUMAN).//P08547
- 5 F-MAMMA1001271//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//4.0e-06:126:38//HOMO SAPIENS (HUMAN).//P54259
- F-MAMMA1001274!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.4e-29:57.66//HOMO SAPIENS (HUMAN).//P39194
- 10 F-MAMMA1001280//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//0.27:24.54//ESCHERICHIA COLI.//P05834
- F-MAMMA1001292//HYPOTHETICAL PROTEIN KIAA0176 (FRAGMENT).//1.3e-73:208.69//HOMO SAPIENS (HUMAN).//Q14681
- F-MAMMA1001296!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/6.9e-22:41.80//HOMO SAPIENS (HUMAN).//P39193
- 15 F-MAMMA1001298//HYPOTHETICAL PROTEIN HI0371.//0.99:29.37//HAEMOPHILUS INFLUENZAE.//P44668
- F-MAMMA1001305//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//9.9e-62:222.54//HOMO SAPIENS (HUMAN).//Q07960
- F-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//2.1e-09:46.60//HOMO SAPIENS (HUMAN).//P20931
- 20 F-MAMMA1001324//POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)].//2.5e-43:128.50//FRIEND MURINE LEUKEMIA VIRUS (ISOLATE PVC-211) (F-MULV).//P26808
- F-MAMMA1001330//HEMOGLOBIN ZETA CHAIN (FRAGMENTS).//0.30:51.37//MACROPUS EUGENII (TAMMAR WALLABY).//P81044
- 25 F-MAMMA1001341//TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36) (GROWTH FACTOR- INDUCIBLE NUCLEAR PROTEIN NUP475).//0.024:89.39//HOMO SAPIENS (HUMAN).//P26651
- F-MAMMA1001343//PROBABLE E5 PROTEIN.//0.60:64.29//HUMAN PAPILLOMAVIRUS TYPE 16.//P06927
- F-MAMMA1001346//PROTEINASE INHIBITOR IIB (FRAGMENTS).//0.97:33.45//SOLANUM TUBEROSUM (POTATO).//P01082
- 30 F-MAMMA1001383!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.2e-30:86.77//HOMO SAPIENS (HUMAN).//P39194
- F-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//9.2e-91:195.92//HOMO SAPIENS (HUMAN).//P02750
- 35 F-MAMMA1001397!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.5e-19:55.69//HOMO SAPIENS (HUMAN).//P39188
- F-MAMMA1001408//SALIVARY GLUE PROTEIN SGS-7 PRECURSOR.//0.60:45.35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P02841
- 40 F-MAMMA1001411//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//5.8e-06:153.26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
- F-MAMMA1001419!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.3e-16:99.51//HOMO SAPIENS (HUMAN).//P39194
- 45 F-MAMMA1001420!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!/0.0018:23.65//HOMO SAPIENS (HUMAN).//P39190
- F-MAMMA1001435!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.7e-22:60.58//HOMO SAPIENS (HUMAN).//P39195
- F-MAMMA1001442
- 50 F-MAMMA1001446!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.2e-23:48.75//HOMO SAPIENS (HUMAN).//P39194
- F-MAMMA1001452//GENE 35 PROTEIN (GP35).//0.61:31.45//MYCOBACTERIOPHAGE L5.//Q05245
- F-MAMMA1001465//HYPOTHETICAL PROTEIN E-115.//0.0026:68.38//HUMAN ADENOVIRUS TYPE 2.//P03290
- 55 F-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENT).//3.7e-94:201.92//MUS MUSCULUS (MOUSE).//P52623
- F-MAMMA1001487//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.6e-16:89.41//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
- F-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-

TRAL PROTEINASE) (CANP) (MU-TYPE).//6.2e-59:86:97//HOMO SAPIENS (HUMAN).//P07384  
 F-MAMMA1001502//HYPOTHETICAL 11.4 KD PROTEIN (ORF1).//0.21:79:30//STREPTOMYCES FRADIAE.//  
 P26800  
 F-MAMMA1001510  
 5 F-MAMMA1001522//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.67:98:31//STREPTO-  
 MYCES FRADIAE.//P20186  
 F-MAMMA1001547//PROBABLE MOLYBDENUM-PTERIN BINDING PROTEIN.//0.97:35:42//HAEMOPHILUS  
 INFLUENZAE.//P45183  
 F-MAMMA1001551//HYPOTHETICAL PROTEIN MJ0458.1.//0.038:31:41//METHANOCOCCUS JANNASCHII.//  
 10 P81308  
 F-MAMMA1001575  
 F-MAMMA1001576//TUBULIN GAMMA CHAIN.//1.6e-86:162:99//XENOPUS LAEVIS (AFRICAN CLAWED  
 FROG).//P23330  
 F-MAMMA1001590!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.0035:38:55//HOMO SAPIENS (HUMAN).//  
 15 P39195  
 F-MAMMA1001600//CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.//0.85:53:33//HOMO SAPIENS  
 (HUMAN).//P29279  
 F-MAMMA1001604//HYPOTHETICAL 11.1 KD PROTEIN C30D11.02C IN CHROMOSOME I.//0.14:82:29//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09902  
 20 F-MAMMA1001606//HIGH MOBILITY GROUP PROTEIN HMGI-C.//8.2e-05:77:37//HOMO SAPIENS (HUMAN).//  
 P52926  
 F-MAMMA1001620!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.5e-05:24:66//HOMO SAPIENS (HU-  
 MAN).//P39195  
 F-MAMMA1001627//CUTICLE COLLAGEN 40.//0.82:131:31//CAENORHABDITIS ELEGANS.//P34804  
 25 F-MAMMA1001630!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//8.6e-26:57:78//HOMO SAPIENS (HU-  
 MAN).//P39194  
 F-MAMMA1001633//ZINC FINGER PROTEIN 165.//6.9e-38:160:55//HOMO SAPIENS (HUMAN).//P49910  
 F-MAMMA1001635  
 F-MAMMA1001649//SPERM PROTAMINE P1.//0.39:31:41//TACHYGLOSSUS ACULEATUS ACULEATUS (AUS-  
 30 TRALIAN ECHIDNA).//P35311  
 F-MAMMA1001654//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-  
 TEIN KINASE 1).//5.6e-06:99:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P18160  
 F-MAMMA1001663//VERY HYPOTHETICAL XYLU PROTEIN.//0.99:27:37//ESCHERICHIA COLI.//P05056  
 F-MAMMA1001670//CUTICLE COLLAGEN 1.//0.033:97:37//CAENORHABDITIS ELEGANS.//P08124  
 35 F-MAMMA1001671  
 F-MAMMA1001679//PROCOLLAGEN ALPHA 2(IV) CHAIN PRECURSOR.//0.92:32:50//HOMO SAPIENS (HU-  
 MAN).//P08572  
 F-MAMMA1001683//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.00026:147:34//STREP-  
 40 TOMYCES FRADIAE.//P20186  
 F-MAMMA1001686  
 F-MAMMA1001692//SMALL HYDROPHOBIC PROTEIN (SMALL PROTEIN 1A).//1.0:34:26//BOVINE RESPIRA-  
 TORY SYNCYTIAL VIRUS (STRAIN A51908) (BRS).//P24616  
 F-MAMMA1001711!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.1e-28:56:69//HOMO SAPIENS (HU-  
 MAN).//P39194  
 45 F-MAMMA1001715!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.6e-08:39:71//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-MAMMA1001730//METALLOTHIONEIN-B (MTB).//1.0:17:64//STRONGYLOCENTROTUS PURPURATUS  
 (PURPLE SEA URCHIN).//Q27287  
 F-MAMMA1001735//TUBULIN BETA-5 CHAIN (CLASS-V).//5.1e-121:213:97//GALLUS GALLUS (CHICKEN).//  
 50 P09653  
 F-MAMMA1001740  
 F-MAMMA1001743!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.3e-09:100:42//HOMO SAPIENS (HU-  
 MAN).//P39195  
 F-MAMMA1001744//POU DOMAIN PROTEIN 2.//0.97:59:38//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA  
 55 DANIO).//Q90270  
 F-MAMMA1001745//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.1e-43:199:42//HOMO SAPIENS (HU-  
 MAN).//P08547  
 F-MAMMA1001751//TWK-8 PROTEIN.//2.9e-15:77:36//CAENORHABDITIS ELEGANS.//P34410

- F-MAMMA1001754//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.019:20:45//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645
- F-MAMMA1001757//HYPOTHETICAL 9.2 KD PROTEIN IN RNPA 3'REGION.//0.94:30:43//PSEUDOMONAS PUTIDA.//P25753
- 5 F-MAMMA1001760//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/4.6e-34:103:59//HOMO SAPIENS (HUMAN).//P39191
- F-MAMMA1001764
- F-MAMMA1001768//HYPOTHETICAL PROTEIN UL61.//0.042:167:33//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818
- 10 F-MAMMA1001769//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.0e-29:97:69//HOMO SAPIENS (HUMAN).//P39194
- F-MAMMA1001771//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//3.3e-09:123:32//HOMO SAPIENS (HUMAN).//P51805
- F-MAMMA1001783//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-09:55:61//HOMO SAPIENS (HUMAN).//P39188
- 15 F-MAMMA1001785//RAS-RELATED PROTEIN RABC.//1.9e-06:120:25//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34143
- F-MAMMA1001788//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.3e-29:46:76//HOMO SAPIENS (HUMAN).//P08547
- 20 F-MAMMA1001790//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.7e-24:69:69//HOMO SAPIENS (HUMAN).//P39188
- F-MAMMA1001806//HYPOTHETICAL 21.2 KD PROTEIN IN TOR2-MNN4 INTERGENIC REGION.//0.95:58:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36042
- F-MAMMA1001812//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.8e-12:53:69//HOMO SAPIENS (HUMAN).//P39195
- 25 F-MAMMA1001815//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.11:30:70//HOMO SAPIENS (HUMAN).//P08547
- F-MAMMA1001817//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.9e-16:86:55//HOMO SAPIENS (HUMAN).//P39188
- 30 F-MAMMA1001818
- F-MAMMA1001820//VITTELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-4) (PROTEIN SV23).//0.0030:63:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13238
- F-MAMMA1001824//APTOTOXIN VII (PARALYTIC PEPTIDE VII) (PP VII).//0.99:26:34//APTOSTICHUS SCHLINGERI (TRAP-DOOR SPIDER).//P49271
- 35 F-MAMMA1001836//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.6e-35:77:88//HOMO SAPIENS (HUMAN).//P39195
- F-MAMMA1001837//ZINC FINGER PROTEIN 191.//1.3e-27:106:58//HOMO SAPIENS (HUMAN).//O14754
- F-MAMMA1001848//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.0e-19:92:58//HOMO SAPIENS (HUMAN).//P39188
- 40 F-MAMMA1001851
- F-MAMMA1001854
- F-MAMMA1001858//ISOTOCIN-NEUROPHYSIN I 1 PRECURSOR.//0.93:42:38//CATOSTOMUS COMMERSONI (WHITE SUCKER).//P15210
- 45 F-MAMMA1001864//PROBABLE ABC TRANSPORTER PERMEASE PROTEIN MG189.//0.77:161:27//MYCOPLASMA GENITALIUM.//P47435
- F-MAMMA1001868//FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PIPIASE) (EC 5.2.1.8) (PROLINE ROTAMASE) (NUCLEOLAR PROLINE ISOMERASE) (FKBP-70).//0.00013:219:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38911
- F-MAMMA1001874//SPERM HISTONE P2 PRECURSOR (PROTAMINE MP2).//0.0075:76:31//MUS MUSCULUS (MOUSE).//P07978
- 50 F-MAMMA1001878//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).//0.020:10:80//LYCOPERSICON ESCULENTUM (TOMATO).//Q01157
- F-MAMMA1001880
- F-MAMMA1001890//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/5.1e-34:56:83//HOMO SAPIENS (HUMAN).//P39192
- 55 F-MAMMA1001907//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.7e-12:44:68//HOMO SAPIENS (HUMAN).//P39194
- F-MAMMA1001908//HYPOTHETICAL 16.2 KD PROTEIN IN PRP24-RRN9 INTERGENIC REGION.//0.00013:77:

37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q03525  
 F-MAMMA1001931//HYPOTHETICAL 118.2 KD PROTEIN F43C1.1 IN CHROMOSOME III.//0.41:106:29//  
 CAENORHABDITIS ELEGANS//Q09564  
 5 F-MAMMA1001956//OCTAPEPTIDE-REPEAT PROTEIN T2.//0.00053:149:30//MUS MUSCULUS (MOUSE)//  
 Q06666  
 F-MAMMA1001963//HYPOTHETICAL PROTEIN IN NAC 5'REGION (ORF X) (FRAGMENT)//1.0:46:28//KLEB-  
 SIELLA AEROGES.//Q08600  
 F-MAMMA1001969//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.7e-34:97:68//HOMO SAPIENS (HU-  
 MAN)//P08547  
 10 F-MAMMA1001970//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//6.2e-07:67:37//HOMO SAPIENS (HU-  
 MAN)//P08547  
 F-MAMMA1001992//PROTEIN Q300.//0.53:14:71//MUS MUSCULUS (MOUSE)//Q02722  
 F-MAMMA1002009//PROBABLE E5 PROTEIN//0.17:56:32//HUMAN PAPILLOMAVIRUS TYPE 31//P17385  
 15 F-MAMMA1002011//MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MARCKS) (PROTEIN KINASE  
 C SUBSTRATE, 80 KD PROTEIN, LIGHT CHAIN) (PKCSL) (80K-L PROTEIN)//1.0:100:31//HOMO SAPIENS  
 (HUMAN)//P29966  
 F-MAMMA1002032//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.1e-21:86:65//HOMO SAPIENS (HUMAN)//  
 P39188  
 20 F-MAMMA1002033//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.5e-20:67:58//HOMO SAPIENS (HUMAN)//  
 P39188  
 F-MAMMA1002041//MALE SPECIFIC SPERM PROTEIN MST84DC//1.0:17:52//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY)//Q01644  
 F-MAMMA1002042//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/0.19:45:46//HOMO SAPIENS (HUMAN)//  
 P39192  
 25 F-MAMMA1002047//TYROSINE AMINOTRANSFERASE (EC 2.6.1.5) (L-TYROSINE:2-OXOGLUTARATE AMI-  
 NOTRANSFERASE) (TAT)//0.0017:50:46//RATTUS NORVEGICUS (RAT)//P04694  
 F-MAMMA1002056//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.2e-37:70:77//HOMO SAPIENS (HU-  
 MAN)//P39194  
 30 F-MAMMA1002058//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-08:26:76//HOMO SAPIENS (HUMAN)//  
 P39188  
 F-MAMMA1002068//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//2.0e-11:78:46//HOMO SAPIENS (HU-  
 MAN)//P08547  
 F-MAMMA1002078//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.96:26:46//COTURNIX COTURNIX  
 JAPONICA (JAPANESE QUAIL)//P50682  
 35 F-MAMMA1002082//SUPPRESSOR PROTEIN SRP40.//0.23:95:32//SACCHAROMYCES CEREVISIAE (BAK-  
 ER'S YEAST)//P32583  
 F-MAMMA1002084//HYPOTHETICAL 7.5 KD PROTEIN.//1.0:40:35//VACCINIA VIRUS (STRAIN COPENHA-  
 GEN)//P20520  
 40 F-MAMMA1002093  
 F-MAMMA1002108//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556//0.00079:143:33//STREP-  
 TOMYCES FRADIAE//P20186  
 F-MAMMA1002118//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:43:34//METRIDIDIUM SENILE  
 (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE)//O47493  
 45 F-MAMMA1002125//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.9e-14:60:68//HOMO SAPIENS (HU-  
 MAN)//P39192  
 F-MAMMA1002132  
 F-MAMMA1002140//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.4e-24:69:65//HOMO SAPIENS (HUMAN)//  
 P39188  
 50 F-MAMMA1002143//SERUM PROTEIN MSE55.//2.1e-16:166:43//HOMO SAPIENS (HUMAN)//Q00587  
 F-MAMMA1002145//36.4 KD PROLINE-RICH PROTEIN.//0.00014:84:29//LYCOPERSICON ESCULENTUM (TO-  
 MATO)//Q00451  
 F-MAMMA1002153  
 F-MAMMA1002155  
 55 F-MAMMA1002156//METALLOPROTEINASE INHIBITOR PRECURSOR.//0.90:58:34//STREPTOMYCES NI-  
 GRESCENS//P01077  
 F-MAMMA1002158  
 F-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN)//6.0e-66:157:70//HOMO SAPI-  
 ENS (HUMAN)//P15880

F-MAMMA1002174!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.5e-25:56:64//HOMO SAPIENS (HUMAN).//P39188

5 F-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE 1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PRP) (NATURAL KILLER CELL ENHANCING FACTOR B) (NKEF-B)//9.0e-09:28:100//HOMO SAPIENS (HUMAN).//P32119

F-MAMMA1002209//TRANSCRIPTION INITIATION FACTOR TFIIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130)//0.0023:132:33//HOMO SAPIENS (HUMAN).//O00268

F-MAMMA1002215//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR//0.00032:68:35//HOMO SAPIENS (HUMAN).//P02452

10 F-MAMMA1002219//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1//0.0079:224:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25386

F-MAMMA1002230

F-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR)//1.4e-118:151:94//RATTUS NORVEGICUS (RAT).//P70541

15 F-MAMMA1002243//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP)//0.028:112:33//MUS MUSCULUS (MOUSE).//P70315

F-MAMMA1002250//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11)//0.0012:80:32//ORYZOTOLA-GUS CUNICULUS (RABBIT).//P06333

F-MAMMA1002267//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6)//0.17:139:28//TRYPANOSOMA BRUCEI BRUCEI//P24499

20 F-MAMMA1002268//60S RIBOSOMAL PROTEIN L22//0.00026:163:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P50887

F-MAMMA1002269//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE//0.35:14:57//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251

25 F-MAMMA1002282!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/6.1e-05:32:65//HOMO SAPIENS (HUMAN).//P39192

F-MAMMA1002292//TROPOMYOSIN 2.1//1.4e-05:100:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40414

F-MAMMA1002293!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.8e-25:127:44//HOMO SAPIENS (HUMAN).//P39188

30 F-MAMMA1002294//ALPHA TRANS-INDUCING PROTEIN (ALPHA-TIF)//0.00011:138:38//BOVINE HERPESVIRUS TYPE 1 (STRAIN P8-2).//P30020

F-MAMMA1002297//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR//0.15:144:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323

35 F-MAMMA1002298//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//1.0e-05:40:50//MUS MUSCULUS (MOUSE).//P05143

F-MAMMA1002299//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3)//0.84:65:32//STRUTHIO CAMELUS (OSTRICH).//O21405

F-MAMMA1002308!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.3e-29:61:73//HOMO SAPIENS (HUMAN).//P39188

40 F-MAMMA1002310//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)//0.00016:70:38//MUS MUSCULUS (MOUSE).//P15265

F-MAMMA1002311!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/9.4e-09:84:54//HOMO SAPIENS (HUMAN).//P39188

45 F-MAMMA1002312//HYPOTHETICAL 10.8 KD PROTEIN IN GP30-RIII INTERGENIC REGION (URF Y)//0.48:48:33//BACTERIOPHAGE T4.//P33084

F-MAMMA1002317

F-MAMMA1002319//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE//0.011:128:27//MUS MUSCULUS (MOUSE).//P11369

50 F-MAMMA1002322!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.2e-20:92:57//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1002329//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.051:33:36//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P03931

F-MAMMA1002332//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//6.5e-20:116:51//HOMO SAPIENS (HUMAN).//P08547

55 F-MAMMA1002333//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//0.0017:214:31//BOS TAURUS (BOVINE).//P02453

F-MAMMA1002339//COPPER-METALLOTHIONEIN (CU-MT)//0.59:42:38//HELIX POMATIA (ROMAN SNAIL)

(EDIBLE SNAIL).//P55947

F-MAMMA1002347/!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.43:26.61//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002351//HYPOTHETICAL PROTEIN MJ0304 //2.3e-07:139:25//METHANOCOCCUS JANNAS-CHII.//Q57752

F-MAMMA1002352

F-MAMMA1002353/!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00028:31:80//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002355/!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.2e-28:87:73//HOMO SAPIENS (HUMAN).//P39193

F-MAMMA1002356//RELAXIN //0.95:31:35//SQUALUS ACANTHIAS (SPINY DOGFISH).//P11953

F-MAMMA1002359//CHLOROPLAST 50S RIBOSOMAL PROTEIN L33.//0.93:44:36//GUILLARDIA THETA (CRYPTOMONAS PHI).//O78487

F-MAMMA1002360//LATE L2 MU CORE PROTEIN PRECURSOR (PROTEIN X).//0.94:30:43//BOVINE ADENOVIRUS TYPE 2 (MASTADENOVIRUS BOS2).//Q96626

F-MAMMA1002361/!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.0e-08:45:68//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002362//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.58:23:26//LUMBRICUS TERRESTRIS (COMMON EARTHWORM).//Q34942

F-MAMMA1002380//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR //0.23:100:27//DROSOPHILA SIMULANS (FRUIT FLY).//P13729

F-MAMMA1002384

F-MAMMA1002385//HYPOTHETICAL 40.9 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION //3.8e-14:125:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38241

F-MAMMA1002392//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:17:58//BRANCHIOSTOMA LANCEOLATUM (COMMON LANCELET) (AMPHIOXUS).//O21003

F-MAMMA1002411//30S RIBOSOMAL PROTEIN S17.//0.85:49:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73311

F-MAMMA1002413//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRAGMENT).//0.97:41:39//DROSOPHILA AFFINIS (FRUIT FLY).//P51926

F-MAMMA1002417//RFBJ PROTEIN.//0.99:31:35//SHIGELLA FLEXNERI.//P37786

F-MAMMA1002427/!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.6e-33:135:59//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1002428//HYPOTHETICAL PROTEIN C18.//0.97:34:44//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//P32217

F-MAMMA1002434/!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/3.1e-36:56:78//HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1002446

F-MAMMA1002454//EARLY NODULIN 20 PRECURSOR (N-20).//0.77:57:45//MEDICAGO TRUNCATULA (BARREL MEDIC).//P93329

F-MAMMA1002461//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//1.3e-05:193:32//CANIS FAMILIARIS (DOG).//P50551

F-MAMMA1002470//HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION //1.0e-75:231:60//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38795

F-MAMMA1002475//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L4 (SNF2-BETA) (BRG-1 PROTEIN) (MITOTIC GROWTH AND TRANSCRIPTION ACTIVATOR) (BRAHMA PROTEIN HOMOLOG 1).//0.013:99:30//HOMO SAPIENS (HUMAN).//P51532

F-MAMMA1002480//NONSTRUCTURAL PROTEIN 5B.//1.0:23:43//HUMAN CORONAVIRUS (STRAIN 229E).//P19741

F-MAMMA1002485//STANNIocalcin PRECURSOR.//2.1e-23:88:46//HOMO SAPIENS (HUMAN).//P52823

F-MAMMA1002494//MOLT-INHIBITING HORMONE (MIH).//1.0:32:37//PROCAMBARUS CLARKII (RED SWAMP CRAYFISH).//P55848

F-MAMMA1002498//6.7 KD PROTEIN (ORF 5).//1.0:26:42//BARLEY YELLOW DWARF VIRUS (ISOLATE PAV) (BYDV).//P09517

F-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION //5.0e-26:222:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43571

F-MAMMA1002530//CYTOSOLIC PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE) / LYSOPHOSPHOLIPASE (EC 3.1.1.5).//4.5e-12:88:44//HOMO SAPIENS (HUMAN).//



P47712

F-MAMMA1002545!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.3e-29:97.71//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1002554//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//0.46:54:40//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414

F-MAMMA1002556//METALLOTHIONEIN 20-I ISOFORMS A AND B (MT-20-IA AND MT-20-IB).//0.99:21:47//MYTILUS EDULIS (BLUE MUSSEL).//P80251

F-MAMMA1002566//TRANSCRIPTION FACTOR P65 (NUCLEAR FACTOR NF-KAPPA-B P65 SUBUNIT).//0.70:130:30//MUS MUSCULUS (MOUSE).//Q04207

F-MAMMA1002571//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (FRAGMENT).//0.54:45:51//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P35084

F-MAMMA1002573//PARATHYMOXIN.//1.5e-07:69:46//HOMO SAPIENS (HUMAN).//P20962

F-MAMMA1002585//MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR ISOFORM (FRAGMENT).//0.38:36:36//MUS MUSCULUS (MOUSE).//P09542

F-MAMMA1002590!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.99:22:77//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1002597!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.1e-18:44:70//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1002598//60S RIBOSOMAL PROTEIN L7.//1.8e-16:40:100//HOMO SAPIENS (HUMAN).//P18124

F-MAMMA1002603

F-MAMMA1002612//30S RIBOSOMAL PROTEIN S16 (FRAGMENT).//1.0:29:37//THERMUS AQUATICUS.//O07348

F-MAMMA1002617//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.00041:81:34//RATTUS NORVEGICUS (RAT).//P10164

F-MAMMA1002618//ESCARGOT/NAIIL PROTEIN HOMOLOG (FRAGMENT).//0.11:18:50//PSYCHODA CINE-REA.//Q02027

F-MAMMA1002619//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//1.8e-13:110:40//CAENORHABDITIS ELEGANS.//Q09931

F-MAMMA1002622!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/8.4e-05:53:58//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002623//PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (EC 1.14.17.3) (PAM).//2.6e-07:37:78//HOMO SAPIENS (HUMAN).//P19021

F-MAMMA1002625

F-MAMMA1002629!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.4e-19:49:73//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002636//COLLAGEN ALPHA 2(VI) CHAIN (FRAGMENT).//1.7e-07:189:32//HOMO SAPIENS (HUMAN).//P12110

F-MAMMA1002637//KINESIN LIGHT CHAIN (KLC).//7.7e-54:227:52//RATTUS NORVEGICUS (RAT).//P37285

F-MAMMA1002646//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//0.034:199:25//MUS MUSCULUS (MOUSE).//P19246

F-MAMMA1002650//TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2).//1.7e-07:104:32//MUS MUSCULUS (MOUSE).//P97303

F-MAMMA1002655//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//1.0:25:44//HOMO SAPIENS (HUMAN).//P22532

F-MAMMA1002662

F-MAMMA1002665!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.3e-07:54:57//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL-AC-TIVATING ENZYME).//1.4e-10:144:31//ESCHERICHIA COLI.//P27550

F-MAMMA1002673//BREVICAN CORE PROTEIN PRECURSOR.//0.76:64:39//BOS TAURUS (BOVINE).//Q28062

F-MAMMA1002684//HYPOTHETICAL 11.8 KD PROTEIN IN GP55-NRDG INTERGENIC REGION.//0.094:77:27//BACTERIOPHAGE T4.//P07079

F-MAMMA1002685//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.0017:177:34//RATTUS NORVEGICUS (RAT).//P02454

F-MAMMA1002698

F-MAMMA1002699//HYPOTHETICAL 45.1 KD PROTEIN IN RP55-ZMS1 INTERGENIC REGION.//1.2e-28:127:

47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47160  
 F-MAMMA1002701//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.0:14:92//HOMO SAPIENS (HUMAN).//  
 P39188  
 5 F-MAMMA1002708//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/7.9e-27:52:65//HOMO SAPIENS (HU-  
 MAN).//P39193  
 F-MAMMA1002711//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.7e-24:54:75//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-MAMMA1002721  
 F-MAMMA1002727//SOX-13 PROTEIN (FRAGMENT).//0.70:36:38//MUS MUSCULUS (MOUSE).//Q04891  
 10 F-MAMMA1002728//HYPOTHETICAL 6.0 KD PROTEIN.//1.0:25:44//THERMOPROTEUS TENAX VIRUS 1  
 (STRAIN KRA1) (TTV1).//P19305  
 F-MAMMA1002744//HYPOTHETICAL 13.4 KD PROTEIN IN ACT5-YCK1 INTERGENIC REGION.//1.0:52:34//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38834  
 F-MAMMA1002746//HYPOTHETICAL 5.6 KD PROTEIN (ORF A-45).//1.0:22:40//SULFOLOBUS VIRUS-LIKE  
 15 PARTICLE SSV1.//P20198  
 F-MAMMA1002748  
 F-MAMMA1002754//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.1e-21:56:64//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-MAMMA1002758//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.37:14:64//DROSOPHILA MELA-  
 20 NOGASTER (FRUIT FLY).//Q01645  
 F-MAMMA1002764//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.7e-32:79:60//HOMO SAPIENS (HU-  
 MAN).//P39194  
 F-MAMMA1002765//PARATHYMOSIN.//0.79:63:28//BOS TAURUS (BOVINE).//P08814  
 F-MAMMA1002769//GAR2 PROTEIN.//0.00037:192:27//SCHIZOSACCHAROMYCES POMBE (FISSION  
 25 YEAST).//P41891  
 F-MAMMA1002775//HYPOTHETICAL 36.7 KD PROTEIN C2F7.14C IN CHROMOSOME I.//5.4e-54:240:49//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09704  
 F-MAMMA1002780  
 F-MAMMA1002782//MARGATOXIN (MGTX).//1.0:31:38//CENTRUROIDES MARGARITATUS (SCORPION).//  
 30 P40755  
 F-MAMMA1002796//ICE NUCLEATION PROTEIN.//0.0018:100:41//PSEUDOMONAS FLUORESCENS.//  
 P09815  
 F-MAMMA1002807//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/9.3e-23:100:59//HOMO SAPIENS (HUMAN).//  
 P39188  
 35 F-MAMMA1002820//NEUROTOXIN IV (LQ IV).//1.0:18:50//LEIURUS QUINQUESTRIATUS QUINQUESTRIA-  
 TUS (EGYPTIAN SCORPION).//P01489  
 F-MAMMA1002830//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.7e-24:55:74//HOMO SAPIENS (HU-  
 MAN).//P39195  
 F-MAMMA1002833//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.6e-31:95:73//HOMO SAPIENS (HU-  
 40 MAN).//P39189  
 F-MAMMA1002835//HYPOTHETICAL 42.1 KD PROTEIN F13G3.3 IN CHROMOSOME I.//1.0:54:37//  
 CAENORHABDITIS ELEGANS.//Q19417  
 F-MAMMA1002838//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.5e-27:99:70//HOMO SAPIENS (HU-  
 MAN).//P39193  
 45 F-MAMMA1002842//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.3e-13:65:63//HOMO SAPIENS (HU-  
 MAN).//P39195  
 F-MAMMA1002843//METALLOTHIONEIN-II (MT-II).//0.97:19:47//MUS MUSCULUS (MOUSE).//P02798  
 F-MAMMA1002844//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//4.9e-08:119:36//  
 AUTOGRAPH CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479  
 50 F-MAMMA1002858//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.98:37:37//IPAN TROGLODYTES  
 (CHIMPANZEE).//Q35647  
 F-MAMMA1002868//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.8e-10:51:62//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-MAMMA1002869//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//1.8e-95:194:  
 78//HOMO SAPIENS (HUMAN).//P48059  
 55 F-MAMMA1002871//G-PROTEIN COUPLED RECEPTOR HOMOLOG R33.//1.0:51:35//RAT CYTOMEGALOVIRUS  
 (STRAIN MAASTRICHT).//O12000  
 F-MAMMA1002880

F-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN).//3.3e-22:180:35//HO-  
 MO SAPIENS (HUMAN).//P48060  
 F-MAMMA1002886//MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL).//0.00011:148:39//ACANTHAMOE-  
 BA CASTELLANII (AMOEB).//P19706  
 5 F-MAMMA1002887  
 F-MAMMA1002890//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.030:142:25//SACCHAROMY-  
 CES CEREVISIAE (BAKER'S YEAST).//P32323  
 F-MAMMA1002892  
 10 F-MAMMA1002895//HYPOTHETICAL PROTEIN UL61.//0.00099:143:35//HUMAN CYTOMEGALOVIRUS  
 (STRAIN AD169).//P16818  
 F-MAMMA1002908//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).//0.12:44:43//ORYCTOLAGUS  
 CUNICULUS (RABBIT).//P06333  
 F-MAMMA1002909//ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00011:28:75//HOMO SAPIENS (HUMAN).//  
 P39188  
 15 F-MAMMA1002930//BOMBYXIN A-7 PRECURSOR (BBX-A7) (4K-PROTHORACICOTROPIC HORMONE) (4K-  
 PTTH).//0.99:45:46//BOMBYX MORI (SILK MOTH).//P26730  
 F-MAMMA1002937//ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1).//6.5e-24:147:34//HOMO  
 SAPIENS (HUMAN).//P28698  
 20 F-MAMMA1002938//CERULOPLASMIN PRECURSOR (EC 1.16.3.1) (FERROXIDASE).//4.7e-11:44:68//MUS  
 MUSCULUS (MOUSE).//Q61147  
 F-MAMMA1002941//PROTEIN Q300.//0.0076:21:61//MUS MUSCULUS (MOUSE).//Q02722  
 F-MAMMA1002947//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//1.9e-08:152:38//STREP-  
 TOMYCES FRADIAE.//P20186  
 F-MAMMA1002964  
 25 F-MAMMA1002970//ALU SUBFAMILY SB WARNING ENTRY !!!!!/0.0057:55:43//HOMO SAPIENS (HUMAN).//  
 P39189  
 F-MAMMA1002972//BRAIN-SPECIFIC HOMEBOX/POU DOMAIN PROTEIN 3A (BRN-3A) (OCT-T1) (HOME-  
 OBOX/POU DOMAIN PROTEIN RDC-1).//0.84:53:41//HOMO SAPIENS (HUMAN).//Q01851  
 F-MAMMA1002973//ALU SUBFAMILY SC WARNING ENTRY !!!!!/4.6e-11:54:68//HOMO SAPIENS (HU-  
 30 MAN).//P39192  
 F-MAMMA1002982  
 F-MAMMA1002987//HYPOTHETICAL 11.9 KD PROTEIN IN RPC8-MFA2 INTERGENIC REGION.//0.17:47:29//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53906  
 F-MAMMA1003003//ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.6e-09:30:73//HOMO SAPIENS (HU-  
 35 MAN).//P39195  
 F-MAMMA1003004//ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.0071:41:58//HOMO SAPIENS (HUMAN).//  
 P39195  
 F-MAMMA1003007//SPERM PROTAMINE P1.//0.0076:51:37//TACHYGLOSSUS ACULEATUS ACULEATUS  
 (AUSTRALIAN ECHIDNA).//P35311  
 40 F-MAMMA1003011//HISTONE MACRO-H2A.1.//1.8e-60:175:70//RATTUS NORVEGICUS (RAT).//Q02874  
 F-MAMMA1003013//ACTIN BINDING PROTEIN.//0.097:83:31//SACCHAROMYCES EXIGUUS (YEAST).//  
 P38479  
 F-MAMMA1003015  
 F-MAMMA1003019//MYOTUBULARIN.//0.022:56:37//HOMO SAPIENS (HUMAN).//Q13496  
 45 F-MAMMA1003026//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0014:208:27//ORGANIA PSEUDOTSUGA-  
 TA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341  
 F-MAMMA1003031//PROBABLE E4 PROTEIN (E1\*E4).//0.14:49:32//HUMAN PAPILLOMAVIRUS TYPE 6B.//  
 P06459  
 F-MAMMA1003035//HYPOTHETICAL 24.4 KD PROTEIN IN LPD 3'REGION (ORF4).//5.1e-12:112:34//ZY-  
 MOMONAS MOBILIS.//O66114  
 50 F-MAMMA1003039//ALU SUBFAMILY J WARNING ENTRY !!!!!/2.4e-07:68:54//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-MAMMA1003040//ALU SUBFAMILY SB1 WARNING ENTRY !!!!!/2.8e-39:90:57//HOMO SAPIENS (HU-  
 MAN).//P39190  
 55 F-MAMMA1003044  
 F-MAMMA1003047//SPERM HISTONE P2 PRECURSOR (PROTAMINE 2).//0.18:25:44//BOS TAURUS (BO-  
 VINE).//P19782  
 F-MAMMA1003049//PROBABLE E4 PROTEIN.//0.50:67:29//HUMAN PAPILLOMAVIRUS TYPE 6C.//P20969

- F-MAMMA1003055//WEAK TOXIN CM-2.//0.99:23:30//NAJA HAJE HAJE (EGYPTIAN COBRA).//P01415  
 F-MAMMA1003056//EXPORTED PROTEIN 7 (FRAGMENT).//1.0:52:32//STREPTOCOCCUS PNEUMONIAE.//P35597
- 5 F-MAMMA1003057//MD6 PROTEIN.//1.5e-85:168:95//MUS MUSCULUS (MOUSE).//Q60584  
 F-MAMMA1003066//REGB PROTEIN.//1.0:62:27//PSEUDOMONAS AERUGINOSA.//Q03381  
 F-MAMMA1003089//ALU SUBFAMILY SB1 WARNING ENTRY !!!!!/5.1e-15:44:77//HOMO SAPIENS (HUMAN).//P39190
- 10 F-MAMMA1003099//ENDOTHELIAL ACTIN-BINDING PROTEIN (ABP-280) (NONMUSCLE FILAMIN) (FILAMIN 1).//4.8e-20:80:62//HOMO SAPIENS (HUMAN).//P21333  
 F-MAMMA1003104//PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII.//0.98:22:40//SYNECHOCOCCUS ELONGATUS NAEGLI.//P25900  
 F-MAMMA1003113//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS).//0.67:35:45//GALLUS GALLUS (CHICKEN).//P02467
- 15 F-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA).//5.2e-34:141:56//MUS MUSCULUS (MOUSE).//P46735  
 F-MAMMA1003135//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.//3.6e-05:91:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170  
 F-MAMMA1003140  
 F-MAMMA1003146//MALE SPECIFIC SPERM PROTEIN MST87F.//1.0:33:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175
- 20 F-MAMMA1003150//HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II.//4.4e-10:254:30//CAENORHABDITIS ELEGANS.//Q09625  
 F-MAMMA1003166//BRAIN PROTEIN H5.//4.0e-42:182:48//HOMO SAPIENS (HUMAN).//O43236  
 F-NT2RM1000001//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70).//0.15:38:34//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779
- 25 F-NT2RM1000018  
 F-NT2RM1000032//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.51:17:41//CYPRINUS CARPIO (COMMON CARP).//P24948  
 F-NT2RM1000035//3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE (EC 1.1.1.34) (HMG-COA REDUCTASE).//0.00011:114:27//BLATTELLA GERMANICA (GERMAN COCKROACH).//P54980
- 30 F-NT2RM1000037//METALLOTHIONEIN-II (MT-II).//0.025:19:47//SCYLLA SERRATA (MUD CRAB).//P02806  
 F-NT2RM1000039//VITELLINE MEMBRANE VM34CA PROTEIN PRECURSOR.//0.00083:84:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q06521  
 F-NT2RM1000055//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.//1.1e-07:34:55//PLASMODIUM LOPHURAE.//P04929
- 35 F-NT2RM1000059//MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACTOR-LIKE PROTEIN 2) (XMEF2) (RSRFR2).//0.18:83:36//HOMO SAPIENS (HUMAN).//Q02080  
 F-NT2RM1000062//PROLINE-RICH PEPTIDE P-B.//0.54:34:44//HOMO SAPIENS (HUMAN).//P02814  
 F-NT2RM1000080//HYPOTHETICAL 35.7 KD PROTEIN SLR1128.//2.1e-20:119:40//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P72655
- 40 F-NT2RM1000086//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.20:56:35//HOMO SAPIENS (HUMAN).//P10162  
 F-NT2RM1000092//COLLAGEN-LIKE PROTEIN.//0.0017:44:45//HERPESVIRUS SAIMIRI (SUBGROUP C / STRAIN 488).//P22576  
 F-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//5.7e-07:109:28//NEUROSPORA CRASSA.//P87072
- 45 F-NT2RM1000119//TRANSCRIPTIONAL REGULATOR IE63 (VMW63) (ICP27).//0.0050:135:32//HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).//P28276  
 F-NT2RM1000127//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.032:68:32//SORGHUM VULGARE (SORGHUM).//P24152
- 50 F-NT2RM1000131//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).//0.82:33:39//BOS TAURUS (BOVINE).//P37359  
 F-NT2RM1000132//NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-A SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-13KD-A) (CI-13KD-A).//2.7e-59:124:91//HOMO SAPIENS (HUMAN).//O75380  
 F-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//2.5e-08:148:29//HOMO SAPIENS (HUMAN).//P49902
- 55 F-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.9e-07:109:27//NEUROSPORA CRASSA.//P87072  
 F-NT2RM1000187//PUTATIVE PRE-mRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE

- SPAC10F6.02C//1.0e-12:94.46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O42643  
 F-NT2RM1000199//CUTICLE COLLAGEN 12 PRECURSOR.//0.46:130:33//CAENORHABDITIS ELEGANS.//P20630
- 5 F-NT2RM1000242//PUTATIVE ATP SYNTHASE J CHAIN, MITOCHONDRIAL (EC 3.6.1.34).//0.85:38:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13931  
 F-NT2RM1000244//HYPOTHETICAL 131.5 KD PROTEIN C02F12.7 IN CHROMOSOME X.//0.0055:98:36//CAENORHABDITIS ELEGANS.//Q11102  
 F-NT2RM1000252//TRICHOHYALIN.//2.9e-06:88:36//OVIS ARIES (SHEEP).//P22793
- 10 F-NT2RM1000256//GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZING] (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GFAF).//2.9e-54:153:67//MUS MUSCULUS (MOUSE).//P47856  
 F-NT2RM1000257//MAGO NASHI PROTEIN.//5.9e-64:136:89//DROSOPHILA MELANOGASTER (FRUIT FLY).//P49028  
 F-NT2RM1000260
- 15 F-NT2RM1000271//GALACTOKINASE (EC 2.7.1.6).//0.99:41:39//BACILLUS SUBTILIS.//P39574  
 F-NT2RM1000272//HYPOTHETICAL 55.5 KD PROTEIN ZK1128.2 IN CHROMOSOME III.//8.8e-25:131:45//CAENORHABDITIS ELEGANS.//Q09357  
 F-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V-ATPASE 28 KD ACCESSORY PROTEIN).//2.5e-63:121:94//BOS TAURUS (BOVINE).//P39942
- 20 F-NT2RM1000300//TREACLE PROTEIN (TREACHER COLLINS SYNDROME PROTEIN).//0.51:145:26//HOMO SAPIENS (HUMAN).//Q13428  
 F-NT2RM1000314  
 F-NT2RM1000318//50S RIBOSOMAL PROTEIN L23.//0.83:28:35//AQUIFEX AEOLICUS.//O66433  
 F-NT2RM1000341
- 25 F-NT2RM1000354//HYPOTHETICAL 5.8 KD PROTEIN IN PUHA 5'REGION (ORF55).//0.95:43:37//RHODOBACTER CAPSULATUS (RHODOSPIRILLUM RUBRUM) (RHODOSPHELODENDROMONAS CAPSULATA).//P26159  
 F-NT2RM1000355//SPERM-SPECIFIC PROTEIN PHI-1.//0.0016:73:43//MYTILUS EDULIS (BLUE MUSSEL).//Q04621  
 F-NT2RM1000365//HYPOTHETICAL PROTEIN KIAA0140.//3.5e-10:83:49//HOMO SAPIENS (HUMAN).//Q14153
- 30 F-NT2RM1000377//DUAL SPECIFICITY PROTEIN PHOSPHATASE 9 (EC 3.1.3.48) (EC 3.1.3.16) (MITOGEN-ACTIVATED PROTEIN KINASE PHOSPHATASE 4) (MAP KINASE PHOSPHATASE 4) (MKP-4).//4.9e-18:113:38//HOMO SAPIENS (HUMAN).//Q99956  
 F-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.00023:67:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53915
- 35 F-NT2RM1000394//HISTONE H3.3 (H3.B) (H3.3Q).//4.7e-52:71:91//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), ORYCTOLAGUS CUNICULUS (RABBIT), GALLUS GALLUS (CHICKEN), SPISULA SOLIDISSIMA (ATLANTIC SURF-CLAM), DROSOPHILA MELANOGASTER (FRUIT FLY), AND DROSOPHILA HYDEI (FRUIT FLY).//P06351  
 F-NT2RM1000399//ENDOTHELIN-2 PRECURSOR (ET-2) (FRAGMENT).//0.92:24:45//CANIS FAMILIARIS (DOG).//P12064  
 F-NT2RM1000421//CUTICLE COLLAGEN 2C (FRAGMENT).//0.12:93:33//HAEMONCHUS CONTORTUS.//P16252
- 40 F-NT2RM1000430//PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP).//0.13:86:31//NICOTIANA TABACUM (COMMON TOBACCO).//Q03211  
 F-NT2RM1000449//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT).//2.9e-17:75:49//HOMO SAPIENS (HUMAN).//Q15057  
 F-NT2RM1000539//HYPOTHETICAL 10.4 KD PROTEIN IN FTR1-SPT15 INTERGENIC REGION.//2.9e-16:82:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40089
- 50 F-NT2RM1000553//GLYCOLIPID TRANSFER PROTEIN (GLTP).//6.4e-06:103:33//SUS SCROFA (PIG).//P17403  
 F-NT2RM1000555//UNR PROTEIN.//8.7e-77:105:95//RATTUS NORVEGICUS (RAT).//P18395  
 F-NT2RM1000563//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.15:20:50//HOMO SAPIENS (HUMAN).//P30808
- 55 F-NT2RM1000623//CLARA CELL PHOSPHOLIPID-BINDING PROTEIN PRECURSOR (CCBP) (CLARA CELLS 10 KD SECRETORY PROTEIN) (CC10).//0.17:70:34//HOMO SAPIENS (HUMAN).//P11684  
 F-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//2.0e-22:133:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43636

F-NT2RM1000661//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF) (GIFB) //0.0060:24:33//HOMO SAPIENS (HUMAN).//P25713

F-NT2RM1000666//COLD SHOCK PROTEIN SCOF.//9.1e-07:67:41//STREPTOMYCES COELICOLOR.//P48859

5 F-NT2RM1000669//CHLOROPLAST 50S RIBOSOMAL PROTEIN L31.//0.071:69:31//PORPHYRA PURPUREA.//P51290

F-NT2RM1000672//SIGNAL RECOGNITION PARTICLE SEC65 SUBUNIT (FRAGMENT).//0.27:42:42//KLUYVEROMYCES LACTIS (YEAST).//O13475

10 F-NT2RM1000691//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2).//4.3e-42:241:42//HOMO SAPIENS (HUMAN).//P29375

F-NT2RM1000699//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR (EC 2.1.1.32).//0.94:48:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P15565

F-NT2RM1000702//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 1.//0.0013:139:25//DROSOPHILA MELANOGASTER (FRUIT FLY).//P26308

15 F-NT2RM1000725//BASIC PROLINE-RICH PEPTIDE P-E (IB-P).//1.0:15:60//HOMO SAPIENS (HUMAN).//P02811

F-NT2RM1000741//STATHMIN (CLONE XO20) (FRAGMENT).//1.0:53:32//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q09005

F-NT2RM1000742//HYPOTHETICAL 24.1 KD PROTEIN IN DHFR 3'REGION (ORF2).//1.0:54:42//HERPESVIRUS SAIMIRI (STRAIN 484-77).//P25049

20 F-NT2RM1000746//HYPOTHETICAL 16.8 KD PROTEIN C29E6.04 IN CHROMOSOME I.//0.11:87:21//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09858

F-NT2RM1000770//DXS6673E PROTEIN.//2.0e-38:190:48//HOMO SAPIENS (HUMAN).//Q14202

F-NT2RM1000772//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1.//4.3e-12:141:30//PODOSPORA ANSERINA.//Q00808

25 F-NT2RM1000780//MALE SPECIFIC SPERM PROTEIN MST87F.//0.98:34:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175

F-NT2RM1000781

F-NT2RM1000800//24.1 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION.//7.9e-11:135:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P28707

30 F-NT2RM1000802//ALPHA-AMYLASE INHIBITOR PAIMI (PIG PANCREATIC ALPHA-AMYLASE INHIBITOR OF MICROBES I).//0.43:62:35//STREPTOMYCES OLIVACEOVIRIDIS (STREPTOMYCES CORCHORUSII).//P09921

F-NT2RM1000811

35 F-NT2RM1000826//UNR PROTEIN.//1.1e-110:144:83//RATTUS NORVEGICUS (RAT).//P18395

F-NT2RM1000829//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:38:34//DROSOPHILA SIMULANS (FRUIT FLY).//P50270

F-NT2RM1000833//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.4e-62:145:841//CANIS FAMILIARIS (DOG).//P38377

40 F-NT2RM1000850//TESTIS-SPECIFIC PROTEIN KINASE 1 (EC 2.7.1.-).//6.1e-08:136:33//RATTUS NORVEGICUS (RAT).//Q63572

F-NT2RM1000852//ATP-DEPENDENT RNA HELICASE ROK1.//1.6e-34:212:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P45818

F-NT2RM1000857//HISTONE H1.M6.1.//0.76:31:48//TRYPANOSOMA CRUZI.//P40273

45 F-NT2RM1000867//MICROSOMAL SIGNAL PEPTIDASE 10.8 KD SUBUNIT (EC 3.4.-.-).//0.0082:76:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P46965

F-NT2RM1000874//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.38:12:58//HOMO SAPIENS (HUMAN).//P30808

F-NT2RM1000882//CYTOCHROME B5.//9.0e-13:92:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40312

50 F-NT2RM1000883//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.79:22:59//HOMO SAPIENS (HUMAN).//P30808

F-NT2RM1000885//HYPOTHETICAL 5.8 KD PROTEIN.//0.76:18:38//CLOVER YELLOW MOSAIC VIRUS (CYMV).//P16485

55 F-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE I135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT).//6.2e-70:153:88//RATTUS NORVEGICUS (RAT).//O54888

F-NT2RM1000898//ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR).//4.3e-12:159:28//OXYTRICHA FAL-

LAX.//P02583

F-NT2RM1000905//GLUTATHIONE S-TRANSFERASE 1-1 (EC 2.5.1.18)/(CLASS-THETA).//0.98:39:35//LUCILIA CUPRINA (GREENBOTTLE FLY) (AUSTRALIAN SHEEP BLOWFLY).//P42860

F-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//1.3e-11:169:28//CAENORHABDITIS ELEGANS.//P46577

F-NT2RM1000927//CUTICLE COLLAGEN 1.//0.00048:141:31//CAENORHABDITIS ELEGANS.//P08124

F-NT2RM1000962//HYPOTHETICAL 35.8 KD PROTEIN C4F8.04 IN CHROMOSOME I.//7.1e-13:169:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14180

F-NT2RM1000978//HYPOTHETICAL 20.2 KD PROTEIN IN MNN4-PTK1 INTERGENIC REGION.//0.61:82:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36045

F-NT2RM1001003//ALPHA-2 CATENIN (ALPHA N-CATENIN) (NEURAL ALPHA-CATENIN).//1.6e-21:211:31//GALLUS GALLUS (CHICKEN).//P30997

F-NT2RM1001008//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//3.2e-15:119:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701

F-NT2RM1001043//ENDOTHELIN-1 (ET-1) (FRAGMENT).//0.78:32:34//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//Q28469

F-NT2RM1001044

F-NT2RM1001059//LORICRIN.//8.6e-08:108:39//HOMO SAPIENS (HUMAN).//P23490

F-NT2RM1001068//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//0.99:24:50//LYCOPERSICON ESCULENTUM (TOMATO).//Q43513

F-NT2RM1001072//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148).//4.7e-15:148:33//HOMO SAPIENS (HUMAN).//P19174

F-NT2RM1001074//HYPOTHETICAL PROTEIN F-215.//8.6e-05:126:30//HUMAN ADENOVIRUS TYPE 2.//P03291

F-NT2RM1001082//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!.//6.5e-19:75:54//HOMO SAPIENS (HUMAN).//P39195

F-NT2RM1001085//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.49:29:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643

F-NT2RM1001092//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//2.8e-42:200:38//HOMO SAPIENS (HUMAN).//P51522

F-NT2RM1001102//HYPOTHETICAL 62.8 KD PROTEIN IN TAF145-YOR1 INTERGENIC REGION.//1.7e-18:161:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53331

F-NT2RM1001105//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//4.0e-05:157:35//STREPTOMYCES FRADIAE.//P20186

F-NT2RM1001121//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.18:20:55//BOS TAURUS (BOVINE).//P02313

F-NT2RM1001115

F-NT2RM1001139//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).//2.0e-25:156:46//PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).//P10496

F-NT2RM2000006//MITOCHONDRIAL RIBOSOMAL PROTEIN S12.//0.76:45:35//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//Q34940

F-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//3.9e-87:238:65//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25167

F-NT2RM2000030//TOXINS 1 AND 2.//0.98:21:42//TRIMERESURUS WAGLERI (WAGLER'S PIT VIPER) (TROPIDOLAEMUS WAGLERI).//P24335

F-NT2RM2000032//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!.//0.00059:53:49//HOMO SAPIENS (HUMAN).//P39188

F-NT2RM2000042//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//1.0:68:26//HOMO SAPIENS (HUMAN).//P22532

F-NT2RM2000092//HYPOTHETICAL 67.5 KD PROTEIN IN PRPS4-STE20 INTERGENIC REGION.//7.0e-11:80:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38748

F-NT2RM2000093//OVARY MATURATING PARSIN (OMP).//1.0:26:38//LOCUSTA MIGRATORIA (MIGRATORY LOCUST).//P80045

F-NT2RM2000101//HYPOTHETICAL 39.3 KD PROTEIN C02B8.6 IN CHROMOSOME X.//3.3e-09:56:35//CAENORHABDITIS ELEGANS.//Q11096

F-NT2RM2000124//CAMP-DEPENDENT PROTEIN KINASE, ALPHA-CATALYTIC SUBUNIT (EC 2.7.1.37) (PKA C-ALPHA).//3.1e-35:77:96//MUS MUSCULUS (MOUSE).//P05132

- F-NT2RM2000191//3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA)/J3.3e-05:181:27//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//Q23917
- F-NT2RM2000192//REPLICATION PROTEIN E1 (FRAGMENTS)/J0.019:148:25//COTTONTAIL RABBIT (SHOPE) PAPILLOMAVIRUS (STRAIN WASHINGTON B) (CRPV)/J51894
- 5 F-NT2RM2000239//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)/J0.00032:111:32//MUS MUSCULUS (MOUSE)//P05143
- F-NNNNNNNNNN//METALLOTHIONEIN-LIKE PROTEIN TYPE 2/J0.046:59:33//LYCOPERSICON ESCULENTUM (TOMATO)//Q43512
- 10 F-NT2RM2000250//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29)/J0.054:46:34//RATTUS NORVEGICUS (RAT)//P08699
- F-NT2RM2000259//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6)/J0.27:112:33//BOVINE HERPES VIRUS TYPE 1 (STRAIN JURA)//P29128
- 15 F-NT2RM2000260//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)/J4.7e-22:191:35//MUS MUSCULUS (MOUSE)//P05143
- F-NT2RM2000287//HYPOTHETICAL 11.8 KD PROTEIN C1B3.02C IN CHROMOSOME I/J5.0e-19:83:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)/J013868
- F-NT2RM2000322//DIAMINOPIMELATE DECARBOXYLASE (EC 4.1.1.20) (DAP DECARBOXYLASE)/J0.47:117:29//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI)//P56129
- 20 F-NT2RM2000359//SPORE GERMINATION PROTEIN 270-11/J0.12:83:36//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P22698
- F-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN/J1.3e-16:203:30//HOMO SAPIENS (HUMAN)//P11274
- F-NT2RM2000368//DEK PROTEIN/J0.00027:100:32//HOMO SAPIENS (HUMAN)//P35659
- 25 F-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE PHOSPHORYLASE) (PNPASE)/J6.8e-36:170:47//ESCHERICHIA COLI//P05055
- F-NT2RM2000374//NODAL PRECURSOR/J1.1e-32:64:95//MUS MUSCULUS (MOUSE)//P43021
- F-NT2RM2000395//IMMEDIATE-EARLY PROTEIN IE180/J0.31:41:43//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV)//P11675
- 30 F-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT)/J1.2e-30:228:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32802
- F-NT2RM2000407//TRANSMEMBRANE PROTEIN SEX PRECURSOR/J0.032:105:30//HOMO SAPIENS (HUMAN)//P51805
- 35 F-NT2RM2000420//METALLOTHIONEIN (MT)/J0.88:42:38//PLEURONECTES PLATESSA (PLAICE)/J07216
- F-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73/J2.0e-117:237:87//RATTUS NORVEGICUS (RAT)//Q08469
- F-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC-BINDING/J1.1e-08:157:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36113
- 40 F-NT2RM2000469//70 KD ANTIGEN/J0.050:207:23//SHIGELLA FLEXNERI//P18010
- F-NT2RM2000490//BASIC PROLINE-RICH PEPTIDE P-E (IB-9)/J0.022:25:44//HOMO SAPIENS (HUMAN)//P02811
- F-NT2RM2000502//MALE SPECIFIC SPERM PROTEIN MST84DD/J0.0037:17:58//DROSOPHILA MELANOGASTER (FRUIT FLY)/JQ01645
- 45 F-NT2RM2000504//HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17/J1.7e-22:195:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)/J042908
- F-NT2RM2000522//RAS-RELATED PROTEIN RABA (FRAGMENT)/J3.6e-05:67:29//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)/P34141
- 50 F-NT2RM2000540//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III/J8.4e-33:214:38//CAENORHABDITIS ELEGANS//Q18262
- F-NT2RM2000556//HYPOTHETICAL PROTEIN KIAA0288 (HA6116)/J1.7e-09:133:36//HOMO SAPIENS (HUMAN)//P56524
- F-NT2RM2000566//INTEGRIN ALPHA-6 PRECURSOR (VLA-6) (CD49F)/J2.2e-60:244:51//HOMO SAPIENS (HUMAN)/P23229
- 55 F-NT2RM2000567//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)/J2.3e-09:192:34//MUS MUSCULUS (MOUSE)//P05143
- F-NT2RM2000569/////ALU SUBFAMILY J WARNING ENTRY!!!!/J9.0e-08:43:72//HOMO SAPIENS (HUMAN)/P39188



F-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS).//  
 9.1e-54:225:45//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73505  
 F-NT2RM2000581//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.079:111:34//HOMO SAPIENS (HUMAN).//Q15427  
 5 F-NT2RM2000588//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//2.3e-09:193:32//HOMO SAPIENS (HUMAN).//P56524  
 F-NT2RM2000594//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.18:33:42//HOMO SAPIENS (HUMAN).//P02811  
 10 F-NT2RM2000599//DNA (CYTOSINE-5)-METHYLTRANSFERASE (EC 2.1.1.37) (DNA METHYLTRANSFERASE) (DNA METASE) (MCMT) (M.MMUJ).//1.5e-09:68:45//MUS MUSCULUS (MOUSE).//P13864  
 F-NT2RM2000609//GRANULIN 2.//0.83:42:35//CYPRINUS CARPIO (COMMON CARP).//P81014  
 F-NT2RM2000612//ZINC FINGER PROTEIN GCS1.//7.2e-05:155:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35197  
 15 F-NT2RM2000623//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//1.8e-09:196:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323  
 F-NT2RM2000624//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.070:113:27//DROSOPHILA ERECTA (FRUIT FLY).//P13730  
 F-NT2RM2000635//SPERM PROTAMINE P1.//0.54:47:38//ANTECHINUS STUARTII.//P42129  
 20 F-NT2RM2000636//OUTER MEMBRANE PROTEIN H.8 PRECURSOR.//0.096:62:35//NEISSERIA GONORRHOEA.//P11910  
 F-NT2RM2000639//HYPOTHETICAL PROTEIN MJ0243.//0.99:32:34//METHANOCOCCUS JANNASCHII.//Q57694  
 F-NT2RM2000649//NEURONAL CALCIUM SENSOR 1 (NCS-1).//0.00049:70:35//RATTUS NORVEGICUS (RAT), AND GALLUS GALLUS (CHICKEN).//P36610  
 25 F-NT2RM2000669//50S RIBOSOMAL PROTEIN L34.//1.0:34:44//BACILLUS SUBTILIS.//P05647  
 F-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//7.0e-116:243:87//HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE).//P32391  
 F-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-I).//3.8e-21:174:35//HOMO SAPIENS (HUMAN).//Q15404  
 30 F-NT2RM2000718//HYPOTHETICAL 52.9 KD SERINE-RICH PROTEIN C11G7.01 IN CHROMOSOME I.//0.0022:174:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q13695  
 F-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.6e-102:246:74//HOMO SAPIENS (HUMAN).//P28160  
 F-NT2RM2000740//HYPOTHETICAL 131.1 KD HELICASE IN ALG7-ENP1 INTERGENIC REGION.//8.5e-51:212:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38144  
 35 F-NT2RM2000795//ALU SUBFAMILY SB WARNING ENTRY.//9.0e-41:125:53//HOMO SAPIENS (HUMAN).//P39189  
 F-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP).//1.1e-128:291:89//RATTUS NORVEGICUS (RAT).//P23514  
 40 F-NT2RM2000837//CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR P57) (P57KIP2).//3.9e-05:113:36//HOMO SAPIENS (HUMAN).//P49918  
 F-NT2RM2000851//HYPOTHETICAL 60.3 KD PROTEIN R08D7.7 IN CHROMOSOME III.//2.5e-49:273:39//CAENORHABDITIS ELEGANS.//P30646  
 45 F-NT2RM2000952//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H) (FRAGMENT).//0.037:234:23//RATTUS NORVEGICUS (RAT).//P16884  
 F-NT2RM2000984//HYPOTHETICAL 54.7 KD PROTEIN F37A4.1 IN CHROMOSOME III.//6.3e-44:216:43//CAENORHABDITIS ELEGANS.//P41879  
 F-NT2RM2001004//SYNAPSINS IA AND IB.//0.15:178:32//RATTUS NORVEGICUS (RAT).//P09951  
 50 F-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.4e-87:188:90//MUS MUSCULUS (MOUSE).//Q60809  
 F-NT2RM2001065//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.53:122:31//TRYPANOSOMA BRUCEI BRUCEI.//P24499  
 F-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//3.4e-13:171:30//CAENORHABDITIS ELEGANS.//P46577  
 55 F-NT2RM2001105//SPORE COAT PROTEIN SP96.//7.8e-06:141:34//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P14328  
 F-NT2RM2001131//PROBABLE EUKARYOTIC INITIATION FACTOR C17C9.03.//2.3e-18:249:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10475

F-NT2RM2001141//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.//0.050:134:26//  
CAENORHABDITIS ELEGANS.//P34681  
F-NT2RM2001152  
5 F-NT2RM2001177//COLLAGEN ALPHA 1(XIV) CHAIN PRECURSOR (UNDULIN).//0.86:42:40//GALLUS GAL-  
LUS (CHICKEN).//P32018  
F-NT2RM2001194//SMOOTHENIN.//4.7e-05:77:32//HOMO SAPIENS (HUMAN).//P53814  
F-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.7e-18:218:35//MUS MUSCULUS  
(MOUSE).//P05143  
10 F-NT2RM2001201//CYSTEINE STRING PROTEIN (CCCS1).//0.041:22:59//TORPEDO CALIFORNICA (PACIFIC  
ELECTRIC RAY).//P56101  
F-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10).//1.3e-13:183:32//  
RATTUS NORVEGICUS (RAT).//P97924  
F-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMI-  
DOHYDROLASE).//6.5e-121:218:98//RATTUS NORVEGICUS (RAT).//P13264  
15 F-NT2RM2001243//HYPOTHETICAL 200.0 KD PROTEIN IN GZF3-IME2 INTERGENIC REGION.//0.00019:177:  
27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42945  
F-NT2RM2001247//LEGUMIN B (FRAGMENT).//0.22:54:35//PISUM SATIVUM (GARDEN PEA).//P14594  
F-NT2RM2001256//PROTEIN TSG4 (MEIOTIC CHECK POINT REGULATOR).//1.8e-109:207:98//MUS MUS-  
CULUS (MOUSE).//P53995  
20 F-NT2RM2001291//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.016:22:40//HOMO SAPIENS  
(HUMAN).//P22531  
F-NT2RM2001306//REF(2)P PROTEIN.//0.61:51:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//P14199  
F-NT2RM2001312//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//7.2e-11:33:72//HOMO SAPIENS (HUMAN).//  
P39195  
25 F-NT2RM2001319  
F-NT2RM2001324//ZYXIN.//5.1e-22:91:38//GALLUS GALLUS (CHICKEN).//Q04584  
F-NT2RM2001345//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//7.4e-10:159:27//PODOSPORA AN-  
SERINA.//Q00808  
F-NT2RM2001360//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONIAL PEPTIDE B).//1.0:27:48//  
30 DROSOPHILA MELANOGASTER (FRUIT FLY).//P05623  
F-NT2RM2001370//NAPE PROTEIN.//0.98:44:31//PARACOCCLUS DENITRIFICANS (SUBSP. THIOSPHAERA  
PANTOTROPHA).//Q56348  
F-NT2RM2001393//VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN  
LV-1C; LIPOVITELLIN LV-2].//0.0024:163:31//ICHTHYOMYZON UNICUSPUS (SILVER LAMPREY).//Q91062  
35 F-NT2RM2001420  
F-NT2RM2001424//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U).//2.4e-41:140:59//  
HOMO SAPIENS (HUMAN).//Q00839  
F-NT2RM2001499//HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+  
BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR)  
40 (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG).//3.7e-71:201:68//HOMO SAPIENS (HUMAN).//P30825  
F-NT2RM2001504//CUTICLE COLLAGEN 2.//0.028:41:39//CAENORHABDITIS ELEGANS.//P17656  
F-NT2RM2001524//HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III.//6.7e-47:190:42//  
CAENORHABDITIS ELEGANS.//Q09316  
45 F-NT2RM2001544//TELOMERE-BINDING PROTEIN 51 KD SUBUNIT.//0.0027:136:33//EUPLOTES  
CRASSUS.//Q06184  
F-NT2RM2001547//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION.//8.5e-18:91:50//  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40564  
F-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//3.9e-  
35:212:41//HOMO SAPIENS (HUMAN).//P19474  
50 F-NT2RM2001582//RESA PROTEIN.//0.0033:72:27//BACILLUS SUBTILIS.//P35160  
F-NT2RM2001588//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//1.0e-06:115:32//ZEA MAYS  
(MAIZE).//P14918  
F-NT2RM2001592//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.033:156:23//HO-  
MO SAPIENS (HUMAN).//P26371  
55 F-NT2RM2001605//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2).//1.1e-116:249:82//HOMO SAPIENS  
(HUMAN).//P29375  
F-NT2RM2001613//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.2e-97:192:100//RATTUS  
NORVEGICUS (RAT).//P38378

F-NT2RM2001632//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.00068:145:28//SACCHARO-  
 MYCES CEREVISIAE (BAKER'S YEAST).//P32323  
 F-NT2RM2001635//NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PRO-  
 TEIN OF 121 KD) (P145).//1.1e-39:235:47//RATTUS NORVEGICUS (RAT).//P52591  
 5 F-NT2RM2001637//HYPOTHETICAL BHLF1 PROTEIN.//0.075:197:29//EPSTEIN-BARR VIRUS (STRAIN B95-8)  
 (HUMAN HERPESVIRUS 4).//P03181  
 F-NT2RM2001641//NADH-CYTOCHROME B5 REDUCTASE (EC 1.6.2.2) (B5R).//0.013:29:68//HOMO SAPIENS  
 (HUMAN).//P00387  
 10 F-NT2RM2001648//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//3.2e-65:132:100//CANIS FA-  
 MILIARIS (DOG).//P38377  
 F-NT2RM2001652//PROTEIN TRANSPORT PROTEIN SEC7.//1.6e-32:261:32//SACCHAROMYCES CEREVI-  
 SIAE (BAKER'S YEAST).//P11075  
 F-NT2RM2001659//CARBOXYPEPTIDASE A INHIBITOR.//0.83:30:46//ASCARIS SUUM (PIG ROUNDWORM)  
 (ASCARIS LUMBRICOIDES).//P19399  
 15 F-NT2RM2001664//HK13 PROTEIN.//1.3e-31:265:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
 Q06706  
 F-NT2RM2001668//TONB PROTEIN.//0.32:39:41//XANTHOMONAS CAMPESTRIS (PV. CAMPESTRIS).//  
 Q34261  
 F-NT2RM2001670//ZINC FINGER PROTEIN 174.//3.6e-21:172:39//HOMO SAPIENS (HUMAN).//Q15697  
 20 F-NT2RM2001671//HYPOTHETICAL 118.6 KD PROTEIN C29E6.03C IN CHROMOSOME I.//1.6e-10:229:24//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09857  
 F-NT2RM2001675//DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52) (DHDS).//1.0:184:21//METHANO-  
 COCCUS JANNASCHII.//Q57695  
 F-NT2RM2001681//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//0.0039:199:22//  
 25 DROSOPHILA MELANOGASTER (FRUIT FLY).//P54399  
 F-NT2RM2001688//HYPOTHETICAL 28.1 KD PROTEIN IN SIPU-PBPC INTERGENIC REGION.//2.6e-21:162:  
 33//BACILLUS SUBTILIS.//P42966  
 F-NT2RM2001695//ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.9e-41:60:81//HOMO SAPIENS (HUMAN).//  
 P39194  
 30 F-NT2RM2001696//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//9.8e-16:126:38//  
 AUTOGRAPHICA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMPNV).//P41479  
 F-NT2RM2001698//PENAEIDIN-3B PRECURSOR (P3-B).//0.36:52:34//PENAEUS VANNAMEI (PENOEID  
 SHRIMP) (EUROPEAN WHITE SHRIMP).//P81059  
 35 F-NT2RM2001699//TRANSCRIPTION INITIATION FACTOR TFIID 30 KD SUBUNIT (TAFII-30) (TAFII30).//  
 0.0012:79:40//HOMO SAPIENS (HUMAN).//Q12962  
 F-NT2RM2001700//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VLCAD)  
 (FRAGMENT).//1.0e-30:140:53//MUS MUSCULUS (MOUSE).//P50544  
 F-NT2RM2001706//ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.5e-33:95:75//HOMO SAPIENS (HUMAN).//  
 P39195  
 40 F-NT2RM2001716//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECUR-  
 SOR.//0.010:116:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47179  
 F-NT2RM2001718//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB.//0.00029:77:37//BACILLUS SUBTI-  
 LIS.//P39217  
 45 F-NT2RM2001723//POSTERIOR PITUITARY PEPTIDE.//0.94:26:53//BOS TAURUS (BOVINE).//P01154  
 F-NT2RM2001727//E7 PROTEIN.//0.91:46:34//HUMAN PAPILLOMAVIRUS TYPE 23.//P50781  
 F-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15)  
 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-  
 ZYME).//4.9e-07:139:29//CAENORHABDITIS ELEGANS.//Q09931  
 50 F-NT2RM2001743//PROENKEPHALIN A PRECURSOR.//0.75:65:35//CAVIA PORCELLUS (GUINEA PIG).//  
 P47969  
 F-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210.//1.5e-14:119:36//HOMO SAPIENS (HUMAN).//  
 Q92609  
 F-NT2RM2001760//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//8.3e-58:119:99//CANIS FA-  
 MILIARIS (DOG).//P38377  
 55 F-NT2RM2001768//HYPOTHETICAL PROTEIN UL25.//0.45:77:32//HUMAN CYTOMEGALOVIRUS (STRAIN  
 AD169).//P16761  
 F-NT2RM2001771//ZINC FINGER PROTEIN 135.//4.6e-80:224:60//HOMO SAPIENS (HUMAN).//P52742  
 F-NT2RM2001782//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-

- PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//7.0e-06:61:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41940
- F-NT2RM2001784//HYPOTHETICAL PROTEIN UL61.//0.00070:145:33//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818
- 5 F-NT2RM2001785//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE).//1.5e-08:127:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q08871
- F-NT2RM2001797//ZINC FINGER PROTEIN 135.//1.6e-73:267:49//HOMO SAPIENS (HUMAN).//P52742
- F-NT2RM2001800//HYPOTHETICAL HELICASE MG018/MG017/MG016 HOMOLOG.//3.9e-12:171:33//MYCOPLASMA PNEUMONIAE.//P75093
- 10 F-NT2RM2001803//IKI3 PROTEIN.//1.6e-38:283:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06706
- F-NT2RM2001805//KOLD SHOCK-LIKE PROTEIN CSPH.//0.51:46:32//SALMONELLA TYPHIMURIUM.//Q33793
- 15 F-NT2RM2001813//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHROMOSOME III.//5.0e-05:82:32//CAENORHABDITIS ELEGANS.//Q17963
- F-NT2RM2001823//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2).//3.6e-49:233:45//HOMO SAPIENS (HUMAN).//O14647
- F-NT2RM2001839//RETICULOCALBIN 1 PRECURSOR.//5.2e-65:222:56//HOMO SAPIENS (HUMAN).//Q15293
- F-NT2RM2001840//ALU SUBFAMILY SQ WARNING ENTRY.//9.6e-33:102:68//HOMO SAPIENS (HUMAN).//P39194
- 20 F-NT2RM2001855//BASP1 PROTEIN.//0.054:120:30//HOMO SAPIENS (HUMAN).//P80723
- F-NT2RM2001867//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//4.1e-19:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867
- F-NT2RM2001879//HYPOTHETICAL 47.3 KD PROTEIN C22G7.07C IN CHROMOSOME I.//5.9e-15:76:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09800
- 25 F-NT2RM2001886//HYPOTHETICAL 126.9 KD PROTEIN C22G7.04 IN CHROMOSOME I.//1.4e-41:249:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09798
- F-NT2RM2001898//HYPOTHETICAL 83.2 KD PROTEIN IN KAR4-PBN1 INTERGENIC REGION.//2.1e-59:197:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25582
- 30 F-NT2RM2001903//HYPOTHETICAL PROTEIN MJ0263.//0.070:132:31//METHANOCOCCUS JANNASCHII.//O06917
- F-NT2RM2001930//THROMBOSPONDIN 2 PRECURSOR.//7.1e-05:53:47//MUS MUSCULUS (MOUSE).//Q03350
- 35 F-NT2RM2001935//PUTATIVE CUTICLE COLLAGEN F55C10.3.//0.00046:116:35//CAENORHABDITIS ELEGANS.//Q21184
- F-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//4.5e-27:216:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P28320
- F-NT2RM2001950//HIRUDIN HV1 (BUFRUDIN).//0.59:43:34//HIRUDINARIA MANILLENSIS (BUFFALO LEECH).//P81492
- 40 F-NT2RM2001982//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)(G)(S)(G)(O) GAMMA-8 SUBUNIT (G GAMMA-C).//0.72:35:42//BOS TAURUS (BOVINE).//P50154
- F-NT2RM2001983//PROLINE-RICH PEPTIDE P-B.//0.00035:23:52//HOMO SAPIENS (HUMAN).//P02814
- F-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//8.6e-24:197:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P37838
- 45 F-NT2RM2001997
- F-NT2RM2001998//IMMEDIATE-EARLY PROTEIN IE180.//0.076:92:27//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675
- F-NT2RM2002004//SLF1 PROTEIN.//3.5e-06:235:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12034
- 50 F-NT2RM2002014//HYPOTHETICAL PROTEIN HI0568.//2.1e-17:235:29//HAEMOPHILUS INFLUENZAE.//P71353
- F-NT2RM2002030//GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZING] (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GFAT).//9.5e-105:271:76//MUS MUSCULUS (MOUSE).//P47856
- 55 F-NT2RM2002049//SMALL PROLINE-RICH PROTEIN 2-1.//0.099:41:41//HOMO SAPIENS (HUMAN).//P35326
- F-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.012:217:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q07878
- F-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//

- 1.1e-09:65:53//MUS MUSCULUS (MOUSE).//Q61990  
 F-NT2RM2002091//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.072:74:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214
- 5 F-NT2RM2002100//ATP-DEPENDENT RNA HELICASE ROK1.//4.5e-50:289:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P45818  
 F-NT2RM2002109//NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C).//1.4e-14:203:32//RATTUS NORVEGICUS (RAT).//Q03351  
 F-NT2RM2002128//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.0025:139:31//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437
- 10 F-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//9.2e-20:42:73//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//P47805  
 F-NT2RM2002145//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT 12 PRECURSOR.//0.0085:200:26//TRITICUM AESTIVUM (WHEAT).//P08488  
 F-NT2RM2002178//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//5.8e-05:56:39//BOS TAURUS (BOVINE).//P25508
- 15 F-NT2RM2002580//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//2.9e-14:96:37//PETROMYZON MARINUS (SEA LAMPREY).//P25210  
 F-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//8.6e-95:271:67//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25167
- 20 F-NT2RM4000027//INTERFERON-ACTIVABLE PROTEIN 202 (IFI-202).//0.99:72:31//MUS MUSCULUS (MOUSE).//P15091  
 F-NT2RM4000030//LAS1 PROTEIN.//1.4e-14:184:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36146
- 25 F-NT2RM4000046//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.99:120:28//RATTUS NORVEGICUS (RAT).//P13941  
 F-NT2RM4000061  
 F-NT2RM4000085//ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (NDH II) (DEAD BOX PROTEIN 9) (MHEL-5).//8.5e-40:263:38//MUS MUSCULUS (MOUSE).//O70133
- 30 F-NT2RM4000086//HYPOTHETICAL PROTEIN HI1497.//1.0:27:37//HAEMOPHILUS INFLUENZAE.//P44221  
 F-NT2RM4000104//ZINC FINGER PROTEIN 134.//1.0e-26:64:56//HOMO SAPIENS (HUMAN).//P52741  
 F-NT2RM4000139//PREPROTEIN TRANSLOCASE SECE SUBUNIT.//0.99:38:42//THERMOTOGA MARITIMA.//P35874
- 35 F-NT2RM4000155//THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE--TRNA LIGASE) (THRRS).//6.3e-34:181:40//HOMO SAPIENS (HUMAN).//P26639  
 F-NT2RM4000156//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//4.6e-12:142:33//NICOTIANA TABACUM (COMMON TOBACCO).//P13983  
 F-NT2RM4000167//KINESIN-LIKE PROTEIN KIF4.//3.4e-123:269:91//MUS MUSCULUS (MOUSE).//P33174
- 40 F-NT2RM4000169//M PROTEIN, SEROTYPE 2.2 PRECURSOR.//9.7e-10:229:26//STREPTOCOCCUS PYOGENES.//P50469  
 F-NT2RM4000191//P68-LIKE PROTEIN.//2.1e-11:104:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P24783  
 F-NT2RM4000197//CUTICLE PROTEIN CP463 (CPCP463).//0.84:29:37//CANCER PAGURUS (ROCK CRAB).//P81587
- 45 F-NT2RM4000199//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//1.8e-06:187:34//HOMO SAPIENS (HUMAN).//P10162  
 F-NT2RM4000200//HYPOTHETICAL 9.4 KD PROTEIN IN FLA1 3'REGION (ORF3).//0.52:42:40//BACILLUS LICHENIFORMIS.//P22754  
 F-NT2RM4000202//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN).//0.00044:168:32//ORYCTOLAGUS CUNICULUS (RABBIT).//P14282
- 50 F-NT2RM4000210//EXTENSIN PRECURSOR.//0.27:129:27//DAUCUS CAROTA (CARROT).//P06599  
 F-NT2RM4000215//MAK16 PROTEIN.//2.0e-65:234:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P10962  
 F-NT2RM4000229//GAR2 PROTEIN.//0.13:217:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891
- 55 F-NT2RM4000233//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.047:108:30//HOMO SAPIENS (HUMAN).//P51805  
 F-NT2RM4000244//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.67:59:27//BALAENOPTERA

PHYSALUS (FINBACK WHALE) (COMMON RORQUAL).//P24947  
 F-NT2RM4000251//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.0059:108:35//MUS MUSCULUS (MOUSE).//P05143  
 F-NT2RM4000265//ALU SUBFAMILY J WARNING ENTRY !!!!!/8.1e-38:70:70//HOMO SAPIENS (HUMAN).//P39188  
 F-NT2RM4000290//TRANSDUCIN-LIKE ENHANCER PROTEIN 3 (ESG3).//1.6e-115:209:94//HOMO SAPIENS (HUMAN).//Q04726  
 F-NT2RM4000324//PRESPORE PROTEIN DP87 PRECURSOR.//0.14:136:30//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//Q04503  
 F-NT2RM4000327//HYPOTHETICAL 8.9 KD PROTEIN IN IE0-IE1 INTERGENIC REGION.//0.91:73:28//AUTOGRAPH CALIFORNIA NUCLEAR POLYHEDROSIS VIRUS (ACMPNV).//P41703  
 F-NT2RM4000344//YME1 PROTEIN HOMOLOG (EC 3.4.24.-).//9.4e-78:241:55//CAENORHABDITIS ELEGANS.//P54813  
 F-NT2RM4000349//CYSTEINE STRING PROTEIN (CCCS1).//0.055:22:59//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P56101  
 F-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//4.6e-26:208:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24371  
 F-NT2RM4000356//COAT PROTEIN.//0.11:105:36//SATELLITE TOBACCO MOSAIC VIRUS (STMV).//P17574  
 F-NT2RM4000366//IMMEDIATE-EARLY PROTEIN.//1.2e-05:215:24//HERPES VIRUS SAIMIRI (STRAIN 11).//Q01042  
 F-NT2RM4000368//HYPOTHETICAL 7.3 KD PROTEIN IN RPBA-GP46 INTERGENIC REGION.//0.54:46:36//BACTERIOPHAGE RB69.//O64300  
 F-NT2RM4000386//RHSC PROTEIN PRECURSOR.//0.0096:162:29//ESCHERICHIA COLI.//P16918  
 F-NT2RM4000395//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION.//4.5e-66:256:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43616  
 F-NT2RM4000414//HYPOTHETICAL 6.0 KD PROTEIN IN TH12 5'REGION.//0.13:33:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53820  
 F-NT2RM4000421//MRNA TRANSPORT REGULATOR MTR10.//5.0e-13:171:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q99189  
 F-NT2RM4000425//ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.1e-25:46:80//HOMO SAPIENS (HUMAN).//P39193  
 F-NT2RM4000433//CUTICLE COLLAGEN 3A3.//2.5e-06:77:38//HAEMONCHUS CONTORTUS.//P16253  
 F-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//4.3e-09:215:22//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10297  
 F-NT2RM4000471//TRNA SPLICING PROTEIN SPL1.//6.7e-73:163:65//CANDIDA ALBICANS (YEAST).//P87185  
 F-NT2RM4000486//COLLAGEN ALPHA 2(VI) CHAIN PRECURSOR.//0.0012:121:34//GALLUS GALLUS (CHICKEN).//P15988  
 F-NT2RM4000496//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RNA POLYMERASE II SUBUNIT 1).//5.9e-09:175:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P36594  
 F-NT2RM4000511//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.020:122:31//DROSOPHILA SIMULANS (FRUIT FLY).//P13729  
 F-NT2RM4000514//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.46:68:32//ARTEMIA SANFRANCISCANA (BRINE SHRIMP) (ARTEMIA FRANCISCANA).//Q37708  
 F-NT2RM4000515//GAR2 PROTEIN.//3.2e-05:198:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891  
 F-NT2RM4000520//HYPOTHETICAL 7.5 KD PROTEIN (ORF 63).//0.011:55:38//SPINACIA OLERACEA (SPINACH).//P08974  
 F-NT2RM4000531//ZINC FINGER PROTEIN 169 (FRAGMENT).//3.6e-44:244:42//HOMO SAPIENS (HUMAN).//Q14929  
 F-NT2RM4000532//PUTATIVE MEMBRANE PROTEIN 53.//1.0:47:34//HERPES VIRUS SAIMIRI (STRAIN 11).//Q01049  
 F-NT2RM4000534//HYPOTHETICAL 5.9 KD PROTEIN IN WRBA-PUTA INTERGENIC REGION.//0.75:26:46//ESCHERICHIA COLI.//P56614  
 F-NT2RM4000585//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P16: CORE PROTEIN P26].//0.019:86:34//HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE SBLIS Y) (HIV-2).//P12450  
 F-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).//5.0e-23:224:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

- F-NT2RM4000595//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III.//3.8e-62:226:50//CAENORHABDITIS ELEGANS.//P34284
- F-NT2RM4000603//SRC SUBSTRATE CORTACTIN (EMSL ONCOGENE).//0.077:132:22//HOMO SAPIENS (HUMAN).//Q14247
- 5 F-NT2RM4000611//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHROMOSOME III.//1.9e-06:82:32//CAENORHABDITIS ELEGANS.//Q17963
- F-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//5.3e-79:213:62//ESCHERICHIA COLI.//P27550
- 10 F-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL1374.//1.3e-11:147:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P74168
- F-NT2RM4000689
- F-NT2RM4000698//CHORION CLASS HIGH-CYSTEINE HCA PROTEIN 12 PRECURSOR (HC-A.12).//0.26:45:33//BOMBYX MORI (SILK MOTH).//P05687
- 15 F-NT2RM4000700//THIOPHENE AND FURAN OXIDATION PROTEIN THDF.//0.95:165:25//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//P53364
- F-NT2RM4000712//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//2.2e-82:152:63//CAENORHABDITIS ELEGANS.//P34547
- 20 F-NT2RM4000717//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.80:54:40//DROSOPHILA SIMULANS (FRUIT FLY).//P13729
- F-NT2RM4000733//OCTAPEPTIDE-REPEAT PROTEIN T2.//1.5e-08:139:28//MUS MUSCULUS (MOUSE).//Q06666
- F-NT2RM4000734//GASTRULA ZINC FINGER PROTEIN XLCGF26.1 (FRAGMENT).//7.2e-20:205:28//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18715
- 25 F-NT2RM4000741//SPERM PROTAMINE P1.//0.89:52:38//ISOODON MACROURUS (SHORT-NOSED BANDICOOT).//P42136
- F-NT2RM4000751//ZINC FINGER PROTEIN 26 (ZFP-26) (MKR3 PROTEIN) (FRAGMENT).//5.2e-77:246:52//MUS MUSCULUS (MOUSE).//P10076
- 30 F-NT2RM4000764//KERATIN, GLYCINE/TYROSINE-RICH OF HAIR.//0.062:33:42//OVIS ARIES (SHEEP).//Q02958
- F-NT2RM4000778
- F-NT2RM4000779//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.014:53:45//VOLVOX CARTERI.//P21997
- 35 F-NT2RM4000787//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).//0.00011:73:39//MUS MUSCULUS (MOUSE).//P98063
- F-NT2RM4000790//SPORE COAT PROTEIN SP96.//0.00083:157:29//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P14328
- F-NT2RM4000795//CHOLINESTERASE PRECURSOR (EC 3.1.1.8) (ACYLCHOLINE ACYLHYDROLASE) (CHOLINE ESTERASE II) (BUTYRYLCHOLINE ESTERASE) (PSEUDOCOLINESTERASE).//7.4e-41:271:36//HOMO SAPIENS (HUMAN).//P06276
- 40 F-NT2RM4000796//5-METHYLCYTOSINE-SPECIFIC RESTRICTION ENZYME B (EC 3.1.21.-).//0.28:82:30//ESCHERICHIA COLI.//P15005
- F-NT2RM4000798//PROTEIN TRANSPORT PROTEIN SEC7.//4.7e-38:165:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11075
- 45 F-NT2RM4000813//METALLOTHIONEIN-IB.//0.0025:25:44//OVIS ARIES (SHEEP).//P09577
- F-NT2RM4000820
- F-NT2RM4000833//HYPOTHETICAL PROTEIN MJ1136.//6.5e-42:206:41//METHANOCOCCUS JANNASCHII.//Q58536
- 50 F-NT2RM4000848//BRAIN-SPECIFIC HOMEOBOX/POU DOMAIN PROTEIN 3A (BRN-3A) (BRN-3.0).//0.00060:159:33//MUS MUSCULUS (MOUSE).//P17208
- F-NT2RM4000852//SMALL PROLINE-RICH PROTEIN 2B (SPR-2B).//0.0076:13:69//HOMO SAPIENS (HUMAN).//P35325
- F-NT2RM4000855//ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.0060:68:44//HOMO SAPIENS (HUMAN).//P39194
- 55 F-NT2RM4000887//RTS1 PROTEIN (SCS1 PROTEIN).//0.23:153:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38903
- F-NT2RM4000895//HYPOTHETICAL 53.5 KD PROTEIN IN PHO2-POL3 INTERGENIC REGION.//3.3e-09:80:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43123

- F-NT2RM4000950//HYPOTHETICAL PROTEIN MJ0572 //0.090:68:29//METHANOCOCCUS JANNASCHII // Q57992
- F-NT2RM4000971//KINESIN LIGHT CHAIN (KLC) //0.79:201:24//LOLIGO PEALEII (LONGFIN SQUID) //P46825
- 5 F-NT2RM4000979//MYOSIN REGULATORY LIGHT CHAIN 2, NONSARCOMERIC (MYOSIN RLC) //1.2e-07:25:96//HOMO SAPIENS (HUMAN) //P19105
- F-NT2RM4000996//ZINC FINGER PROTEIN 37 (ZFP-37) (MALE GERM CELL SPECIFIC ZINC FINGER PROTEIN) //1.4e-56:253:46//MUS MUSCULUS (MOUSE) //P17141
- F-NT2RM4001002
- 10 F-NT2RM4001016//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30] //0.25:101:31//FBR MURINE OSTEOSARCOMA VIRUS //P29175
- F-NT2RM4001032//CUTICLE COLLAGEN 2 //2.6e-07:130:39//CAENORHABDITIS ELEGANS //P17656
- F-NT2RM4001047//MO25 PROTEIN //5.6e-107:252:80//MUS MUSCULUS (MOUSE) //Q06138
- F-NT2RM4001054//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT //9.0e-109:209:94//CANIS FAMILIARIS (DOG) //P38377
- 15 F-NT2RM4001084//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN UXUR-IADA INTERGENIC REGION //0.57:95:30//ESCHERICHIA COLI //P39376
- F-NT2RM4001092//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III //2.5e-47:231:47//CAENORHABDITIS ELEGANS //Q09531
- F-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II //1.3e-08:243:23//CAENORHABDITIS ELEGANS //Q09417
- 20 F-NT2RM4001140//HOMEOBOX PROTEIN MSH-D //7.1e-13:103:38//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO) //Q01704
- F-NT2RM4001151//SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1) //0.26:96:34//HOMO SAPIENS (HUMAN) //P17600
- 25 F-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN //3.6e-103:201:91//BOS TAURUS (BOVINE) //Q27969
- F-NT2RM4001160//GLUTATHIONE S-TRANSFERASE (EC 2.5.1.18) (CLASS-PHI) (FRAGMENTS) //1.0:33:36//BRASSICA OLERACEA (CAULIFLOWER) //P48438 F-NT2RM4001187//PREPROTEIN TRANSLOCASE SECA SUBUNIT //0.44:158:27//MYCOPLASMA GENITALIUM //P47318
- 30 F-NT2RM4001191//LONG NEUROTOXIN 2 (TOXIN C) //0.99:44:43//ASTROTIA STOKESI (STOKES'S SEA SNAKE) (DISTEIRA STOKES) //P01381
- F-NT2RM4001200//ZINC FINGER PROTEIN 135 //2.2e-82:245:59//HOMO SAPIENS (HUMAN) //P52742
- F-NT2RM4001203//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION //0.028:94:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P53214
- 35 F-NT2RM4001204//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66) //0.0096:182:34//HOMO SAPIENS (HUMAN) //Q15428
- F-NT2RM4001217//RING CANAL PROTEIN (KELCH PROTEIN) //2.1e-21:221:29//DROSOPHILA MELANOGASTER (FRUIT FLY) //Q04652
- 40 F-NT2RM4001256//CBP3 PROTEIN PRECURSOR //0.30:55:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P21560
- F-NT2RM4001258//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556 //0.00031:132:39//STREPTOMYCES FRADIAE //P20186
- F-NT2RM4001309//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT) //0.048:132:28//HOMO SAPIENS (HUMAN) //P02812
- 45 F-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-LIKE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-3-KINASE) (PI3K) //2.6e-37:124:65//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD) //P54676
- F-NT2RM4001316//ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.3) (MCAD) //1.7e-10:185:30//RATTUS NORVEGICUS (RAT) //P08503
- F-NT2RM4001320//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-CIOGENITAL DYSPLASIA PROTEIN HOMOLOG) //1.5e-08:197:26//MUS MUSCULUS (MOUSE) //P52734
- 50 F-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN) //7.7e-14:82:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P32626
- F-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOL1 INTERGENIC REGION //3.3e-16:128:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P53742
- 55 F-NT2RM4001347//HYPOTHETICAL 76.9 KD PROTEIN IN RPM2-TUB1 INTERGENIC REGION //0.067:111:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //Q04511
- F-NT2RM4001371
- F-NT2RM4001382//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR //1.0e-08:82:39//PLASMODIUM LOPHU-



- RAE.//P04929  
F-NT2RM4001384  
F-NT2RM4001410//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//2.1e-08:185:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
- 5 F-NT2RM4001411//EARLY NODULIN 20 PRECURSOR (N-20).//5.3e-05:105:38//MEDICAGO TRUNCATULA (BARREL MEDIC).//P93329  
F-NT2RM4001412//GTPASE-ACTIVATING PROTEIN (GAP) (RAS P21 PROTEIN ACTIVATOR) (P120GAP) (RASGAP).//6.2e-17:109:41//RATTUS NORVEGICUS (RAT).//P50904  
F-NT2RM4001414//ZINC FINGER PROTEIN 177.//8.3e-06:54:50//HOMO SAPIENS (HUMAN).//Q13360
- 10 F-NT2RM4001437//ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.1e-24:87:65//HOMO SAPIENS (HUMAN).//P39192  
F-NT2RM4001444//PROBABLE ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS) (FRAGMENT).//2.6e-45:197:47//CIONA INTESTINALIS.//Q94425  
F-NT2RM4001454//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT).//0.0060:95:29//HOMO SAPIENS (HUMAN).//Q15057
- 15 F-NT2RM4001455//PROBABLE E5B PROTEIN.//0.41:44:36//HUMAN PAPILLOMAVIRUS TYPE 6B.//P06461  
F-NT2RM4001483//ZINC FINGER PROTEIN 136.//1.7e-28:85:64//HOMO SAPIENS (HUMAN).//P52737  
F-NT2RM4001489//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.086:111:34//HOMO SAPIENS (HUMAN).//P23246
- 20 F-NT2RM4001519//ACID UREASE ALPHA SUBUNIT (EC 3.5.1.5) (UREA AMIDOHYDROLASE).//0.82:51:47//LACTOBACILLUS FERMENTUM.//P26929  
F-NT2RM4001522//TROPOMYOSIN.//0.030:117:23//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q02088  
F-NT2RM4001557
- 25 F-NT2RM4001565//HYPOTHETICAL 44.3 KD PROTEIN C1F7.07C IN CHROMOSOME I.//0.99:42:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09919  
F-NT2RM4001566//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//0.054:190:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
- 30 F-NT2RM4001569//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (ACTIVATED PROTEIN KINASE C RECEPTOR HOMOLOG).//0.72:64:31//TRYPAANOMA BRUCEI BRUCEI.//Q94775  
F-NT2RM4001582  
F-NT2RM4001592//DNA REPAIR PROTEIN RAD9.//0.00037:198:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P14737
- 35 F-NT2RM4001594//IMMEDIATE-EARLY PROTEIN IE180.//1.9e-05:147:34//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479  
F-NT2RM4001597//THIOL:DISULFIDE INTERCHANGE PROTEIN TLPA (CYTOCHROME C BIOGENESIS PROTEIN TLPA).//5.7e-06:122:29//BRADYRHIZOBIUM JAPONICUM.//P43221  
F-NT2RM4001605//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//1.7e-28:249:96//RATTUS NORVEGICUS (RAT).//P37199
- 40 F-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).//1.5e-35:128:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36024  
F-NT2RM4001629//MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE HOMOLOG 3).//5.8e-42:254:37//HOMO SAPIENS (HUMAN).//Q13368  
F-NT2RM4001650//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4).//0.62:19:57//GALLUS GALLUS (CHICKEN).//P17277
- 45 F-NT2RM4001662//PROTEIN KINASE C, ALPHA TYPE (EC 2.7.1.-) (PKC-ALPHA).//0.29:90:32//HOMO SAPIENS (HUMAN).//P17252  
F-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION.//1.1e-31:137:44//ESCHERICHIA COLI.//P37339  
F-NT2RM4001682//PROBABLE 60S RIBOSOMAL PROTEIN L22.//0.09:55:29//CAENORHABDITIS ELEGANS.//P52819
- 50 F-NT2RM4001710//HYPOTHETICAL PROTEIN KIAA0039 (FRAGMENT).//0.56:113:28//HOMO SAPIENS (HUMAN).//Q15054  
F-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT).//1.4e-108:255:77//HOMO SAPIENS (HUMAN).//Q14141  
F-NT2RM4001715//HYPOTHETICAL PROTEIN C19G10.16 IN CHROMOSOME I (FRAGMENT).//2.1e-36:148:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10342

- F-NT2RM4001731//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III.//1.1e-05:90:33//CAENORHABDITIS ELEGANS.//P34284
- F-NT2RM4001741//TALIN.//1.1e-106:208:99//MUS MUSCULUS (MOUSE).//P26039
- 5 F-NT2RM4001746//EBNA-1 NUCLEAR PROTEIN.//1.6e-09:155:38//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03211
- F-NT2RM4001754//COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR.//0.93:158:33//HOMO SAPIENS (HUMAN).//P29400
- F-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//5.1e-113:277:79//HOMO SAPIENS (HUMAN).//P27448
- 10 F-NT2RM4001776//MYOSIN I ALPHA (MMI-ALPHA).//2.2e-73:262:54//MUS MUSCULUS (MOUSE).//P46735
- F-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1) (FRAGMENT).//5.3e-26:169:39//MUS MUSCULUS (MOUSE).//P55200
- F-NT2RM4001810//MALE SPECIFIC SPERM PROTEIN MST84DB.//2.3e-05:68:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01843
- 15 F-NT2RM4001813//RHODOCETIN ALPHA SUBUNIT.//2.3e-05:115:34//AGKISTRODON RHODOSTOMA (MALAYAN PIT VIPER) (CALLOSELASMIA RHODOSTOMA).//P81397
- F-NT2RM4001819//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR) (CELL SURFACE GLYCOPROTEIN F4/80).//1.7e-06:159:25//MUS MUSCULUS (MOUSE).//Q61549
- 20 F-NT2RM4001823//ZINC FINGER PROTEIN ZIC1 (ZINC FINGER PROTEIN OF THE CEREBELLUM 1).//2.6e-18:114:40//MUS MUSCULUS (MOUSE).//P46684
- F-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//4.0e-81:253:59//HOMO SAPIENS (HUMAN).//P51523
- F-NT2RM4001836//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.21:176:30//NEPHILA CLAVIPES (ORB SPIDER).//P46804
- 25 F-NT2RM4001841//PROLINE-RICH PEPTIDE P-B.//0.046:27:40//HOMO SAPIENS (HUMAN).//P02814
- F-NT2RM4001842//HYPOTHETICAL 7.0 KD PROTEIN B03B8.1 IN CHROMOSOME III.//0.98:35:42//CAENORHABDITIS ELEGANS.//Q11104
- F-NT2RM4001856//HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION.//2.3e-37:242:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39722
- 30 F-NT2RM4001858//T-BOX PROTEIN VEGT (T-BOX PROTEIN BRAT) (T-BOX PROTEIN ANTIPODEAN).//1.8e-23:78:64//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P87377
- F-NT2RM4001865//NEURONAL CALCIUM SENSOR 2 (NCS-2).//0.012:83:28//CAENORHABDITIS ELEGANS.//P36609
- F-NT2RM4001876//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.//3.8e-10:242:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47179
- 35 F-NT2RM4001880//EC PROTEIN HOMOLOG.//0.22:59:32//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P93746
- F-NT2RM4001905//60S RIBOSOMAL PROTEIN L40 (CEP52).//0.57:20:60//HOMO SAPIENS (HUMAN), RAT, RATTUS NORVEGICUS (RAT), AND GALLUS GALLUS (CHICKEN).//P14793
- 40 F-NT2RM4001922
- F-NT2RM4001930//PUTATIVE GLUCOSYLTRANSFERASE C08B11.8 (EC 2.4.1.-).//5.5e-45:167:53//CAENORHABDITIS ELEGANS.//Q09226
- F-NT2RM4001938//RTOA PROTEIN (RATIO-A).//0.0036:120:32//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P54681
- 45 F-NT2RM4001940//IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-1 (FRAGMENT).//0.32:31:48//HOMO SAPIENS (HUMAN).//P78415
- F-NT2RM4001953//ALU SUBFAMILY SC WARNING ENTRY.//2.2e-43:56:85//HOMO SAPIENS (HUMAN).//P39192
- 50 F-NT2RM4001965//IG ALPHA-1 CHAIN C REGION.//0.56:73:34//GORILLA GORILLA GORILLA (LOWLAND GORILLA).//P20758
- F-NT2RM4001969//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//0.0016:140:27//HOMO SAPIENS (HUMAN).//P04280
- F-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.9e-21:103:51//HOMO SAPIENS (HUMAN).//P51523
- 55 F-NT2RM4001984//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.0034:50:40//MUS MUSCULUS (MOUSE).//P15974
- F-NT2RM4001987//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN).//6.9e-17:115:31//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q08180

- F-NT2RM4002013//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHROMOSOME V.//0.0062:117-28//CAENORHABDITIS ELEGANS.//Q23256
- F-NT2RM4002018//SPORE COAT PROTEIN SP96.//4.3e-06:203-28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P14328
- 5 F-NT2RM4002034//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//0.78:132-25//HOMO SAPIENS (HUMAN).//P98171
- F-NT2RM4002044//VITELLOGENIN I PRECURSOR (MINOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LVI); PHOSVITIN (PV); LIPOVITELLIN II (LVII); YGP42].//0.062:201-24//GALLUS GALLUS (CHICKEN).//P87498
- 10 F-NT2RM4002054//DUPLICATE PROCYCLIN.//0.0079:44-52//TRYPANOSOMA BRUCEI BRUCEI.//P14044
- F-NT2RM4002055//PUTATIVE Z PROTEIN.//0.82:39-30//OVIS ARIES (SHEEP).//P08105
- F-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE-TRNA LIGASE) (ASPRS).//7.0e-37:80:52//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P36419
- F-NT2RM4002063//SARCOSINE OXIDASE (EC 1.5.3.1).//2.2e-25:216:31//BACILLUS SP. (STRAIN NS-129).//P23342
- 15 F-NT2RM4002066//HYPOTHETICAL PROTEIN KIAA0192 (FRAGMENT).//1.1e-94:260:71//HOMO SAPIENS (HUMAN).//Q93074
- F-NT2RM4002067//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!.//1.5e-15:51:70//HOMO SAPIENS (HUMAN).//P39188
- F-NT2RM4002073//ELASTIN PRECURSOR (TROPOELASTIN).//4.9e-05:88:36//HOMO SAPIENS (HUMAN).//P15502
- 20 F-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//7.2e-43:220:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
- F-NT2RM4002093//POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I) (57 KD RNA-BINDING PROTEIN PPTB-1).//1.8e-93:255:72//HOMO SAPIENS (HUMAN).//P26599
- 25 F-NT2RM4002109//KINESIN-LIKE PROTEIN KIF4.//3.7e-101:260:78//MUS MUSCULUS (MOUSE).//P33174
- F-NT2RM4002128//HYPOTHETICAL PROTEIN IN CYCB 3'REGION PRECURSOR (ORF2) (FRAGMENT).//0.91e-37:80:52//PARACOCCLUS DENITRIFICANS.//P29969
- F-NT2RM4002140//GROUCHO PROTEIN (ENHANCER OF SPLIT M9/10).//0.36:104:22//DROSOPHILA MELANOGASTER (FRUIT FLY).//P16371
- 30 F-NT2RM4002145//SLIT PROTEIN PRECURSOR.//8.6e-13:127:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//P24014
- F-NT2RM4002146//MAGO NASHI PROTEIN.//7.9e-69:143:91//DROSOPHILA MELANOGASTER (FRUIT FLY).//P49028
- 35 F-NT2RM4002161//DUAL SPECIFICITY PROTEIN PHOSPHATASE (EC 3.1.3.48) (EC 3.1.3.16).//0.0062:99:26//CHLAMYDOMONAS EUGAMETOS.//Q39491
- F-NT2RM4002174//MRP PROTEIN.//4.5e-50:183:55//ESCHERICHIA COLI.//P21590
- F-NT2RM4002189//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//2.6e-14:233:29//HOMO SAPIENS (HUMAN).//Q02817
- 40 F-NT2RM4002194//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.92:108:28//HOMO SAPIENS (HUMAN).//P51805
- F-NT2RM4002205//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//5.8e-39:122:72//RATTUS NORVEGICUS (RAT).//Q07803
- 45 F-NT2RM4002213//HYPOTHETICAL 88.4 KD PROTEIN B0464.7 IN CHROMOSOME III.//9.9e-27:110:43//CAENORHABDITIS ELEGANS.//Q03565
- F-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//1.3e-21:147:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//P40809
- F-NT2RM4002251//PROTEIN EF-7 (FRAGMENT).//0.00082:45:42//MUS MUSCULUS (MOUSE).//P97805
- 50 F-NT2RM4002256//COLD-REGULATED PROTEIN 1 (FRAGMENT).//0.00015:114:42//HORDEUM VULGARE (BARLEY).//P23251
- F-NT2RM4002268//CUTICLE COLLAGEN 2.//0.00013:142:33//CAENORHABDITIS ELEGANS.//P17656
- F-NT2RM4002278//HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC REGION.//1.0:40:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53288
- F-NT2RM4002281
- 55 F-NT2RM4002287//GAR2 PROTEIN.//0.00055:225:23//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891
- F-NT2RM4002294//HYPOTHETICAL PROTEIN KIAA0281 (HA6725).//1.1e-60:152:75//HOMO SAPIENS (HUMAN).//Q92556

- F-NT2RM4002301//GENERAL STRESS PROTEIN CTC (FRAGMENT)//0.56:43:39//BACILLUS CALDOLYTI-CUS.//P42832
- F-NT2RM4002323//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.0080:73:35//BOS TAURUS (BO-VINE).//P02313
- 5 F-NT2RM4002339//METALLOTHIONEIN 10-III (MT-10-III)//0.67:34:38//MYTILUS EDULIS (BLUE MUSSEL)//P80248
- F-NT2RM4002344//METALLOTHIONEIN-I (MT-I)//0.84:41:31//MUS MUSCULUS (MOUSE)//P02802
- F-NT2RM4002373//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT DY10 PRECURSOR//0.0019:190:28//TRITICUM AESTIVUM (WHEAT)//P10387
- 10 F-NT2RM4002374//SE5 ANTIGEN//0.0059:170:32//RATTUS NORVEGICUS (RAT)//Q63003
- F-NT2RM4002383//ALU SUBFAMILY SP WARNING ENTRY !!!!!/0.13:17:88//HOMO SAPIENS (HUMAN)//P39193
- F-NT2RM4002390
- 15 F-NT2RM4002398//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN)//0.034:110:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38074
- F-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL-AC-TIVATING ENZYME)//4.0e-20:179:31//METHANOTRIX SOEHNGENII//P27095
- F-NT2RM4002438//ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.7e-15:41:95//HOMO SAPIENS (HUMAN)//P39194
- 20 F-NT2RM4002446//CRYPTIDIN-RELATED PROTEIN 4C-1 PRECURSOR (CRS4C)//0.0058:24:50//MUS MUSCULUS (MOUSE)//P17534
- F-NT2RM4002452//METALLOTHIONEIN 10-II (MT-10-II)//0.83:48:37//MYTILUS EDULIS (BLUE MUSSEL)//P80247
- F-NT2RM4002457//ALU SUBFAMILY SC WARNING ENTRY !!!!!/4.9e-07:52:63//HOMO SAPIENS (HUMAN)//P39192
- 25 F-NT2RM4002460//C-HORDEIN (CLONE PC-919) (FRAGMENT)//0.92:43:30//HORDEUM VULGARE (BAR-LEY)//P17992
- F-NT2RM4002479//RNA HELICASE-LIKE PROTEIN DB10.//1.7e-28:200:41//NICOTIANA SYLVESTRIS (WOOD TOBACCO)//P46942
- 30 F-NT2RM4002482//HYPOTHETICAL 65.9 KD PROTEIN YPR065W//8.8e-26:123:49//SACCHAROMYCES CER-EVISIAE (BAKER'S YEAST)//Q12514 F-NT2RM4002493//LARVAL CUTICLE PROTEIN I PRECURSOR//0.17:126:27//DROSOPHILA MIRANDA (FRUIT FLY)//P91627
- F-NT2RM4002499//ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.4e-34:92:80//HOMO SAPIENS (HUMAN)//P39194
- 35 F-NT2RM4002504//ALU SUBFAMILY SB WARNING ENTRY !!!!!/3.4e-19:55:83//HOMO SAPIENS (HUMAN)//P39189
- F-NT2RM4002527//WD-40 REPEAT PROTEIN MS12.//3.0e-07:193:27//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q22468
- 40 F-NT2RM4002532//AEROLYSIN REGULATORY PROTEIN//0.97:19:47//AEROMONAS SOBRIA.//P09165
- F-NT2RM4002534//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L32 PRECURSOR (YML32).//0.76:86:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P25348
- F-NT2RM4002558//LONG-CHAIN FATTY ACID TRANSPORT PROTEIN (FATP).//4.2e-55:204:50//MUS MUSCU-LUS (MOUSE)//Q60714
- 45 F-NT2RM4002565//CHYMOTRYPSIN/ELASTASE ISOINHIBITORS 2 TO 5.//1.0:16:62//ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P07852
- F-NT2RM4002567//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION.//2.7e-10:184:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032
- F-NT2RM4002571//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOS-AMINYLTRANSFERASE) (GALNAC-T1).//2.4e-25:124:47//HOMO SAPIENS (HUMAN)//Q10472
- 50 F-NT2RM4002593//HYPOTHETICAL 9.1 KD PROTEIN IN TETB-EXOA INTERGENIC REGION.//0.95:36:38//BA-CILLUS SUBTILIS.//P37509
- F-NT2RM4002594//MSP1 PROTEIN HOMOLOG.//9.0e-68:227:60//CAENORHABDITIS ELEGANS.//P54815
- F-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE-TRNA LIGASE) (ASPRS).//3.3e-54:243:47//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73851
- 55 F-NT2RP1000018//SUPPRESSOR PROTEIN SRP40.//0.0023:131:25//SACCHAROMYCES CEREVISIAE (BAK-ER'S YEAST).//P32583
- F-NT2RP1000035//RING CANAL PROTEIN (KELCH PROTEIN).//1.0e-06:63:34//DROSOPHILA MELA-

NOGASTER (FRUIT FLY).//Q04652  
 F-NT2RP1000040//LETHAL NEUROTOXIN TX1.//0.69:21:47//PHONEUTRIA NIGRIVENTER (BRAZILIAN ARMED SPIDER).//P17727  
 5 F-NT2RP1000063//HYPOTHETICAL 25.1 KD PROTEIN IN SMC3-MRPL8 INTERGENIC REGION.//3.8e-14:130:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40359  
 F-NT2RP1000086//HYPOTHETICAL 9.4 KD PROTEIN IN RNPA-THDF INTERGENIC REGION.//0.16:44:40//ESCHERICHIA COLI.//P22847  
 F-NT2RP1000101//45.8 KD PROTEIN IN SHM1-MRPL37 INTERGENIC REGION.//1.9e-06:74:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38344  
 10 F-NT2RP1000111//COP1 REGULATORY PROTEIN (FUSCA PROTEIN FUS1).//2.7e-19:135:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P43254  
 F-NT2RP1000112//DUAL SPECIFICITY PROTEIN KINASE TTK (EC 2.7.1.-) (PYT).//1.2e-39:91:62//HOMO SAPIENS (HUMAN).//P33981  
 F-NT2RP1000124//ATP-DEPENDENT PROTEASE LA 2 (EC 3.4.21.53).//0.074:131:24//MYXOCOCCUS XANTHUS.//P36774  
 15 F-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//1.5e-49:186:56//MUS MUSCULUS (MOUSE).//P51859  
 F-NT2RP1000163//METALLOTHIONEIN (MT).//0.98:41:34//PLEURONECTES PLATESSA (PLAICE).//P07216  
 F-NT2RP1000170//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.85:64:35//HOMO SAPIENS (HUMAN).//P10162  
 20 F-NT2RP1000174//IMMEDIATE-EARLY PROTEIN IE180.//0.00056:89:37//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479  
 F-NT2RP1000191//NIFU PROTEIN.//0.53:78:35//FRANKIA ALNI.//P46045  
 F-NT2RP1000202//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//9.1e-21:148:39//HOMO SAPIENS (HUMAN).//Q01485  
 25 F-NT2RP1000243//HYPOTHETICAL PROTEIN MJ1136.//1.4e-37:219:36//METHANOCOCCUS JANNASCHII.//Q58536  
 F-NT2RP1000259//HYPOTHETICAL PROTEIN TP0318.//0.18:25:44//TREPONEMA PALLIDUM.//O83338  
 F-NT2RP1000272//SPLICING FACTOR, ARGININE/SERINE-RICH 3 (PRE-MRNA SPLICING FACTOR SRP20) (X16 PROTEIN).//1.6e-18:133:36//HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE).//P23152  
 30 F-NT2RP1000324  
 F-NT2RP1000326//HYPOTHETICAL 29.8 KD PROTEIN ZC97.1 IN CHROMOSOME III.//1.0e-23:129:36//CAENORHABDITIS ELEGANS.//P34599  
 F-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//2.5e-45:147:57//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32447  
 35 F-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//4.8e-14:119:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25343  
 F-NT2RP1000357//TRYPMAGISTOTE DECAY-ACCELERATING FACTOR (T-DAF) (FRAGMENT).//1.0:43:32//TRYPANOSOMA CRUZI.//Q26327  
 40 F-NT2RP1000358//HYPOTHETICAL 84.4 KD PROTEIN IN RPC2/RET1 3'REGION.//7.9e-28:244:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39744  
 F-NT2RP1000363//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//2.2e-07:178:30//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437  
 F-NT2RP1000376//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//1.5e-20:254:31//HOMO SAPIENS (HUMAN).//P16157  
 45 F-NT2RP1000409//CYTOCHROME C3 (CYTOCHROME C7) (C551.5).//1.0:34:26//DESULFUROMONAS ACETOXIDANS (CHLOROPSEUDOMONAS ETHYLICA).//P00137  
 F-NT2RP1000413//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN).//3.7e-131:230:97//RATUS NORVEGICUS (RAT).//P55161  
 50 F-NT2RP1000416//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.83:54:40//DROSOPHILA SIMULANS (FRUIT FLY).//P13729  
 F-NT2RP1000418//HYPOTHETICAL 9.9 KD PROTEIN IN GCVT-SPOIIIAA INTERGENIC REGION.//0.24:91:35//BACILLUS SUBTILIS.//P49779  
 F-NT2RP1000439//HYPOTHETICAL 100.5 KD PROTEIN C1B9.04 IN CHROMOSOME I.//0.13:172:22//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10429  
 55 F-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN).//1.9e-08:167:24//HOMO SAPIENS (HUMAN).//Q08257  
 F-NT2RP1000460//NUCLEAR MOVEMENT PROTEIN NUDC.//1.0e-18:149:34//EMERICELLA NIDULANS (AS-

PERGILLUS NIDULANS) //P17624

F-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//1.3e-43:

180:47//CAENORHABDITIS ELEGANS.//P34580

F-NT2RP1000478//TUBULIN BETA-6 CHAIN (CLASS-VI).//1.5e-45:85:63//GALLUS GALLUS (CHICKEN).//P09207

F-NT2RP1000481//HYPOTHETICAL 5.8 KD PROTEIN IN PUHA 5'REGION (ORF55).//0.083:21:47//RHODOBACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA).//P26159

F-NT2RP1000493//POSSIBLE DNA-REPAIR PROTEIN XP-E (POSSIBLE XERODERMA PIGMENTOSUM GROUP E PROTEIN) (UV-DAMAGED DNA-BINDING PROTEIN) (UV-DBD).//6.6e-11:139:31//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).//P33194

F-NT2RP1000513//60S RIBOSOMAL PROTEIN L22.//0.017:92:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P50887

F-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//0.0055:86:36//MUS MUSCULUS (MOUSE).//Q81068

F-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.2e-09:69:36//CRICETULUS GRISEUS (CHINESE HAMSTER).//P49020

F-NT2RP1000574//HOMEODOMAIN PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//6.0e-39:141:65//MUS MUSCULUS (MOUSE).//P97367

F-NT2RP1000577//PUTATIVE ATP-DEPENDENT RNA HELICASE YDL031W.//0.00016:48:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12389

F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR.//0.00017:61:50//HOMO SAPIENS (HUMAN).//P04275

F-NT2RP1000609//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE).//4.4e-07:128:31//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q08871

F-NT2RP1000629//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//4.2e-70:167:86//MUS MUSCULUS (MOUSE).//P35585

F-NT2RP1000630//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.//0.0011:238:21//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47179

F-NT2RP1000677//COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.//0.99:71:33//HOMO SAPIENS (HUMAN).//Q07092

F-NT2RP1000688//ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.0024:19:94//HOMO SAPIENS (HUMAN).//P39193

F-NT2RP1000695//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III.//2.2e-30:185:37//CAENORHABDITIS ELEGANS.//Q18262

F-NT2RP1000701//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.2e-65:128:93//RATTUS NORVEGICUS (RAT).//P54319

F-NT2RP1000721//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//2.3e-06:139:34//HOMO SAPIENS (HUMAN).//O00268

F-NT2RP1000730//MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR ISOFORM (FRAGMENT).//0.89:40:40//MUS MUSCULUS (MOUSE).//P09542

F-NT2RP1000733//METALLOTHIONEIN-LIKE PROTEIN CR55.//0.024:24:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41902

F-NT2RP1000738//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1 / PRP-3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C) [CAPAINS: PEPTIDE P-C].//0.040:82:36//HOMO SAPIENS (HUMAN).//P02810

F-NT2RP1000746//HYPOTHETICAL 27.1 KD PROTEIN UFD4-CAP1 INTERGENIC REGION.//2.0e-30:170:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33201

F-NT2RP1000767//PSEUDOMONAS PEPSIN PRECURSOR (EC 3.4.23.37) (PEPSTATIN-INSENSITIVE CARBOXYL PROTEINASE).//0.99:75:34//PSEUDOMONAS SP. (STRAIN 101).//P42790

F-NT2RP1000782//CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1).//2.3e-23:159:35//HOMO SAPIENS (HUMAN).//P41732

F-NT2RP1000796//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP) (SMALL PROLINE-RICH SCROFA (PIG)).//P35323

F-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//3.1e-37:89:64//HOMO SAPIENS (HU-

MAN).//Q07960  
 F-NT2RP1000833//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.32:29:48//HOMO SAPIENS (HUMAN).//P22531  
 5 F-NT2RP1000834//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-).//6.4e-67:202:68//RATTUS NORVEGICUS (RAT).//P70473  
 F-NT2RP1000836//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION.//1.0:35:54//HUMAN ADENOVIRUS TYPE 41.//P23691  
 F-NT2RP1000846//SMALL PROLINE-RICH PROTEIN 2-1.//0.013:35:48//HOMO SAPIENS (HUMAN).//P35326  
 10 F-NT2RP1000851//PERIOD CLOCK PROTEIN (FRAGMENT).//0.082:28:57//DROSOPHILA SALTANS (FRUIT FLY).//Q04536  
 F-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//2.5e-26:190:30//MUS MUSCULUS (MOUSE).//Q35566  
 F-NT2RP1000860//POTENTIAL TRANSCRIPTIONAL ADAPTOR.//0.13:86:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q02336  
 15 F-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//7.6e-11:200:35//CAENORHABDITIS ELEGANS.//Q09531  
 F-NT2RP1000915//HYPOTHETICAL GTP-BINDING PROTEIN IN PM140-PAC2 INTERGENIC REGION.//1.4e-06:88:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40010  
 F-NT2RP1000916//SUPPRESSOR PROTEIN SRP40.//0.40:90:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583  
 20 F-NT2RP1000943//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//0.099:75:34//HOMO SAPIENS (HUMAN).//Q02817  
 F-NT2RP1000944//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//7.6e-06:65:41//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341  
 25 F-NT2RP1000947//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//3.6e-12:27:77//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P51669  
 F-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//2.8e-15:169:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652  
 30 F-NT2RP1000958//HYPOTHETICAL GTP-BINDING PROTEIN IN PM140-PAC2 INTERGENIC REGION.//4.2e-16:162:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40010  
 F-NT2RP1000959//CORNIFIN A (SMALL PROLINE-RICH PROTEIN IA) (SPR-IA) (SPRK).//0.0031:34:44//HOMO SAPIENS (HUMAN).//P35321  
 35 F-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//1.5e-52:110:95//HOMO SAPIENS (HUMAN).//P19338  
 F-NT2RP1000980//LIGHT-HARVESTING PROTEIN B-1015, ALPHA CHAIN PRECURSOR (ANTENNA PIGMENT PROTEIN, ALPHA CHAIN).//0.87:37:45//RHODOPSEUDOMONAS VIRIDIS.//P04123  
 F-NT2RP1000988  
 F-NT2RP1001011//PROTEIN P19.//0.96:30:50//BACTERIOPHAGE PRD1.//P17638  
 40 F-NT2RP1001013//DNA-BINDING PROTEIN 65 (PROTEIN GP65).//1.0:20:45//BACTERIOPHAGE T4.//P16012  
 F-NT2RP1001014  
 F-NT2RP1001033//TUBULIN GAMMA CHAIN.//2.5e-16:112:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P25295  
 F-NT2RP1001073//HYPOTHETICAL 10.4 KD PROTEIN IN FTR1-SPT15 INTERGENIC REGION.//7.6e-16:82:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40089  
 45 F-NT2RP1001079//SARCOSINE OXIDASE (EC 1.5.3.1).//4.8e-15:95:40//ARTHROBACTER SP. (STRAIN TE1826).//P40873  
 F-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9.//2.4e-29:126:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06218  
 50 F-NT2RP1001113//SMALL PROLINE-RICH PROTEIN 2-1.//0.49:38:39//HOMO SAPIENS (HUMAN).//P35326  
 F-NT2RP1001173//RHOMBOTIN-1 (CYSTEINE RICH PROTEIN TTG-1) (T-CELL TRANSLOCATION PROTEIN 1) (LIM-ONLY PROTEIN 1).//0.99:54:37//HOMO SAPIENS (HUMAN).//P25800  
 F-NT2RP1001177//HISTONE MACRO-H2A.1.//1.6e-29:85:76//RATTUS NORVEGICUS (RAT).//Q02874  
 F-NT2RP1001185  
 55 F-NT2RP1001199//NEUROTOXIN 1.//1.0:23:47//CENTRUROIDES SCULPTURATUS (BARK SCORPION).//P01491  
 F-NT2RP1001247//TRANSFORMING GROWTH FACTOR BETA 4 PRECURSOR (TGF-BETA 4) (ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR).//3.3e-08:28:89//HOMO SAPIENS (HUMAN).//O00292

F-NT2RP1001248//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.33:49:28//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18804

F-NT2RP1001253//GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10) (GLUCOSAMINE-6-PHOSPHATE DEAMINASE) (GNPDA) (OSCILLIN) (KIAA0060).//3.8e-46:115:81//HOMO SAPIENS (HUMAN).//P46926

5 F-NT2RP1001286//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-34 GALACTOSIDE-BINDING LECTIN).//0.16:48:37//MUS MUSCULUS (MOUSE).//P16110

F-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//6.1e-05:92:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12024

10 F-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.2e-05:92:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12024

F-NT2RP1001310//PROBABLE E4 PROTEIN.//0.99:109:26//HUMAN PAPILLOMAVIRUS TYPE 5.//P06924

F-NT2RP1001311//SODIUM/HYDROGEN EXCHANGER 5 (NA(+)/H(+) EXCHANGER 5) (NHE-5) (FRAGMENT).//0.99:94:31//HOMO SAPIENS (HUMAN).//Q14940

15 F-NT2RP1001313//CYTOCHROME B5.//9.0e-13:92:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40312

F-NT2RP1001361//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B).//1.2e-47:117:74//BOS TAURUS (BOVINE).//Q02827

F-NT2RP1001385//CELL DIVISION PROTEIN FTSN.//0.64:107:28//ESCHERICHIA COLI.//P29131

20 F-NT2RP1001395//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS).//0.25:35:45//GALLUS GALLUS (CHICKEN).//P02467

F-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//2.2e-41:129:67//CAENORHABDITIS ELEGANS.//P91917

F-NT2RP1001424//UREASE ACCESSORY PROTEIN UREAF (FRAGMENT).//0.87:24:45//ESCHERICHIA COLI.//Q03286

25 F-NT2RP1001432//CYSTEINE PROTEINASE INHIBITOR B (CYSTATIN B) (SCB).//1.0:35:42//HELIANTHUS ANNUUS (COMMON SUNFLOWER).//Q10993

F-NT2RP1001449//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.053:37:37//OVIS ARIES (SHEEP).//P26372

30 F-NT2RP1001457//HYPOTHETICAL 57.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN CPR4-SSK22 INTERGENIC REGION.//2.9e-16:159:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25382

F-NT2RP1001466//HYPOTHETICAL PROTEIN MJ0284.//5.3e-15:162:35//METHANOCOCCUS JANNASCHII.//Q57732

F-NT2RP1001475//HYPOTHETICAL 195.1 KD PROTEIN IN DNA43-UB1 INTERGENIC REGION.//0.69:119:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40457

35 F-NT2RP1001482//PROTEASOME COMPONENT C9 (EC 3.4.99.46) (MACROPAIN SUBUNIT C9) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C9).//1.0:58:32//HOMO SAPIENS (HUMAN).//P25789

F-NT2RP1001494//MALE STERILITY PROTEIN 2.//2.4e-12:84:42//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q08891

40 F-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//6.3e-37:94:52//SPIRODELA POLYRRHIZA.//P42803

F-NT2RP1001546//LEUKOCYTE SURFACE ANTIGEN CD53 (CELL SURFACE GLYCOPROTEIN CD53).//9.3e-11:98:29//HOMO SAPIENS (HUMAN).//P19387

F-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//2.2e-64:159:84//MUS MUSCULUS (MOUSE).//P47758

45 F-NT2RP1001616//HYPOTHETICAL 13.5 KD PROTEIN C45G9.7 IN CHROMOSOME III.//9.2e-05:49:42//CAENORHABDITIS ELEGANS.//Q09506

F-NT2RP1001665//REGB PROTEIN.//0.99:29:37//PSEUDOMONAS AERUGINOSA.//Q03381

F-NT2RP2000001//SMALL PROLINE-RICH PROTEIN 2-1.//0.64:36:41//HOMO SAPIENS (HUMAN).//P35326

50 F-NT2RP2000006//DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40).//1.7e-19:74:52//HOMO SAPIENS (HUMAN).//P25685

F-NT2RP2000007//TROPOMYOSIN, FIBROBLAST AND EPITHELIAL MUSCLE-TYPE (TM36) (TME1) (TM1).//0.93:126:23//HOMO SAPIENS (HUMAN).//P06468

F-NT2RP2000008//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) (FRAGMENT).//4.2e-35:156:54//HOMO SAPIENS (HUMAN).//Q06730

55 F-NT2RP2000027//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.95:41:39//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//P50665

F-NT2RP2000032//BAX PROTEIN, CYTOPLASMIC ISOFORM GAMMA.//1.0:35:34//HOMO SAPIENS (HU-



- MAN).//Q07815  
 F-NT2RP2000040//BASIC PROLINE-RICH PEPTIDE IB-1.//0.0024:58:36//HOMO SAPIENS (HUMAN).//P04281  
 F-NT2RP2000045//DNAJ PROTEIN.//1.1e-12:42:66//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//Q56237
- 5 F-NT2RP2000054//GONADOLIBERIN III PRECURSOR (GONADOTROPIN-RELEASING HORMONE III) (GN-RH-III) (LH-RH III) (LULIBERIN III).//0.20:46:36//ONCORHYNCHUS MASOU (CHERRY SALMON) (MASU SALMON).//P30973  
 F-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP-EP-SILON).//1.3e-18:45:100//MUS MUSCULUS (MOUSE).//P49446
- 10 F-NT2RP2000067//HOMEBOX PROTEIN HOX-A5 (S12-B) (FRAGMENT).//0.71:44:40//SALMO SALAR (ATLANTIC SALMON).//P09637  
 F-NT2RP2000070//INSULIN.//0.94:30:43//HYSTRIX CRISTATA (CRESTED PORCUPINE).//P01328  
 F-NT2RP2000076//ETS-LIKE PROTEIN POINTED P1 (D-ETS-2).//0.0013:76:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P51022
- 15 F-NT2RP2000077//U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (U1-C).//0.24:49:40//HOMO SAPIENS (HUMAN).//P09234  
 F-NT2RP2000079//PLATELET FACTOR 4 (PF-4).//0.15:52:30//SUS SCROFA (PIG).//P30034  
 F-NT2RP2000088//HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC REGION.//1.0:36:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53245
- 20 F-NT2RP2000091//HYPOTHETICAL PROTEIN HI0149 PRECURSOR.//0.22:38:47//HAEMOPHILUS INFLUENZAE.//P43953  
 F-NT2RP2000097//VIRUS ATTACHMENT PROTEIN (O61R).//0.75:33:36//AFRICAN SWINE FEVER VIRUS (STRAIN BA71V) (ASFV).//P32510  
 F-NT2RP2000098
- 25 F-NT2RP2000108//ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.4e-09:50:70//HOMO SAPIENS (HUMAN).//P39195  
 F-NT2RP2000114//WISKOTT-ALDRICH SYNDROME PROTEIN (WASP).//0.024:52:44//HOMO SAPIENS (HUMAN).//P42768  
 F-NT2RP2000120//5.8 KD PROTEIN IN HMC OPERON (ORF 4).//0.67:37:32//DESULFOVIBRIO VULGARIS (STRAIN HILDENBOROUGH).//P33391
- 30 F-NT2RP2000126//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//1.5e-23:94:47//HOMO SAPIENS (HUMAN).//O14646  
 F-NT2RP2000133//SPICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//5.6e-10:82:39//HOMO SAPIENS (HUMAN).//Q15427
- 35 F-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//6.7e-89:96:98//MUS MUSCULUS (MOUSE).//P35585  
 F-NT2RP2000153//PEPTIDYLPROLYL ISOMERASE CYP-1 (EC 5.2.1.8) (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE).//1.7e-05:136:33//BRUGIA MALAYI.//Q27450
- 40 F-NT2RP2000157//ML02 PROTEIN.//2.7e-06:62:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09329  
 F-NT2RP2000161//DIS3 PROTEIN HOMOLOG.//2.7e-33:173:45//CAENORHABDITIS ELEGANS.//Q17632  
 F-NT2RP2000173//HYPOTHETICAL 10.5 KD PROTEIN IN SODA-COMGA INTERGENIC REGION.//0.99:62:25//BACILLUS SUBTILIS.//P54499
- 45 F-NT2RP2000175//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.19:41:43//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643  
 F-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SPECIFIC PROTEIN NSP60).//4.1e-19:114:44//BOS TAURUS (BOVINE).//Q02675  
 F-NT2RP2000195//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:30:33//MICROTUS PENNSYLVANICUS (MEADOW VOLE).//P29499
- 50 F-NT2RP2000205//MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR (PERIPLASMIC MERCURY ION BINDING PROTEIN) (MERCURY SCAVENGER PROTEIN).//0.098:88:25//SH-EWANELLA PUTREFACIENS (PSEUDOMONAS PUTREFACIENS).//Q54463  
 F-NT2RP2000208//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.020:19:57//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645
- 55 F-NT2RP2000224//PUTATIVE CUTICLE COLLAGEN C09G5.4.//0.0058:159:32//CAENORHABDITIS ELEGANS.//Q09455  
 F-NT2RP2000232//P55-C-FOS PROTO-ONCOGENE PROTEIN (FRAGMENT).//1.0:44:38//OVIS ARIES

(SHEEP).//O02761  
 F-NT2RP2000233//GASTRIN/CHOLECYSTOKININ TYPE B RECEPTOR (CCK-B RECEPTOR) (CCK-BR).//  
 0.34:53:43//CANIS FAMILIARIS (DOG).//P30552  
 F-NT2RP2000239//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//O.019:  
 5 69:33//RATTUS NORVEGICUS (RAT).//P10164  
 F-NT2RP2000248//OVOMUCOID (FRAGMENT).//O.88:18:55//POLYLECTRON EMPHANUM (PALAWAN PEA-  
 COCK-PHEASANT).//P52250  
 F-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//6.4e-09:83:37//SACCHAROMYCES  
 CEREVISIAE (BAKER'S YEAST).//P40556  
 10 F-NT2RP2000258//MYOSIN II HEAVY CHAIN, NON MUSCLE.//O.081:217:28//DICTYOSTELIUM DISCOIDEUM  
 (SLIME MOLD).//P08799  
 F-NT2RP2000270//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-17:80:57//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-NT2RP2000274//HYPOTHETICAL 5.8 KD PROTEIN.//O.082:22:45//CLOVER YELLOW MOSAIC VIRUS  
 15 (CYMV).//P16485  
 F-NT2RP2000283//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III.//O.39:38:34//  
 CAENORHABDITIS ELEGANS.//P34535  
 F-NT2RP2000288  
 F-NT2RP2000289//HYPOTHETICAL 9.4 KD PROTEIN IN RNPA-THDF INTERGENIC REGION.//O.40:38:42//ES-  
 20 CHERICHIA COLI.//P22847  
 F-NT2RP2000297//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//2.3e-62:206:47//HO-  
 MO SAPIENS (HUMAN).//Q03923  
 F-NT2RP2000298//CUTICLE COLLAGEN 12 PRECURSOR.//O.55:81:40//CAENORHABDITIS ELEGANS.//  
 P20630  
 25 F-NT2RP2000310//RUBREDOXIN (RD).//O.13:43:41//TREPNEMA PALLIDUM.//O83956  
 F-NT2RP2000327//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:46:30//GADUS MORHUA (ATLANTIC  
 COD).//P15996  
 F-NT2RP2000328//HYPOTHETICAL 86.6 KD PROTEIN IN PFK1-TDS4 INTERGENIC REGION.//2.0e-21:198:  
 31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53313  
 30 F-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//1.8e-91:155:  
 92//BOS TAURUS (BOVINE).//P08760  
 F-NT2RP2000337//PROTEIN A54.//O.75:48:35//VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS  
 (STRAIN COPENHAGEN).//P21072  
 F-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//9.7e-13:114:42//  
 35 MUS MUSCULUS (MOUSE).//P17564  
 F-NT2RP2000369//CALTRIN (CALCIUM TRANSPORT INHIBITOR).//O.98:47:34//MUS MUSCULUS (MOUSE).//  
 Q09098  
 F-NT2RP2000412//SHORT NEUROTOXIN D PRECURSOR.//O.66:57:36//AIPYSURUS LAEVIS (OLIVE SEA  
 SNAKE).//P19960  
 40 F-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).//1.0e-27:96:67//HO-  
 MO SAPIENS (HUMAN).//P52597  
 F-NT2RP2000420//ZINC FINGER PROTEIN 191.//O.16:47:38//HOMO SAPIENS (HUMAN).//O14754  
 F-NT2RP2000422//PUTATIVE PHOSPHOACETYLGLUCOSAMINE MUTASE (EC 5.4.2.3) (ACETYLGLU-  
 COSAMINE PHOSPHOMUTASE) (N-ACETYLGLUCOSAMINE-PHOSPHATE MUTASE).//3.6e-19:148:36//  
 45 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09687  
 F-NT2RP2000438//TUBULIN GAMMA CHAIN.//O.86:190:27//RETICULOMYXA FILOSA.//P54405  
 F-NT2RP2000448//OXYSTEROL-BINDING PROTEIN.//3.7e-13:140:42//HOMO SAPIENS (HUMAN).//P22059  
 F-NT2RP2000459//NEURONAL PROTEIN 3.1 (P311 PROTEIN).//1.0:45:35//HOMO SAPIENS (HUMAN).//  
 Q16612  
 50 F-NT2RP2000498//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//O.062:25:68//HOMO SAPIENS (HUMAN).//  
 P39194  
 F-NT2RP2000503  
 F-NT2RP2000510//TOXIN IV-5.//1.0:51:33//TITYUS BAHIIENSIS (BRAZILIAN SCORPION).//P56608  
 F-NT2RP2000516//SLYX PROTEIN.//1.0:52:32//ESCHERICHIA COLI.//P30857  
 55 F-NT2RP2000523//PHORBOLIN I (FRAGMENTS).//1.4e-06:36:47//HOMO-SAPIENS (HUMAN).//P31941  
 F-NT2RP2000603//ALPHA/BETA-GLIADIN PRECURSOR (PROLAMIN) (CLASS A-III).//O.93:119:26//TRITICUM  
 AESTIVUM (WHEAT).//P04723  
 F-NT2RP2000617//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//O.056:16:62//OVIS ARIES

(SHEEP), AND CAPRA HIRCUS (GOAT).//P04102  
 F-NT2RP2000634//NEDD-4 PROTEIN (EC 6.3.2.-) (KIAA0093) (FRAGMENT).//1.8e-05:128:28//HOMO SAPIENS (HUMAN).//P46934  
 F-NT2RP2000644//HYPOTHETICAL PROTEIN HI1566 PRECURSOR.//0.85:48:39//HAEMOPHILUS INFLUENZAE.//P44257  
 F-NT2RP2000656//EARLY GROWTH RESPONSE PROTEIN 1 (EGR-1) (NERVE GROWTH FACTOR-INDUCED PROTEIN A) (NGFI-A).//1.0:111:24//RATTUS NORVEGICUS (RAT).//P08154  
 F-NT2RP2000658//URONATE ISOMERASE (EC 5.3.1.12) (GLUCURONATE ISOMERASE) (URONIC ISOMERASE).//0.49:79:31//ESCHERICHIA COLI.//P42607  
 F-NT2RP2000668//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (45 KD MEROZOITE SURFACE ANTIGEN).//0.020:115:30//PLASMODIUM FALCIPARUM (ISOLATE 3D7).//P50498  
 F-NT2RP2000678//ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00085:38:28//HOMO SAPIENS (HUMAN).//P39188  
 F-NT2RP2000704//ALU SUBFAMILY J WARNING ENTRY !!!!!/2.2e-17:55:74//HOMO SAPIENS (HUMAN).//P39188  
 F-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//8.9e-47:106:59//TREPONEMA PALLIDUM.//O83950  
 F-NT2RP2000715  
 F-NT2RP2000731//CONIDATION-SPECIFIC PROTEIN 10.//0.094:31:41//NEUROSPORA CRASSA.//P10713  
 F-NT2RP2000758//ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00027:31:74//HOMO SAPIENS (HUMAN).//P39188  
 F-NT2RP2000764//NIFS PROTEIN.//2.7e-27:175:47//ANABAENA SP. (STRAIN PCC 7120).//P12623  
 F-NT2RP2000809//HYPOTHETICAL PROTEIN MG381 HOMOLOG.//0.91:85:25//MYCOPLASMA PNEUMONIAE.//P75219  
 F-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//2.8e-07:133:31//MUS MUSCULUS (MOUSE).//Q99104  
 F-NT2RP2000814//40S RIBOSOMAL PROTEIN S27A.//0.93:44:38//LYCOPERSICON ESCULENTUM (TOMATO), AND SOLANUM TUBEROSUM (POTATO).//P27083  
 F-NT2RP2000816//HYPOTHETICAL 88.4 KD PROTEIN B0464.7 IN CHROMOSOME III.//3.3e-21:123:39//CAENORHABDITIS ELEGANS.//Q03565  
 F-NT2RP2000819//TROPOMYOSIN 5, CYTOSKELETAL TYPE.//1.0:71:30//MUS MUSCULUS (MOUSE).//P21107  
 F-NT2RP2000841//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//0.0011:133:26//MUS MUSCULUS (MOUSE).//P27671  
 F-NT2RP2000842//LYSOPHOSPHATIDIC ACID RECEPTOR (EDG-2).//6.4e-13:22:95//HOMO SAPIENS (HUMAN).//Q92633  
 F-NT2RP2000845//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (MSTI).//0.92:24:41//MEDICAGO SCUTELLATA (SNAIL MEDIC).//P80321  
 F-NT2RP2000863//N-MYC PROTO-ONCOGENE PROTEIN.//0.010:148:27//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P24793  
 F-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2.//4.0e-100:199:94//HOMO SAPIENS (HUMAN).//O60841  
 F-NT2RP2000892//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].//0.43:45:44//MUS MUSCULUS (MOUSE).//P28481  
 F-NT2RP2000931//MATRIN 3.//2.8e-48:104:92//RATTUS NORVEGICUS (RAT).//P43244  
 F-NT2RP2000932//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).//3.9e-07:113:31//MUS MUSCULUS (MOUSE).//Q05921  
 F-NT2RP2000938//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID).//0.026:59:45//RATTUS NORVEGICUS (RAT).//Q01956  
 F-NT2RP2000943//HYPOTHETICAL PROTEIN KIAA0079 (HA3543).//5.9e-18:161:42//HOMO SAPIENS (HUMAN).//P53992  
 F-NT2RP2000965//INNER CENTROMERE PROTEIN (INCENP).//0.062:156:25//GALLUS GALLUS (CHICKEN).//P53352  
 F-NT2RP2000970//EC PROTEIN HOMOLOG.//1.0:50:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P93746  
 F-NT2RP2000985//HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION.//2.5e-06:53:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36159  
 F-NT2RP2000987//INSECT TOXIN 4 (INSECT TOXIN AAHIT4).//1.0:32:34//ANDROCTONUS AUSTRALIS HEC-

- TOR (SAHARA SCORPION).//P21150  
F-NT2RP2001036!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.2e-33:65:81//HOMO SAPIENS (HUMAN).//P39193
- 5 F-NT2RP2001044//HIRUSTASIN.//0.97:15:66//HIRUDO MEDICINALIS (MEDICINAL LEECH).//P80302  
F-NT2RP2001056!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.0e-24:85:65//HOMO SAPIENS (HUMAN).//P39194  
F-NT2RP2001065//BOWMAN-BIRK TYPE SEED TRYPSIN AND CHYMOTRYPSIN INHIBITOR (BTCI).//0.41:50:32//MIGNA UNGUICULATA (COWPEA).//P17734  
F-NT2RP2001070//PROBABLE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE) (FPPA PROTEIN).//6.2e-18:64:48//MYXOCOCCUS XANTHUS.//P21159
- 10 F-NT2RP2001081//SYNAPTOTAGMIN IV.//7.8e-16:94:46//RATTUS NORVEGICUS (RAT).//P50232  
F-NT2RP2001094//METALLOTHIONEIN-I (MT-I).//1.0:24:33//RATTUS NORVEGICUS (RAT).//P02803  
F-NT2RP2001119!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/7.5e-11:61:63//HOMO SAPIENS (HUMAN).//P39195
- 15 F-NT2RP2001127//XE169 PROTEIN (SMCX PROTEIN) (FRAGMENTS).//1.0e-47:155:58//MUS MUSCULUS (MOUSE).//P41230  
F-NT2RP2001137//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.10:68:39//BOS TAURUS (BOVINE).//P25508  
F-NT2RP2001149!!!! ALU SUBFAMILY J WARNING ENTRY!!!!/1.1e-13:81:59//HOMO SAPIENS (HUMAN).//P39188
- 20 F-NT2RP2001168//PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENTS).//0.0071:77:33//RATTUS NORVEGICUS (RAT).//P20468  
F-NT2RP2001173//CYTOSKELETON-ASSOCIATED PROTEIN CKAP1 (TUBULIN FOLDING COFACTOR B).//1.0:36:41//HOMO SAPIENS (HUMAN).//Q39426
- 25 F-NT2RP2001174//ZINC FINGER PROTEIN 137.//7.2e-11:65:43//HOMO SAPIENS (HUMAN).//P52743  
F-NT2RP2001196//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).//1.0:95:26//CAPRA HIRCUS (GOAT).//Q36346  
F-NT2RP2001218//HYPOTHEICAL 59.2 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION.//0.00024:80:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40486
- 30 F-NT2RP2001228//RABPHILIN-3A (FRAGMENT).//4.6e-05:121:39//MUS MUSCULUS (MOUSE).//P47708  
F-NT2RP2001233//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.2e-61:153:56//HOMO SAPIENS (HUMAN).//P16415  
F-NT2RP2001245//SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN).//4.9e-05:230:21//HOMO SAPIENS (HUMAN).//Q15431
- 35 F-NT2RP2001268//HOMEBOX PROTEIN CEH-32.//0.23:159:25//CAENORHABDITIS ELEGANS.//Q23175  
F-NT2RP2001277  
F-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-ALPHA HOMOLOG) (BRAIN PROTEIN I47) (FRAGMENT).//1.0e-86:131:97//MUS MUSCULUS (MOUSE).//P28663  
F-NT2RP2001295
- 40 F-NT2RP2001312//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).//0.64:80:33//CAPRA HIRCUS (GOAT).//P50426  
F-NT2RP2001327//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//1.0e-36:118:65//HOMO SAPIENS (HUMAN).//Q13829  
F-NT2RP2001328//PROBABLE E5 PROTEIN.//1.0:46:41//HUMAN PAPILLOMAVIRUS TYPE 33.//P06426
- 45 F-NT2RP2001347!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.5e-19:66:62//HOMO SAPIENS (HUMAN).//P39193  
F-NT2RP2001366//SPERM-SPECIFIC PROTEIN PHI-1.//0.66:55:32//MYTILUS EDULIS (BLUE MUSSEL).//Q04621  
F-NT2RP2001378//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID) (FRAGMENT).//0.060:78:33//HOMO SAPIENS (HUMAN).//Q14003
- 50 F-NT2RP2001381//26S PROTEASE REGULATORY SUBUNIT 8 (SUG1 HOMOLOG) (XSUG1).//1.0:167:26//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P46470  
F-NT2RP2001392//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIA3.//0.0080:82:32//OVIS ARIES (SHEEP).//P02441
- 55 F-NT2RP2001394//POLYHOMEOTIC-PROXIMAL CHROMATIN PROTEIN.//0.024:39:53//DROSOPHILA MELANOGASTER (FRUIT FLY).//P39769  
F-NT2RP2001397//G2/MITOTIC-SPECIFIC CYCLIN B2.//1.4e-46:125:78//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//P37883

- F-NT2RP2001420//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H]//0.00018:113:38//HOMO SAPIENS (HUMAN)//P04280
- F-NT2RP2001423//HYPOTHETICAL 9.4 KD PROTEIN IN GP31-CD INTERGENIC REGION (ORF A)//0.90:23:43//BACTERIOPHAGE T4//P17307
- 5 F-NT2RP2001427//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.2e-11:38:68//HOMO SAPIENS (HUMAN)//P39188
- F-NT2RP2001436//DYNEIN LIGHT INTERMEDIATE CHAIN 2, CYTOSOLIC (LIC53/55) (LIC-2)//0.25:124:28//RATTUS NORVEGICUS (RAT)//Q62698
- 10 F-NT2RP2001440//14-3-3 PROTEIN GAMMA (PROTEIN KINASE C INHIBITOR PROTEIN-1) (KCIP-1)//4.8e-62:145:90//RATTUS NORVEGICUS (RAT)//P35214
- F-NT2RP2001445
- F-NT2RP2001449//CLEFTAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT)//9.5e-118:226:95//BOS TAURUS (BOVINE)//Q10568
- F-NT2RP2001450
- 15 F-NT2RP2001467//SHORT NEUROTOXIN 1 (TOXIN V-II-1)//1.0:25:40//BUNGARUS FASCIATUS (BANDIED KRAIT)//P10808
- F-NT2RP2001506
- F-NT2RP2001511//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III//0.49:124:29//CAENORHABDITIS ELEGANS//P34681
- 20 F-NT2RP2001520//VITAMIN D-DEPENDENT CALCIUM-BINDING PROTEIN, INTESTINAL (CABP) (CALBINDIN D9K)//0.035:71:33//HOMO SAPIENS (HUMAN)//P29377
- F-NT2RP2001526
- F-NT2RP2001536//METALLOTHIONEIN-I (MT-1)//1.0:19:42//COLUMBA LIVIA (DOMESTIC PIGEON)//P15786
- F-NT2RP2001560//CUTICLE COLLAGEN 12 PRECURSOR//0.0018:144:35//CAENORHABDITIS ELEGANS//P20630
- 25 F-NT2RP2001569//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.7e-31:102:67//HOMO SAPIENS (HUMAN)//P39194
- F-NT2RP2001576//SMP3 PROTEIN//0.00016:75:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q04174
- 30 F-NT2RP2001581//TRANSMEMBRANE PROTEIN SEX PRECURSOR//0.040:46:36//HOMO SAPIENS (HUMAN)//P51805
- F-NT2RP2001597//PROBABLE E4 PROTEIN//0.00042:113:34//HUMAN PAPILLOMAVIRUS TYPE 5//P06924
- F-NT2RP2001601
- 35 F-NT2RP2001613//HOMEOBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT)//0.14:59:32//GALLUS GALLUS (CHICKEN)//P19601
- F-NT2RP2001628//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR//0.056:140:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32323
- 40 F-NT2RP2001634//ALPHA-CATENIN//7.1e-12:152:35//DROSOPHILA MELANOGASTER (FRUIT FLY)//P35220
- F-NT2RP2001660//HYPOTHETICAL 80.4 KD PROTEIN IN SMC3-MRPL8 INTERGENIC REGION//0.43:119:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40358
- F-NT2RP2001663//ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE)//1.2e-26:126:56//HOMO SAPIENS (HUMAN)//P06733
- 45 F-NT2RP2001675//HYPOTHETICAL 107.7 KD PROTEIN IN RP50 5'REGION (ORF1)//0.25:148:25//CAMPYLOBACTER JEJUNI//Q46089
- F-NT2RP2001677//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT)//0.010:101:31//RATTUS NORVEGICUS (RAT)//P10164
- 50 F-NT2RP2001678//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.6e-18:83:61//HOMO SAPIENS (HUMAN)//P39188
- F-NT2RP2001699//PROTEIN C14//0.98:51:31//VACCINIA VIRUS (STRAIN COPENHAGEN)//P21045
- F-NT2RP2001720//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (ALLELIC FORM 1)//0.16:145:30//PLASMODIUM FALCIPARUM (ISOLATE CAMP / MALAYSIA)//Q89317
- 55 F-NT2RP2001721//MALE-SPECIFIC LETHAL-2 PROTEIN//0.00090:48:39//DROSOPHILA MELANOGASTER (FRUIT FLY)//P50534
- F-NT2RP2001740//ANNEXIN VI (SYNEXIN) (FRAGMENT)//0.50:43:25//BOS TAURUS (BOVINE)//P20072
- F-NT2RP2001748//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-

- MENT).//0.77:111:28//HOMO SAPIENS (HUMAN).//P10162  
 F-NT2RP2001762  
 F-NT2RP2001813//PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII (PSI-I).//1.0:22:40//PICEA ABIES (NORWAY SPRUCE) (PICEA EXCELSA).//O47040  
 5 F-NT2RP2001839//SCY1 PROTEIN.//6.8e-17:204:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53009  
 F-NT2RP2001861//D15KZ1 PROTEIN (FRAGMENT).//0.31:56:39//MUS MUSCULUS (MOUSE).//Q61466  
 F-NT2RP2001869//CORNEODESMOSIN (S PROTEIN) (FRAGMENT).//0.97:78:30//SUS SCROFA (PIG).//O19084  
 10 F-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM BINDING ADAPTER MOLECULE 1).//3.5e-36:106:66//HOMO SAPIENS (HUMAN).//P55008  
 F-NT2RP2001883//CATHEPSIN L (EC 3.4.22.15).//0.95:29:41//OVIS ARIES (SHEEP).//Q10991  
 F-NT2RP2001898//TYPE II INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) (FRAGMENT).//1.6e-84:185:83//HOMO SAPIENS (HUMAN).//P32019  
 15 F-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5.//1.1e-17:180:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53946  
 F-NT2RP2001907//HYPHAL WALL PROTEIN 1 (CELL ELONGATION PROTEIN 2).//0.13:108:27//CANDIDA ALBICANS (YEAST).//P46593  
 F-NT2RP2001926//HYPOTHETICAL 7.6 KD PROTEIN YCF33.//0.55:57:26//CYANOPHORA PARADOXA.//P48273  
 20 F-NT2RP2001936  
 F-NT2RP2001943//HYPOTHETICAL 57.7 KD PROTEIN IN AIP1-CTF13 INTERGENIC REGION.//1.8e-13:208:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04305  
 F-NT2RP2001946//HYPOTHETICAL 13.0 KD PROTEIN IN ALGR3 3'REGION.//0.59:76:28//PSEUDOMONAS AERUGINOSA.//P21485  
 25 F-NT2RP2001947//ZINC FINGER PROTEIN DAN (N03).//0.53:68:29//RATTUS NORVEGICUS (RAT).//Q06880  
 F-NT2RP2001969//CHLOROPLAST 30S RIBOSOMAL PROTEIN S18.//0.0015:52:34//CHLORELLA VULGARIS.//P58353  
 F-NT2RP2001976//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//9.5e-07:201:22//MUS MUSCULUS (MOUSE).//Q99104  
 30 F-NT2RP2001985//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.016:90:32//MUS MUSCULUS (MOUSE).//P05142  
 F-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//8.0e-14:47:76//RATTUS NORVEGICUS (RAT).//Q08469  
 35 F-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//2.9e-30:211:42//GALLUS GALLUS (CHICKEN).//P35331  
 F-NT2RP2002032//FLOCCULANT-ACTIVE PROTEINS MO2.1 AND MO2.2.//0.23:20:40//MORINGA OLEIFERA (HORSEADISH TREE) (MORINGA PTERYGOSPERMA).//P24303  
 F-NT2RP2002033//!!!! ALU SUBFAMILY SP WARNING ENTRY!!!!//0.88:27:62//HOMO SAPIENS (HUMAN).//P39193  
 40 F-NT2RP2002041  
 F-NT2RP2002046//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1) (PROTEIN KINASE A INTERFERENCE PROTEIN).//1.0:85:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36027  
 F-NT2RP2002047  
 45 F-NT2RP2002058//DOM34 INTERACTING PROTEIN 2.//9.4e-25:165:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12220  
 F-NT2RP2002066//TIGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1).//5.7e-12:108:41//HOMO SAPIENS (HUMAN).//Q07157  
 F-NT2RP2002070//CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) (FRAGMENT).//0.88:28:50//ASTERINA PECTINIFERA (STARFISH).//P11958  
 50 F-NT2RP2002076//TRP-ASP REPEATS CONTAINING PROTEIN RBA-2.//0.0031:124:27//CAENORHABDITIS ELEGANS.//P90916  
 F-NT2RP2002078//KERATIN, GLYCINE/TYROSINE-RICH OF HAIR.//0.82:30:40//OVIS ARIES (SHEEP).//Q02958  
 55 F-NT2RP2002079//OUTER DENSE FIBER PROTEIN.//0.34:41:39//HOMO SAPIENS (HUMAN).//Q14990  
 F-NT2RP2002099//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U).//5.2e-08:81:48//HOMO SAPIENS (HUMAN).//Q00839  
 F-NT2RP2002105//COLLAGEN 1(X) CHAIN PRECURSOR.//0.0012:100:34//BOS TAURUS (BOVINE).//P23206

F-NT2RP2002124//EARLY GROWTH RESPONSE PROTEIN 1 (EGR-1) (KROX24) (TRANSCRIPTION FACTOR ETR103) (ZINC FINGER PROTEIN 225) (AT225)//0.74:72:31//HOMO SAPIENS (HUMAN)//P18146

F-NT2RP2002137//NEUROTOXIN B-II//1.0:27:44//CEREBRATULUS LACTEUS (MILKY RIBBON WORM)//P01526

5 F-NT2RP2002154//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-34 GALACTOSIDE-BINDING LECTIN)//0.0029:112:34//MUS MUSCULUS (MOUSE)//P16110

F-NT2RP2002172

10 F-NT2RP2002185//UBIQUITIN-LIKE PROTEIN DSK2//1.8e-07:87:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P48510

F-NT2RP2002192

F-NT2RP2002193//CUTICLE COLLAGEN 40//0.0062:70:37//CAENORHABDITIS ELEGANS//P34804

F-NT2RP2002208//PEROXISOME ASSEMBLY PROTEIN PEX10 (PEROXIN-10)//0.00011:45:40//HOMO SAPIENS (HUMAN)//060683

15 F-NT2RP2002219

F-NT2RP2002231//V-TYPE SODIUM ATP SYNTHASE SUBUNIT E (EC 3.6.1.34) (NA(+)-TRANSLOCATING ATPASE SUBUNIT E)//1.0:68:32//ENTEROCOCCUS HIRAE//P43436

F-NT2RP2002235//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULANCE FACTOR ICP34.5)//0.0022:66:45//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN CVG-2)//P37318

20 F-NT2RP2002252//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT)//0.071:110:31//CRICETULUS GRAISEUS (CHINESE HAMSTER)//P11414

F-NT2RP2002256//CYTOCHROME P450 26 (EC 1.14.-.-) (RETINOIC ACID-METABOLIZING CYTOCHROME) (P450RA1) (RETINOIC ACID 4-HYDROXYLASE)//3.1e-31:75:84//MUS MUSCULUS (MOUSE)//J055127

F-NT2RP2002259//L-MYC-1 PROTO-ONCOGENE PROTEIN//1.1e-17:41:90//HOMO SAPIENS (HUMAN)//P12524

25 F-NT2RP2002270//HYPOTHETICAL 26.0 KD PROTEIN IN CYB5-LEU4 INTERGENIC REGION//2.1e-27:164:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53930

F-NT2RP2002292//IMMEDIATE-EARLY PROTEIN RSP40//0.018:107:23//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV)//P24827

30 F-NT2RP2002312//PHOSPHATIDATE CYTIDYLTRANSFERASE (EC 2.7.7.41) (CDP-DIGLYCERIDE SYNTHASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLTRANSFERASE) (CDP-DAG SYNTHASE)//1.4e-52:174:55//HOMO SAPIENS (HUMAN)//Q92903

F-NT2RP2002316//HISTONE H1.C6/H1.C9//1.0:40:40//TRYPANOSOMA CRUZI//P40269

35 F-NT2RP2002325//PEROXISOMAL MEMBRANE PROTEIN PMP30A (PMP31) (PEROXIN 11A)//2.2e-06:145:26//CANDIDA BODINII (YEAST)//Q00316

F-NT2RP2002333//HYPOTHETICAL 39.1 KD PROTEIN IN RNPB-SOHA INTERGENIC REGION (ORF 3)//0.30:86:32//ESCHERICHIA COLI//P23524

F-NT2RP2002373//SYNAPSINS IA AND IB//0.080:145:31//BOS TAURUS (BOVINE)//P17599

40 F-NT2RP2002385//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) (CONTAINS: KNOB PROTEIN GP70; SPIKE PROTEIN P15E; R PROTEIN)//0.021:66:28//MINK CELL FOCUS-FORMING MURINE LEUKEMIA VIRUS (ISOLATE CI-3)//P03388

F-NT2RP2002394

45 F-NT2RP2002408//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//0.00030:107:37//BOS TAURUS (BOVINE)//P02453

F-NT2RP2002426

F-NT2RP2002439//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)//0.00032:79:32//PLASMODIUM BERGHEI (STRAIN ANKA)//P23093

F-NT2RP2002442//HESA PROTEIN//6.0e-16:163:30//PLECTONEMA BORYANUM//P46037

50 F-NT2RP2002457

F-NT2RP2002464//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME I//9.3e-18:165:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//J010264

F-NT2RP2002475//CYSTEINE-RICH HEART PROTEIN (HCRHP)//0.91:45:35//HOMO SAPIENS (HUMAN)//P50238

55 F-NT2RP2002479//ATP-BINDING CASSETTE TRANSPORTER 7 PRECURSOR (ABC TRANSPORTER 7 PROTEIN)//6.8e-96:186:94//HOMO SAPIENS (HUMAN)//O75027

F-NT2RP2002498//HYPOTHETICAL MERCURIC RESISTANCE PROTEIN MERC//0.65:37:45//PSEUDOMONAS AERUGINOSA//P04139

- F-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744)//1.3e-31:124:59//HOMO SAPIENS (HUMAN)//Q02386
- F-NT2RP2002504//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140)//1.2e-123:240:92//RATTUS NORVEGICUS (RAT)//P37199
- 5 F-NT2RP2002520//ACIDIC PROLINE-RICH PROTEIN HP43A PRECURSOR//0.94:83:28//MESOCRICETUS AURATUS (GOLDEN HAMSTER)//P06680
- F-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X//4.0e-10:194:23//CAENORHABDITIS ELEGANS//Q11073
- 10 F-NT2RP2002546
- F-NT2RP2002549//G2/MITOTIC-SPECIFIC CYCLIN C13-1 (A-LIKE CYCLIN) (FRAGMENT)//0.98:65:30//DAUCUS CAROTA (CARROT)//P25010
- F-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//2.6e-19:60:61//HOMO SAPIENS (HUMAN)//P51523
- 15 F-NT2RP2002595//ANNEXIN VII (SYNEXIN) //1.2e-15:121:49//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//Q92125
- F-NT2RP2002606//PROTEIN TRANSPORT PROTEIN SEC2//0.00034:98:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P17065
- F-NT2RP2002609//HYPOTHETICAL 52.0 KD PROTEIN IN CLB6-SPT6 INTERGENIC REGION//0.00022:79:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53264
- 20 F-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 1 (EC 2.1.1.-)//6.2e-37:180:44//RATTUS NORVEGICUS (RAT)//Q63009
- F-NT2RP2002621//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT)//0.98:37:35//LEMUR CATTIA (RING-TAILED LEMUR)//Q34879
- 25 F-NT2RP2002643//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP34.5) //0.04:72:32//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN MGH-10) //P37319
- F-NT2RP2002672//PROTEIN Q300//0.0018:41:43//MUS MUSCULUS (MOUSE) //Q02722
- F-NT2RP2002701//HYPOTHETICAL 72.5 KD PROTEIN C2F.7 IN CHROMOSOME I//3.6e-17:100:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //Q09701
- 30 F-NT2RP2002706//IMMEDIATE-EARLY PROTEIN IE180//0.00027:139:33//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV) //P33479
- F-NT2RP2002710//SH3-BINDING PROTEIN 3BP.1//6.9e-09:96:40//MUS MUSCULUS (MOUSE) //P55194
- F-NT2RP2002727//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN) //3.6e-20:160:36//RATTUS NORVEGICUS (RAT) //P49816
- 35 F-NT2RP2002736
- F-NT2RP2002740
- F-NT2RP2002741//RHO1 GDP-GTP EXCHANGE PROTEIN 2//2.0e-07:178:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P51862
- F-NT2RP2002750//ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//1.6e-09:43:72//HOMO SAPIENS (HUMAN) //P39191
- 40 F-NT2RP2002752//LOW CALCIUM RESPONSE LOCUS PROTEIN T//0.95:33:39//YERSINIA PSEUDOTUBERCULOSIS //Q00932
- F-NT2RP2002753//ENDOGLUCANASE EG-1 PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE) (CELLULASE) //0.71:78:33//TRICHODERMA LONGIBRACHIATUM //Q12714
- 45 F-NT2RP2002769//50 KD SPICULE MATRIX PROTEIN PRECURSOR //0.44:76:32//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN) //P11994
- F-NT2RP2002778
- F-NT2RP2002800//CRAMBIN //0.99:20:50//CRAMBE ABYSSINICA (ABYSSINIAN CRAMBE) //P01542
- F-NT2RP2002839//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT) //0.010:87:31//HOMO SAPIENS (HUMAN) //P02812
- 50 F-NT2RP2002857//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33) //0.00018:57:45//RATTUS NORVEGICUS (RAT) //P04474
- F-NT2RP2002862//HYPOTHETICAL 27.1 KD PROTEIN UFD4-CAP1 INTERGENIC REGION //7.2e-27:140:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P33201
- F-NT2RP2002880//DNA REPAIR PROTEIN RAD32 //0.83:67:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //Q09683
- 55 F-NT2RP2002891//HOMEBOX PROTEIN DLX-2 (DLX-5) (FRAGMENT) //0.99:70:24//RATTUS NORVEGICUS (RAT) //Q64204
- F-NT2RP2002925//ALPHA-1D ADRENERGIC RECEPTOR (ALPHA 1D-ADRENOCEPTOR) (ALPHA-1A



ADRENERGIC RECEPTOR.//0.31:48:43//HOMO SAPIENS (HUMAN).//P25100  
 F-NT2RP2002928//CELL DIVISION CONTROL PROTEIN 40.//2.8e-26:142:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40968  
 5 F-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II.//2.0e-31:186:35//CAENORHABDITIS ELEGANS.//Q18964  
 F-NT2RP2002939//ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-INHIBITABLE ADENYL CYCLASE).//0.0022:98:39//CANIS FAMILIARIS (DOG).//P30803  
 F-NT2RP2002954//U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A').//0.0019:107:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P43333  
 10 F-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//2.8e-11:33:81//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P51669  
 F-NT2RP2002979  
 15 F-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//1.1e-09:98:36//MYCOPLASMA CAPRICOLUM.//P10129  
 F-NT2RP2002986//RING CANAL PROTEIN (KELCH PROTEIN).//1.1e-19:141:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652  
 F-NT2RP2002987//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!1.3e-07:78:47//HOMO SAPIENS (HUMAN).//P39192  
 20 F-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT).//8.0e-77:165:85//RATTUS NORVEGICUS (RAT).//O54888  
 F-NT2RP2003000//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!2.8e-19:62:64//HOMO SAPIENS (HUMAN).//P39194  
 25 F-NT2RP2003034//HYPOTHETICAL PROTEIN H1458.//1.0:42:35//HAEMOPHILUS INFLUENZAE.//P44204  
 F-NT2RP2003073//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!0.0051:16:87//HOMO SAPIENS (HUMAN).//P39189  
 F-NT2RP2003099  
 F-NT2RP2003108//BASIC PROLINE-RICH PEPTIDE IB-1.//0.84:47:34//HOMO SAPIENS (HUMAN).//P04281  
 30 F-NT2RP2003117  
 F-NT2RP2003121//HYPOTHETICAL 96.7 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION.//9.0e-08:99:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43572  
 F-NT2RP2003125//TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2).//9.2e-08:134:28//MUS MUSCULUS (MOUSE).//P97303  
 35 F-NT2RP2003129  
 F-NT2RP2003137//UBIQUITIN.//3.4e-06:70:30//NEUROSPORA CRASSA.//P13117  
 F-NT2RP2003157//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//7.8e-13:84:40//CAENORHABDITIS ELEGANS.//Q09217  
 F-NT2RP2003158//26S PROTEASOME REGULATORY SUBUNIT S3 (PROTEASOME SUBUNIT P58).//3.1e-65:155:84//HOMO SAPIENS (HUMAN).//O43242  
 40 F-NT2RP2003161//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.0011:59:42//MUS MUSCULUS (MOUSE).//P05142  
 F-NT2RP2003164//ZYXIN.//0.0037:85:36//MUS MUSCULUS (MOUSE).//Q62523  
 F-NT2RP2003165//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!1.2e-24:77:64//HOMO SAPIENS (HUMAN).//P39194  
 45 F-NT2RP2003177//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.55:38:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643  
 F-NT2RP2003194//HYPOTHETICAL 12.5 KD PROTEIN ZK637.2 IN CHROMOSOME III.//2.3e-14:87:37//CAENORHABDITIS ELEGANS.//P30629  
 50 F-NT2RP2003208//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).//1.0:100:28//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM).//P41306  
 F-NT2RP2003228//DNA REPLICATION LICENSING FACTOR MCM4 (CDC21 HOMOLOG) (P1-CDC21).//9.3e-82:211:81//HOMO SAPIENS (HUMAN).//P33991  
 F-NT2RP2003230//SEC14 CYTOSOLIC FACTOR (PHOSPHATIDYLINOSITOL/PHOSPHATIDYLCHOLINE TRANSFER PROTEIN) (PIPC TP).//1.0:51:31//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA).//P53989  
 55 F-NT2RP2003237//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!5.1e-44:66:84//HOMO SAPIENS (HUMAN).//P39194

F-NT2RP2003243//M PROTEIN, SEROTYPE 5 PRECURSOR.//0.027:204:23//STREPTOCOCCUS PYOGENES.//P02977

F-NT2RP2003265//BP4A PROTEIN.//0.95:35:34//BRASSICA NAPUS (RAPE).//P41505

5 F-NT2RP2003272//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT).//5.5e-06:78:35//BRASSICA NAPUS (RAPE).//P40603

F-NT2RP2003277//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1).//1.9e-19:145:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P30771

F-NT2RP2003280

10 F-NT2RP2003286//RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE).//2.1e-32:137:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q08096

F-NT2RP2003293//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.7e-12:175:33//HOMO SAPIENS (HUMAN).//P51522

F-NT2RP2003295//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.055:44:45//HOMO SAPIENS (HUMAN).//P23246

15 F-NT2RP2003297

F-NT2RP2003307//KINESIN LIGHT CHAIN (KLC).//2.0e-18:87:49//RATTUS NORVEGICUS (RAT).//P37285

F-NT2RP2003308//CROOKED NECK PROTEIN.//2.1e-91:244:67//DROSOPHILA MELANOGASTER (FRUIT FLY).//P17886

F-NT2RP2003329//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III.//5.8e-57:186:55//CAENORHABDITIS ELEGANS.//P34284

20 F-NT2RP2003339//SHORT NEUROTOXIN 1 (NEUROTOXIN ALPHA).//0.98:11:72//DENDROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA).//P01416

F-NT2RP2003347//60S RIBOSOMAL PROTEIN L38.//0.83:42:33//OSTERTAGIA OSTERTAGI.//O61570

F-NT2RP2003367//SYNERGISTIC-TYPE VENOM PROTEIN C9S3, CHAIN 1.//1.0:37:35//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P01408

25 F-NT2RP2003391//MRNA TRANSPORT REGULATOR MTR10.//3.3e-11:229:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q09189

F-NT2RP2003393//PROTOCHLOROPHYLLIDE REDUCTASE CHLB SUBUNIT (EC 1.3.1.33) (NADPH-PROTOCHLOROPHYLLIDE OXIDOREDUCTASE CHLB SUBUNIT) (FRAGMENT).//0.94:29:34//ARAUCARIA HETEROPHYLLA.//P37843

30 F-NT2RP2003394

F-NT2RP2003401//60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN).//0.95:125:28//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P45746

F-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//9.8e-78:178:84//RATTUS NORVEGICUS (RAT).//P38378

35 F-NT2RP2003445

F-NT2RP2003446//HYPOTHETICAL PROTEIN E-115.//0.00030:106:33//HUMAN ADENOVIRUS TYPE 2.//P03290

F-NT2RP2003456//PHOTOSYSTEM II REACTION CENTRE M PROTEIN.//1.0:27:51//MARCHANTIA POLYMORPHA (LIVERWORT).//P12168

40 F-NT2RP2003466//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE).//6.7e-06:108:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q08871

F-NT2RP2003480//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (CBF-2) (T-14-6).//7.2e-15:38:50//GALLUS GALLUS (CHICKEN).//Q98937

45 F-NT2RP2003499//S55 ANTIGEN.//0.090:114:32//RATTUS NORVEGICUS (RAT).//Q63003

F-NT2RP2003506//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//2.0e-11:91:43//SUS SCROFA (PIG).//P04175

F-NT2RP2003511//PARAMYOSIN, SHORT FORM (MIMIPARAMYOSIN).//0.0020:108:25//DROSOPHILA MELANOGASTER (FRUIT FLY).//P35416

50 F-NT2RP2003513//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.2e-05:96:36//HOMO SAPIENS (HUMAN).//P23246

F-NT2RP2003517//HYPOTHETICAL 12.9 KD PROTEIN CY49.27.//0.0059:22:31//MYCOBACTERIUM TUBERCULOSIS.//Q10696

F-NT2RP2003522//HYPOTHETICAL 10.0 KD PROTEIN.//1.0:65:30//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19283

55 F-NT2RP2003533//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//8.7e-18:94:54//HOMO SAPIENS (HUMAN).//P08547

F-NT2RP2003543//SYNAPSINS IA AND IB.//0.045:101:35//RATTUS NORVEGICUS (RAT).//P09951

- F-NT2RP2003559//ITBA2 PROTEIN (DXS9879E)//0.98:37:37//HOMO SAPIENS (HUMAN)//Q14657  
 F-NT2RP2003564//52 KD RO PROTEIN (SJOJGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))//6.4e-35:175:44//HOMO SAPIENS (HUMAN)//P19474  
 F-NT2RP2003567//HYPOTHETICAL 11.2 KD PROTEIN T18D3.7 IN CHROMOSOME X//0.72:82:34//CAENORHABDITIS ELEGANS//Q22544  
 F-NT2RP2003581//HOMEBOX PROTEIN OTX1//0.90:61:37//MUS MUSCULUS (MOUSE)//P80205  
 F-NT2RP2003596//ELONGATION FACTOR P (EF-P)//0.83:61:32//MYCOPLASMA GENITALIUM//P47272  
 F-NT2RP2003604//ALPHA-CATENIN//1.5e-11:152:33//DROSOPHILA MELANOGASTER (FRUIT FLY)//P35220  
 F-NT2RP2003629//PHOSPHOLIPASE A2 ALPHA (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE)//0.97:85:27//CROTALUS ADAMANTEUS (EASTERN DIAMONDBACK RATTLESNAKE)//P00623  
 F-NT2RP2003643//ACYLNEURAMINATE CYTIDYLTRANSFERASE (EC 2.7.7.43) (CMP-N- ACETYLNEURAMINIC ACID SYNTHETASE) (CMP-NEUNAC SYNTHETASE) (CMP-SIALIC ACID SYNTHETASE)//3.9e-12:84:40//NEISSERIA MENINGITIDIS//Q57385  
 F-NT2RP2003668//ALU-SUBFAMILY SX WARNING ENTRY!!!!/5.0e-33:74:81//HOMO SAPIENS (HUMAN)//P39195  
 F-NT2RP2003687//ALU SUBFAMILY J WARNING ENTRY!!!!/5.7e-05:40:67//HOMO SAPIENS (HUMAN)//P39188  
 F-NT2RP2003691//ALU SUBFAMILY SQ WARNING ENTRY!!!!/2.5e-37:56:67//HOMO SAPIENS (HUMAN)//P39194  
 F-NT2RP2003702//HYPOTHETICAL OXIDOREDUCTASE IN INLA 5'REGION (EC 1.-.-.-) (ORFA)//1.3e-07:98:37//LISTERIA MONOCYTOGENES//P25145  
 F-NT2RP2003704//GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (EC 2.3.2.2) (GAMMA-GLUTAMYLTRANSFERASE 5) (GGT-REL)//0.66:23:52//HOMO SAPIENS (HUMAN)//P36269  
 F-NT2RP2003706//GLUTAMYLAMINOPEPTIDASE (EC 3.4.11.7) (EAP) (AMINOPEPTIDASE A) (APA) (DIFFERENTIATION ANTIGEN GP160)//1.2e-22:187:35//HOMO SAPIENS (HUMAN)//Q07075  
 F-NT2RP2003713//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 6 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 6) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 6) (DEUBIQUITINATING ENZYME 6) (PROTO-ONCOGENE TRE-2)//2.7e-06:119:34//HOMO SAPIENS (HUMAN)//P35125  
 F-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//6.7e-27:68:75//HOMO SAPIENS (HUMAN)//Q05481  
 F-NT2RP2003727//HYPOTHETICAL PROTEIN MG007 HOMOLOG//0.64:110:30//MYCOPLASMA PNEUMONIAE//P75105  
 F-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2)//1.2e-72:147:90//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P51669  
 F-NT2RP2003751//EXTRACELLULAR GLOBIN PRECURSOR//0.67:68:30//PSEUDOTERRANOVA DECIPIENS (COD WORM)//P26914  
 F-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP)//1.0e-98:235:82//BOS TAURUS (BOVINE)//P53620  
 F-NT2RP2003764//HYPOTHETICAL 29.3 KD PROTEIN (ORF92)//0.011:69:34//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV)//O10341  
 F-NT2RP2003769//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:33:36//EQUUS CABALLUS (HORSE)//P48663  
 F-NT2RP2003770//PHOSPHATE REGULON SENSOR PROTEIN PHOR (EC 2.7.3.-) (FRAGMENT)//0.029:35:42//PSEUDOMONAS AERUGINOSA//P23621  
 F-NT2RP2003777//HYPOTHETICAL 82 KD AVIRULENCE PROTEIN IN AVRBS3 REGION//0.041:67:34//XANTHOMONAS CAMPESTRIS (PV. VESICATORIA)//P14728  
 F-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II//4.7e-54:204:47//CAENORHABDITIS ELEGANS//Q09201  
 F-NT2RP2003793//PSEUDO-HEVEIN (MINOR HEVEIN)//0.61:30:36//HEVEA BRASILIENSIS (PARA RUBBER TREE)//P80359  
 F-NT2RP2003825//ENDOTHELIN-1 PRECURSOR (ET-1) (FRAGMENT)//1.0:35:37//CANIS FAMILIARIS (DOG)//P13206  
 F-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X//2.5e-05:80:38//CAENORHABDITIS ELEGANS//Q11076  
 F-NT2RP2003857//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17)//0.54:28:50//ESCHERICHIA CO-

LI.//P05834  
 F-NT2RP2003859//DROSOCIN PRECURSOR.//1.0:37:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P36193  
 F-NT2RP2003871  
 5 F-NT2RP2003885//CUTICLE PROTEIN 32 (LM-32) (LM-ACP 32) (FRAGMENT).//1.0:28:50//LOCUSTA MIGRATORIA (MIGRATORY LOCUST).//P11736  
 F-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NEK1 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 1).//4.9e-110:268:80//MUS MUSCULUS (MOUSE).//P51954  
 F-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//0.00024:92:31//RATTUS NORVEGICUS (RAT).//009175  
 10 F-NT2RP2003968//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//9.2e-05:101:36//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437  
 F-NT2RP2003976//ALU SUBFAMILY J WARNING ENTRY !!!!!/1.7e-21:62:62//HOMO SAPIENS (HUMAN).//P39188  
 15 F-NT2RP2003981//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS8.//2.7e-08:165:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39702  
 F-NT2RP2003984//UNC-87 PROTEIN.//0.75:71:28//CAENORHABDITIS ELEGANS.//P37806  
 F-NT2RP2003986//ALU SUBFAMILY SP WARNING ENTRY !!!!!/5.3e-19:47:70//HOMO SAPIENS (HUMAN).//P39193  
 20 F-NT2RP2003988//ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.2e-18:80:58//HOMO SAPIENS (HUMAN).//P39195  
 F-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//1.0e-52:141:77//HOMO SAPIENS (HUMAN).//P20290  
 25 F-NT2RP2004014//MACROPHAGE INFLAMMATORY PROTEIN-2-ALPHA (MIP2-ALPHA) (CINC-2-ALPHA).//0.99:45:26//RATTUS NORVEGICUS (RAT).//Q10746  
 F-NT2RP2004041//SYNAPSINS IA AND IB.//0.0022:51:37//BOS TAURUS (BOVINE).//P17599  
 F-NT2RP2004042//CRUSTACEAN HYPERGLYCEMIC HORMONE PRECURSOR (CHH) (FRAGMENT).//1.0:49:28//PENAEUS VANNAMEI (PENOEID SHRIMP) (EUROPEAN WHITE SHRIMP).//Q26181  
 30 F-NT2RP2004068//CALDES MON (CDM).//2.9e-05:175:21//GALLUS GALLUS (CHICKEN).//P12957  
 F-NT2RP2004081//CADMIUM-METALLOTHIONEIN (CD-MT).//0.93:59:23//HELIIX POMATIA (ROMAN SNAIL) (EDIBLE SNAIL).//P33187  
 F-NT2RP2004098//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//4.6e-09:121:30//HOMO SAPIENS (HUMAN).//Q15404  
 35 F-NT2RP2004124//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.068:63:31//GALLUS GALLUS (CHICKEN).//P02314  
 F-NT2RP2004142//HYPOTHETICAL 59.1 KD PROTEIN IN VPS15-YMC2 INTERGENIC REGION.//7.9e-05:94:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38262  
 F-NT2RP2004152//LAMIN L(I).//0.25:167:19//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P06010  
 40 F-NT2RP2004165//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.0014:124:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214  
 F-NT2RP2004170//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.012:125:30//MUS MUSCULUS (MOUSE).//P05143  
 F-NT2RP2004172//HYPOTHETICAL 105.7 KD PROTEIN IN TPK3-PIR1 INTERGENIC REGION.//4.1e-26:214:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36051  
 45 F-NT2RP2004187//ZINC FINGER PROTEIN 174.//3.7e-12:76:47//HOMO SAPIENS (HUMAN).//Q15697  
 F-NT2RP2004194//HYPOTHETICAL 10.5 KD PROTEIN C31A2.13C IN CHROMOSOME I.//0.0013:92:23//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09730  
 F-NT2RP2004196//METALLOTHIONEIN 10-II (MT-10-II).//0.92:36:36//MYTILUS EDULIS (BLUE MUSSEL).//P80247  
 50 F-NT2RP2004207//MALE ACCESSORY GLAND SECRETORY PROTEIN 355A PRECURSOR.//0.92:62:35//DROSOPHILA SIMULANS (FRUIT FLY).//P33737  
 F-NT2RP2004226//66 KD STRESS PROTEIN (P66).//0.030:113:26//PHYSARUM POLYCEPHALUM (SLIME MOLD).//P90587  
 55 F-NT2RP2004232//PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).//2.0e-48:211:51//HOMO SAPIENS (HUMAN).//Q15139  
 F-NT2RP2004239//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR.//0.00038:111:36//TRITICUM AESTIVUM (WHEAT).//P08489

- F-NT2RP2004240//METALLOTHIONEIN-II (MT-II) (METALLOTHIONEIN-LIKE PROTEIN) (MT-CE) //1.0.39:28//  
CAENORHABDITIS ELEGANS. //P17512
- F-NT2RP2004242//RAS-RELATED PROTEIN RGP1 (GTP-BINDING REGULATORY PROTEIN RGP1) //0.0036:  
64:28//ORYZA SATIVA (RICE). //P25766
- 5 F-NT2RP2004245//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L) //1.0.21:42//PONGO PYGMAEUS PYG-  
MAEUS (BORNEAN ORANGUTAN). //P92896
- F-NT2RP2004270//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT) //0.00023:118:33//NEPHILA CLA-  
VIPES (ORB SPIDER). //P46804
- 10 F-NT2RP2004300//PROBABLE E4 PROTEIN //0.18:77:40//HUMAN PAPILLOMAVIRUS TYPE 8. //P06425
- F-NT2RP2004316  
F-NT2RP2004321//HYPOTHETICAL 10.8 KD PROTEIN SSR2439. //1.0.50:28//SYNECHOCYSTIS SP. (STRAIN  
PCC 6803). //Q01904
- F-NT2RP2004339//ALU SUBFAMILY SX WARNING ENTRY !!!/5.0e-33:84:77//HOMO SAPIENS (HUMAN). //P39195
- 15 F-NT2RP2004347//HYPOTHETICAL 40.9 KD PROTEIN F33H1.3 FROM CHROMOSOME II. //0.78:96:30//  
CAENORHABDITIS ELEGANS. //Q09556
- F-NT2RP2004364//MINOR OUTER CAPSID PROTEIN (NS26) (NONSTRUCTURAL PROTEIN VP9). //0.059:143:  
30//BOVINE ROTAVIRUS (STRAIN UK). //P04515
- F-NT2RP2004365//EAMZP30-47 PROTEIN (FRAGMENT) //0.27:38:39//EIMERIA ACERVULINA. //P21959
- 20 F-NT2RP2004366//GLYCOPROTEIN L PRECURSOR //0.64:71:28//MAREK'S DISEASE HERPESVIRUS  
(STRAIN GA) (MDHV). //P52510
- F-NT2RP2004373//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (HISTIDINE-PROLINE RICH GLYCO-  
PROTEIN) (HPRG) (FRAGMENT). //0.59:50:40//ORYCTOLAGUS CUNICULUS (RABBIT). //Q28640
- F-NT2RP2004389//HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III. //4.0e-16:89:43//  
CAENORHABDITIS ELEGANS. //P34388
- 25 F-NT2RP2004392  
F-NT2RP2004396//SINGLE-STRANDED NUCLEIC ACID-BINDING PROTEIN. //0.42:89:29//SACCHAROMY-  
CES CEREVISIAE (BAKER'S YEAST). //P10080
- F-NT2RP2004399//SOMATOTROPIN PRECURSOR (GROWTH HORMONE). //1.0.72:34//MESOCRICETUS AU-  
RATUS (GOLDEN HAMSTER). //P37886
- 30 F-NT2RP2004400  
F-NT2RP2004412//SPERM PROTAMINE P1. //0.24:38:31//NOTORYCTES TYPHLOPS (MARSUPIAL MOLE). //P42143
- F-NT2RP2004425//SUPPRESSOR PROTEIN SRP40. //0.0087:197:22//SACCHAROMYCES CEREVISIAE (BAK-  
ER'S YEAST). //P32583
- 35 F-NT2RP2004463//ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR). //1.3e-05:  
121:37//MUS MUSCULUS (MOUSE). //Q01338
- F-NT2RP2004476//NICKEL-SENSITIVE T-TYPE CALCIUM CHANNEL ALPHA-1 SUBUNIT (RBE-II). //0.20:68:  
36//RATTUS NORVEGICUS (RAT). //Q07652
- 40 F-NT2RP2004490//FOS-RELATED ANTIGEN 1. //0.94:59:33//HOMO SAPIENS (HUMAN). //P15407
- F-NT2RP2004512//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3) (FRAGMENTS). //1.0.37:  
32//SISATER OCHRACEUS (SEA STAR). //P24998
- F-NT2RP2004523//ALU SUBFAMILY SQ WARNING ENTRY !!!/2.1e-15:57:71//HOMO SAPIENS (HUMAN). //P39194
- 45 F-NT2RP2004538//KINESIN-LIKE PROTEIN KIF1A (AXONAL TRANSPORTER OF SYNAPTIC VESICLES). //1.2e-48:  
121:60//HOMO SAPIENS (HUMAN). //Q12756
- F-NT2RP2004551//HYPOTHETICAL 7.6 KD PROTEIN (ORF 65). //1.0.20:50//EUGLENA GRACILIS. //P32095
- F-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03. //5.2e-07:150:30//SCHIZOSAC-  
CHAROMYCES POMBE (FISSION YEAST). //Q09903
- 50 F-NT2RP2004580//ALU SUBFAMILY SC WARNING ENTRY !!!/3.7e-37:100:78//HOMO SAPIENS (HU-  
MAN). //P39192
- F-NT2RP2004587//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION. //8.2e-06:  
150:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P53214
- F-NT2RP2004594//HYPOTHETICAL 45.3 KD PROTEIN C09F5.7 IN CHROMOSOME II. //0.84:105:24//  
CAENORHABDITIS ELEGANS. //Q09458
- 55 F-NT2RP2004600//MYRISTOYLALANINE-RICH C-KINASE SUBSTRATE (MARCKS). //0.17:127:29//RAT-  
TUS NORVEGICUS (RAT). //P30009
- F-NT2RP2004602//ALU SUBFAMILY J WARNING ENTRY !!!/1.1e-05:50:58//HOMO SAPIENS (HUMAN). //

- P39188  
F-NT2RP2004614//HYPOTHETICAL 11.6 KD PROTEIN.//1.0:68:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20561
- 5 F-NT2RP2004655//GLYCINE-RICH RNA-BINDING PROTEIN 7.//17.0e-05:70:42//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q03250  
F-NT2RP2004664//HYPOTHETICAL 104.0 KD PROTEIN C32A11.03C IN CHROMOSOME I.//0.30:78:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10328  
F-NT2RP2004675  
F-NT2RP2004681
- 10 F-NT2RP2004689//HYPOTHETICAL 78.3 KD PROTEIN IN RAM2-ATP7 INTERGENIC REGION.//0.021:179:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P34243  
F-NT2RP2004709//HYPOTHETICAL PROTEIN MJ0647.//0.90:39:43//METHANOCOCCUS JANNASCHII.//Q58063  
F-NT2RP2004710//GAR2 PROTEIN.//0.085:60:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891  
F-NT2RP2004736//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.4e-15:97:49//HOMO SAPIENS (HUMAN).//P39188  
F-NT2RP2004743//MALE SPECIFIC SPERM PROTEIN MST87F.//0.43:24:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175
- 20 F-NT2RP2004767//36.4 KD PROLINE-RICH PROTEIN.//0.0051:88:27//LYCOPERSICON ESCULENTUM (TOMATO).//Q00451  
F-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).//9.0e-29:166:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38692  
F-NT2RP2004775
- 25 F-NT2RP2004791//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//7.4e-60:226:53//CAENORHABDITIS ELEGANS.//Q09996  
F-NT2RP2004799//SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//2.2e-42:133:57//NEOCALLIMASTIX FRONTALIS (RUMEN FUNGUS).//P53587
- 30 F-NT2RP2004802//HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION.//0.018:86:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898  
F-NT2RP2004816//H<-BETA>58 PROTEIN.//1.0e-68:145:93//MUS MUSCULUS (MOUSE).//P40336  
F-NT2RP2004841//DSRD PROTEIN.//0.83:33:39//ARCHAEOGLOBUS FULGIDUS.//P70742  
F-NT2RP2004861//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIA3A.//0.0072:41:39//OVIS ARIES (SHEEP).//P02443
- 35 F-NT2RP2004897//METALLOTHIONEIN-LIKE PROTEIN 1.//0.99:41:41//CASUARINA GLAUCA (SWAMP OAK).//Q39511  
F-NT2RP2004933//DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1).//8.4e-34:102:67//HOMO SAPIENS (HUMAN).//P53355
- 40 F-NT2RP2004936//HIGH POTENTIAL IRON-SULFUR PROTEIN, ISOZYME 2 (HIPI 2).//0.87:36:33//EC-TOTHIORHODOSPIRA VACUOLATA.//P38524  
F-NT2RP2004959//STEM CELL FACTOR PRECURSOR (SCF) (MAST CELL GROWTH FACTOR) (MGF) (C-KIT LIGAND).//1.0:69:28//CANIS FAMILIARIS (DOG).//Q06220  
F-NT2RP2004961//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) (FRAGMENT).//2.1e-21:73:58//HOMO SAPIENS (HUMAN).//Q06730
- 45 F-NT2RP2004962//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/0.17:28:57//HOMO SAPIENS (HUMAN).//P39189  
F-NT2RP2004967//HYPOTHETICAL 7.3 KD PROTEIN.//0.76:41:31//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19301
- 50 F-NT2RP2004978//SPERMATID-SPECIFIC PROTEIN T2 [CONTAINS: SPERM PROTAMINE SP2].//0.44:40:45//SEPIA OFFICINALIS (COMMON CUTTLEFISH).//P80002  
F-NT2RP2004982  
F-NT2RP2004985//HYPOTHETICAL PROTEIN KIAA0144.//1.2e-51:204:57//HOMO SAPIENS (HUMAN).//Q14157
- 55 F-NT2RP2004999//LONG NEUROTOXIN 1 (ALPHA-BUNGAROTOXIN) (BGTX).//0.23:73:26//BUNGARUS MUL-TICINCTUS (MANY-BANDED KRAIT).//P01378  
F-NT2RP2005000//ATPASE STABILIZING FACTOR 15 KD PROTEIN.//0.12:37:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P16965

- F-NT2RP2005001//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.90:54:31//HOMO SAPIENS (HUMAN).//P22531
- F-NT2RP2005003//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//1.6e-30:78:56//MUS MUSCULUS (MOUSE).//P15533
- 5 F-NT2RP2005012//NPL1 PROTEIN (SEC63 PROTEIN).//0.00024:94:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P14906
- F-NT2RP2005018//GAG POLYPROTEIN (CORE POLYPROTEIN) [CONTAINS: CORE PROTEINS P19, P10] (FRAGMENT).//1.0:91:28//AVIAN ENDOGENOUS ROUS-ASSOCIATED VIRUS-0 (EV-2) (AVIAN RETROVIRUS RAV-0).//P08937
- 10 F-NT2RP2005020
- F-NT2RP2005022//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//4.9e-11:106:35//PODOSPORA ANSERINA.//Q00808
- F-NT2RP2005031
- 15 F-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//2.2e-32:117:55//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32447
- F-NT2RP2005038//DNA NUCLEOTIDYLTRANSFERASE (EC 2.7.7.31) (TERMINAL ADDITION ENZYME) (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFERASE).//9.3e-28:187:40//AMBYSTOMA MEXICANUM (AXOLOTL).//O57486
- F-NT2RP2005108//CUTICLE COLLAGEN 2.//0.33:62:38//CAENORHABDITIS ELEGANS.//P17656
- 20 F-NT2RP2005116//PUTATIVE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 ALPHA SUBUNIT (EIF-3 ALPHA).//4.0e-54:161:63//CAENORHABDITIS ELEGANS.//P34466
- F-NT2RP2005126//CHLOROPLAST 50S RIBOSOMAL PROTEIN L27 (FRAGMENT).//0.23:46:39//PLEUROCHYSIS HAPTONEMOFERA.//P41552
- F-NT2RP2005139//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.016:43:37//BOS TAURUS (BOVINE).//P25508
- 25 F-NT2RP2005140//HYPOTHETICAL 7.4 KD PROTEIN YCF33.//0.96:51:39//GUILLARDIA THETA (CRYPTOMONAS PHI).//O78517
- F-NT2RP2005144//TUBBY PROTEIN.//5.6e-08:66:45//MUS MUSCULUS (MOUSE).//P50586
- F-NT2RP2005147
- 30 F-NT2RP2005159//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR.//0.94:57:29//NICOTIANA TABACUM (COMMON TOBACCO), AND SPINACIA OLERACEA (SPINACH).//P12164
- F-NT2RP2005162//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION.//1.2e-33:139:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38821
- F-NT2RP2005168//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U).//2.8e-33:102:61//HOMO SAPIENS (HUMAN).//Q00839
- 35 F-NT2RP2005204//DNA DAMAGE TOLERANCE PROTEIN RHC31 (RAD31 HOMOLOG).//3.9e-28:141:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06624
- F-NT2RP2005227
- F-NT2RP2005239//TRNA SPLICING PROTEIN SPL1.//2.0e-38:117:64//CANDIDA ALBICANS (YEAST).//P87185
- 40 F-NT2RP2005254//OMEGA-AGATOXIN IB (OMEGA-AGA-IB) (FRAGMENT).//0.26:29:48//AGELLENOPSIS APERTA (FUNNEL-WEB SPIDER).//P15970
- F-NT2RP2005270//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4).//0.037:82:34//GALLUS GALLUS (CHICKEN).//P17277
- F-NT2RP2005278//LONG-CHAIN-FATTY-ACID-COA LIGASE 4 (EC 6.2.1.3) (LONG-CHAIN ACYL-COA SYNTHETASE 4) (LACS 4).//2.0e-59:174:61//RATTUS NORVEGICUS (RAT).//O35547
- 45 F-NT2RP2005287//ZINC FINGER PROTEIN 26 (ZINC FINGER PROTEIN KOX20) (FRAGMENT).//1.5e-05:27:70//HOMO SAPIENS (HUMAN).//P17031
- F-NT2RP2005288//PROBABLE RUBREDOXIN HUPI.//1.0:42:28//RHIZOBIUM LEGUMINOSARUM (BIOVAR VICIAE).//P28151
- 50 F-NT2RP2005289//ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.1e-21:75:70//HOMO SAPIENS (HUMAN).//P39193
- F-NT2RP2005293//TRANSLATION INITIATION FACTOR IF-2.//0.58:170:24//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//P55972
- F-NT2RP2005315//CUTICLE COLLAGEN 7 (FRAGMENT).//0.091:65:38//CAENORHABDITIS ELEGANS.//P18832
- 55 F-NT2RP2005325//CHROMOGRANIN A PRECURSOR (CGA) (PITUITARY SECRETORY PROTEIN I) (SP-I) [CONTAINS: PANCREASTATIN; WE-14].//9.5e-09:98:39//HOMO SAPIENS (HUMAN).//P10645
- F-NT2RP2005336//HYPOTHETICAL 68.7 KD PROTEIN IN STB1-MCK1 INTERGENIC REGION.//0.00011:124:

- 28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P42846  
 F-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 4 (EC 3.6.1.38)//4.7e-21:92:52//SAC-  
 CHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q12675  
 F-NT2RP2005354  
 5 F-NT2RP2005358//MYOSIN IC HEAVY CHAIN//0.012:91:39//ACANTHAMOEBA CASTELLANII (AMOEBA)//  
 P10569  
 F-NT2RP2005360//ACROSIN PRECURSOR (EC 3.4.21.10)//0.0022:73:36//ORYCTOLAGUS CUNICULUS  
 (RABBIT)//P48038  
 10 F-NT2RP2005393//HYPOTHETICAL 25.9 KD PROTEIN AH6.3 IN CHROMOSOME II//0.00085:135:28//  
 CAENORHABDITIS ELEGANS//Q09202  
 F-NT2RP2005407//SQUALENE MONOOXYGENASE (EC 1.14.99.7) (SQUALENE EPOXIDASE) (SE)//0.96:  
 109:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32476  
 F-NT2RP2005436//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN)//0.0011:54:42//ZEA MAYS  
 (MAIZE)//P14918  
 15 F-NT2RP2005441//PROLINE-RICH PROTEIN MP-2 PRECURSOR//0.039:182:29//MUS MUSCULUS  
 (MOUSE)//P05142  
 F-NT2RP2005453  
 F-NT2RP2005457//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3)  
 (COMPLEX I-B14.5B) (CI-B14.5B)//4.0e-10:124:37//BOS TAURUS (BOVINE)//Q02827  
 20 F-NT2RP2005464//HYPOTHETICAL 9.5 KD PROTEIN//0.96:42:33//VACCINIA VIRUS (STRAIN COPENHA-  
 GEN)//P20553  
 F-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2//4.6e-09:92:42//SACCHAROMYCES CERE-  
 VISIAE (BAKER'S YEAST)//P38127  
 F-NT2RP2005472//HYPOTHETICAL PROTEIN BB0129//0.76:80:32//BORRELIA BURGDORFERI (LYME DIS-  
 EASE SPIROCHETE)//O51155  
 25 F-NT2RP2005476//ALU SUBFAMILY SP WARNING ENTRY!!!!/1.0e-31:39:89//HOMO SAPIENS (HUMAN)//  
 P39193  
 F-NT2RP2005490//METALLOTHIONEIN-II (MT-II)//0.14:27:33//SCYLLA SERRATA (MUD CRAB)//P02806  
 F-NT2RP2005491//DNA-DIRECTED RNA POLYMERASE SUBUNIT I (EC 2.7.7.6)//0.95:45:31//METHANO-  
 COCCUS JANNASCHII//Q58785  
 30 F-NT2RP2005495//HYPOTHETICAL 10.8 KD PROTEIN IN GP30-RIII INTERGENIC REGION//0.99:68:30//BAC-  
 TERIOPHAGE T4//Q02407  
 F-NT2RP2005496//ZINC FINGER PROTEIN 135//1.4e-54:120:59//HOMO SAPIENS (HUMAN)//P52742  
 F-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PRO-  
 TEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55)//9.5e-76:146:86//RATTUS NOR-  
 VEGICUS (RAT)//P36876  
 35 F-NT2RP2005501//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PRO-  
 TEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN)  
 (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP)//0.025:70:40//HOMO SAPIENS (HU-  
 MAN)//P17931  
 40 F-NT2RP2005509//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR//1.0:166:27//GALLUS GALLUS (CHICK-  
 EN)//P02457  
 F-NT2RP2005520//CHROMOSOME ASSEMBLY PROTEIN XCAP-E//7.9e-45:118:79//XENOPUS LAEVIS (AF-  
 RICAN CLAWED FROG)//P50533  
 45 F-NT2RP2005525//50S RIBOSOMAL PROTEIN L11//1.0:47:27//BORRELIA BURGDORFERI (LYME DISEASE  
 SPIROCHETE)//O51354  
 F-NT2RP2005531//PROTEIN-TYROSINE PHOSPHATASE MEG1 (EC 3.1.3.48) (PTPASE-MEG1) (MEG)//9.8e-  
 13:84:45//HOMO SAPIENS (HUMAN)//P29074  
 F-NT2RP2005539//RING CANAL PROTEIN (KELCH PROTEIN)//4.9e-10:90:33//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY)//Q04852  
 50 F-NT2RP2005540//NUCLEOTIDE BINDING PROTEIN EXPZ//0.36:119:21//BACILLUS SUBTILIS//P39115  
 F-NT2RP2005549//HYPOTHETICAL 32.0 KD PROTEIN C16C10.10 IN CHROMOSOME III//6.0e-39:179:46//  
 CAENORHABDITIS ELEGANS//Q09253  
 F-NT2RP2005555  
 55 F-NT2RP2005557//HYPOTHETICAL 23.7 KD PROTEIN C13G6.14 IN CHROMOSOME I//4.9e-06:90:35//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09790  
 F-NT2RP2005581  
 F-NT2RP2005600//BASIC PROLINE-RICH PEPTIDE P-E (IB-9)//0.014:37:40//HOMO SAPIENS (HUMAN)//



P02811

F-NT2RP2005605//GONADOLIBERIN I PRECURSOR (LHRH I) (LUTEINIZING HORMONE RELEASING HORMONE I) (GONADOTROPIN RELEASING HORMONE I) (GNRH I) (LULIBERIN I) (FRAGMENT).//0.64:26:42//MACACA MULATTA (RHESUS MACAQUE).//P55247

F-NT2RP2005620//HYPOTHETICAL 45.1 KD PROTEIN IN RP55-ZMS1 INTERGENIC REGION.//8.7e-31:138:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160

F-NT2RP2005622//NEUROTOXIN-LIKE PROTEIN STR1 (ANATOXIN AAH STR1).//0.39:22:40//ANDROCTONUS AUSTRALIS HECTOR (SAHARA SCORPION).//P80950

F-NT2RP2005635//HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION.//5.8e-43:144:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38795

F-NT2RP2005637//VPU PROTEIN (U ORF PROTEIN).//0.91:33:45//CHIMPANZEE IMMUNODEFICIENCY VIRUS (SIV(CPZ)) (CIV).//P17286

F-NT2RP2005640//METALLOTHIONEIN-LIKE PROTEIN LSC54.//0.63:41:31//BRASSICA NAPUS (RAPE).//P43402

F-NT2RP2005645

F-NT2RP2005651//OCTAMER-BINDING TRANSCRIPTION FACTOR 3A (OCT-3A) (OCT-4).//0.0023:50:42//HOMO SAPIENS (HUMAN).//Q01860

F-NT2RP2005654//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION.//6.1e-16:76:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40564

F-NT2RP2005669//METALLOTHIONEIN-II (MT-II).//0.76:16:50//SCYLLA SERRATA (MUD CRAB).//P02806

F-NT2RP2005675//PUTATIVE ORAL CANCER SUPPRESSOR (DELETED IN ORAL CANCER-1).//6.5e-26:116:54//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//P49119

F-NT2RP2005683//HYPOTHETICAL PROTEIN HI0275.//0.17:50:40//HAEMOPHILUS INFLUENZAE.//P43975

F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//1.3e-16:75:30//PISUM SATIVUM (GARDEN PEA).//Q04708

F-NT2RP2005694//HYPOTHETICAL PROTEIN KIAA0032.//9.6e-11:135:34//HOMO SAPIENS (HUMAN).//Q15034

F-NT2RP2005701//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.084:158:32//HOMO SAPIENS (HUMAN).//P10161

F-NT2RP2005712//METALLOTHIONEIN-II (MT-II).//0.19:14:50//STENELLA COERULEALBA (STRIPED DOLPHIN).//P14425

F-NT2RP2005719//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).//1.0:36:41//ORYCTOLAGUS CUNICULUS (RABBIT).//P02456

F-NT2RP2005722//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//7.8e-37:131:62//HOMO SAPIENS (HUMAN).//P16415

F-NT2RP2005723//ALU SUBFAMILY SC WARNING ENTRY !!!!!//0.98:23:60//HOMO SAPIENS (HUMAN).//P39192

F-NT2RP2005726//HYPOTHETICAL PROTEIN TP0375.//0.98:30:43//TREPONEMA PALLIDUM.//O83390

F-NT2RP2005732//PERIOD CLOCK PROTEIN (FRAGMENT).//0.41:20:55//DROSOPHILA ROBUSTA (FRUIT FLY).//Q03296

F-NT2RP2005741//SMR1 PROTEIN PRECURSOR (VCS-ALPHA 1).//0.38:58:36//RATTUS NORVEGICUS (RAT).//P13432

F-NT2RP2005748//ZINC FINGER PROTEIN KOX23 (FRAGMENT).//0.026:19:68//HOMO SAPIENS (HUMAN).//P17034

F-NT2RP2005752//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//0.90:101:31//HOMO SAPIENS (HUMAN).//P02461

F-NT2RP2005753//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.50:22:58//HOMO SAPIENS (HUMAN).//P30808

F-NT2RP2005763//PUTATIVE ATP-DEPENDENT RNA HELICASE STE13.//4.7e-14:108:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09181

F-NT2RP2005767//NONHISTONE CHROMOSOMAL PROTEIN 6B.//4.1e-08:65:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11633

F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//1.2e-14:65:61//HOMO SAPIENS (HUMAN).//P32322

F-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP).//1.3e-103:199:90//ORYCTOLAGUS CUNICULUS (RABBIT).//P42675

F-NT2RP2005781//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1 / PRP-

- 3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C) [CONTAINS: PEPTIDE P-C] //0.090:73:36//HOMO SAPIENS (HUMAN) //P02810
- F-NT2RP2005784//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VWV110) (ALPHA-0 PROTEIN) //3.5e-06:79:37//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17) //P08393
- 5 F-NT2RP2005804//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT) //1.8e-07:43:55//OWENIA FUSIFORMIS //P21260
- F-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION //6.3e-14:143:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P40004
- 10 F-NT2RP2005815//FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) //0.0017:123:37//MYCOBACTERIUM AVIUM //O07401
- F-NT2RP2005835//SHP1 PROTEIN //1.2e-08:135:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P34223
- 15 F-NT2RP2005841//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N) //0.23:28:53//HOMO SAPIENS (HUMAN) //P22532
- F-NT2RP2005853//HYPOTHETICAL 8.5 KD PROTEIN IN ASIA-MOTA INTERGENIC REGION //0.99:33:48//BACTERIOPHAGE T4 //P22917
- F-NT2RP2005857//CHROMOSOME ASSEMBLY PROTEIN XCAP-C //8.6e-84:235:66//XENOPUS LAEVIS (AFRICAN CLAWED FROG) //P50532
- 20 F-NT2RP2005859//MALE SPECIFIC SPERM PROTEIN MST84DB //0.017:60:40//DROSOPHILA MELANOGASTER (FRUIT FLY) //Q01643
- F-NT2RP2005868//ATP SYNTHASE B' CHAIN PRECURSOR (EC 3.6.1.34) (SUBUNIT II) //0.28:121:28//SPINACIA OLERACEA (SPINACH) //P31853
- F-NT2RP2005886//MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA] //0.80:130:28//TETRAHYMENA THERMOPHILA //P40631
- 25 F-NT2RP2005890
- F-NT2RP2005901//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L) //0.35:18:44//DROSOPHILA YAKUBA (FRUIT FLY) //P03933
- 30 F-NT2RP2005908//ALU SUBFAMILY SQ WARNING ENTRY !!!!! //1.0e-28:61:65//HOMO SAPIENS (HUMAN) //P39194
- F-NT2RP2005933//PERIOD CLOCK PROTEIN (P230) (FRAGMENT) //1.7e-11:85:49//ACETABULARIA MEDITERRANEA (MERMAID'S WINE GLASS) //P12347
- F-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) //7.2e-59:216:58//BOS TAURUS (BOVINE) //P25500
- 35 F-NT2RP2005980//HYPOTHETICAL 11.5 KD PROTEIN IN RSP8A-AST1 INTERGENIC REGION //1.0:49:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P38185
- F-NT2RP2006023//DNA REPAIR PROTEIN RECN (RECOMBINATION PROTEIN N) (FRAGMENT) //1.0:40:45//VIBRIO CHOLERAE //P52118
- 40 F-NT2RP2006038//HYPOTHETICAL 30.2 KD PROTEIN C02F5.4 IN CHROMOSOME III //4.0e-11:90:34//CAENORHABDITIS ELEGANS //P34281
- F-NT2RP2006043//LAMININ BETA-1 CHAIN VARIANT (LAMININ BETA-1-2 CHAIN) (FRAGMENT) //0.00067:73:38//GALLUS GALLUS (CHICKEN) //Q01636
- F-NT2RP2006052//METALLOTHIONEIN-I (MT-I) //0.19:31:38//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET) //P02797
- 45 F-NT2RP2006069//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENTS) //1.0:66:34//RATTUS NORVEGICUS (RAT) //P02466
- F-NT2RP2006071//RESTIN //0.40:156:29//GALLUS GALLUS (CHICKEN) //O42184
- F-NT2RP2006098//HYPOTHETICAL 21.7 KD PROTEIN IN TUP1-ABP1 INTERGENIC REGION //0.99:95:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P25651
- 50 F-NT2RP2006100//LONG NEUROTOXIN 4 (ALPHA-NEUROTOXIN) //0.94:43:34//OPHIOPHAGUS HANNAH (KING COBRA) (NAJA HANNAH) //P80156
- F-NT2RP2006103//50S RIBOSOMAL PROTEIN L32 //0.40:36:38//SYNECHOCYSTIS SP. (STRAIN PCC 6803) //P73014
- 55 F-NT2RP2006106//CUTICLE COLLAGEN 1 //0.28:85:29//CAENORHABDITIS ELEGANS //P08124
- F-NT2RP2006141//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I //1.9e-08:57:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //Q09701
- F-NT2RP2006166

F-NT2RP2006184//HYPOTHETICAL 11.2 KD PROTEIN IN CSGC-MDOG INTERGENIC REGION PRECURSOR.//0.95:87:26//ESCHERICHIA COLI.//P75917

F-NT2RP2006186//MICROTUBULE-ASSOCIATED PROTEIN 2.//0.088:124:33//MUS MUSCULUS (MOUSE).//P20357

5 F-NT2RP2006196//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.0e-05:49:61//HOMO SAPIENS (HUMAN).//P39193

F-NT2RP2006200//PROCOLLAGEN ALPHA 2(V) CHAIN PRECURSOR.//0.0013:205:32//HOMO SAPIENS (HUMAN).//P05997

10 F-NT2RP2006219//GONADAL PROTEIN GDL.//3.5e-18:158:37//DROSOPHILA MELANOGASTER (FRUIT FLY).//P22468

F-NT2RP2006237//FIBRINOGEN- AND IG-BINDING PROTEIN PRECURSOR (MRP PROTEIN).//0.79:103:28//STREPTOCOCCUS PYOGENES.//P30141

F-NT2RP2006238//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//4.7e-07:127:39//MUS MUSCULUS (MOUSE).//P05143

15 F-NT2RP2006258//PROBABLE E5 PROTEIN.//0.78:47:34//RHESUS PAPILLOMAVIRUS TYPE 1 (RHPV 1).//P24834

F-NT2RP2006261//PENAEIDIN-3A PRECURSOR (P3-A).//0.61:35:40//PENAEUS VANNAMEI (PENOEID SHRIMP) (EUROPEAN WHITE SHRIMP).//P81058

F-NT2RP2006275//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 2 (FRAGMENT).//1.2e-28:59:57//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P14401

20 F-NT2RP2006312//HIGH-MOBILITY-GROUP PROTEIN (NONHISTONE CHROMOSOMAL PROTEIN).//1.6e-06:53:35//TETRAHYMENA PYRIFORMIS.//P40625

F-NT2RP2006320//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).//0.90:24:41//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1).//P04612

25 F-NT2RP2006321//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/0.0051:25:76//HOMO SAPIENS (HUMAN).//P39193

F-NT2RP2006323//WISKOTT-ALDRICH SYNDROME PROTEIN (WASP).//0.84:33:39//HOMO SAPIENS (HUMAN).//P42768

F-NT2RP2006333//MYOTOXIN 3 PRECURSOR (CROTAMINE 3).//0.56:37:40//CROTALUS DURISSUS TERRIFICUS (SOUTH AMERICAN RATTLESNAKE).//P24333

30 F-NT2RP2006334//SUCCINYL-COA LIGASE [GDP-FORMING], ALPHA-CHAIN 3 PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN 3).//0.00097:46:41//TRICHOMONAS VAGINALIS.//P53401

F-NT2RP2006365//NONSPECIFIC LIPID-TRANSFER PROTEIN 4.3 PRECURSOR (LTP 4.3).//0.18:75:29//HORDEUM VULGARE (BARLEY).//Q42842

35 F-NT2RP2006393//OMEGA-CONOTOXIN MVIIC PRECURSOR (FRAGMENT).//0.82:15:66//CONUS MAGUS (MAGUS CONE).//P37300

F-NT2RP2006436//ANTERIOR-RESTRICTED HOMEBOX PROTEIN (RATHKE POUCH HOMEBOX).//1.4e-08:50:50//MUS MUSCULUS (MOUSE).//Q61658

40 F-NT2RP2006441//METALLOTHIONEIN-LIKE PROTEIN 1.//0.99:22:54//MIMULUS GUTTATUS (SPOTTED MONKEY FLOWER) (YELLOW MONKEY FLOWER).//P20238

F-NT2RP2006454//SPERM PROTAMINE P1.//0.60:47:36//TACHYGLOSSUS ACULEATUS ACULEATUS (AUSTRALIAN ECHIDNA).//P35311

F-NT2RP2006456

45 F-NT2RP2006464//PHOTOSYSTEM I IRON-SULFUR CENTER (PHOTOSYSTEM I SUBUNIT VII) (9 KD POLYPEPTIDE) (PSI-C).//0.91:79:30//SYNECHOCOCCUS SP. (STRAIN PCC 7002) (AGMENEILLUM QUADRUPLICATUM).//P31087

F-NT2RP2006467//PUTATIVE CUTICLE COLLAGEN F55C10.3.//0.15:53:35//CAENORHABDITIS ELEGANS.//Q21184

50 F-NT2RP2006472//HYPOTHETICAL 19 KD PROTEIN (ORF 167).//0.33:98:26//MARCHANTIA POLYMORPHA (LIVERWORT).//P12202

F-NT2RP2006534

F-NT2RP2006554//ANTI-SIGMA F FACTOR ANTAGONIST (STAGE II SPORULATION PROTEIN AA).//0.91:50:34//BACILLUS SPHAERICUS.//O32723

F-NT2RP2006565//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 1 (SCAMP 37).//6.0e-66:93:96//RATTUS NORVEGICUS (RAT).//P56603

55 F-NT2RP2006571//CYTOCHROME P450 2B10 (EC 1.14.14.1) (CYPIB10) (TESTOSTERONE 16-ALPHA HYDROXYLASE) (P450-16-ALPHA) (CLONE PF3/46).//4.5e-40:138:57//MUS MUSCULUS (MOUSE).//P12791

F-NT2RP2006573//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.53:46:39//BOS TAURUS (BO-

VINE).//P02318  
 F-NT2RP2006598!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.3e-12:44:77//HOMO SAPIENS (HUMAN).//  
 P39195  
 5 F-NT2RP3000002!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.4e-19:60:63//HOMO SAPIENS (HUMAN).//  
 P39192  
 F-NT2RP30000031//HYPOTHETICAL 89.8 KD PROTEIN F41H10.6 IN CHROMOSOME IV.//2.1e-39:210:42//  
 CAENORHABDITIS ELEGANS.//Q20296  
 F-NT2RP3000046//POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF.//1.4e-25:149:44//  
 PSEUDOMONAS PUTIDA.//P25755  
 10 F-NT2RP3000047//NPL4 PROTEIN.//4.7e-48:275:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
 P33755  
 F-NT2RP3000050//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//3.2e-72:232:59//HOMO SA-  
 PIENS (HUMAN).//P51522  
 F-NT2RP3000055//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.26:57:36//DROSOPHILA MELA-  
 15 NOGASTER (FRUIT FLY).//Q01643  
 F-NT2RP3000068//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.//0.0014:66:  
 34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170  
 F-NT2RP3000072//HYPOTHETICAL 6.7 KD PROTEIN IN NOHA-CSPI INTERGENIC REGION.//0.95:49:30//ES-  
 CHERICHIA COLI.//P77695  
 20 F-NT2RP3000080!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.1e-17:64:68//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-NT2RP3000085//BIOTIN CARBOXYLASE (EC 6.3.4.14) (A SUBUNIT OF ACETYL-COA CARBOXYLASE (EC  
 6.4.1.2)) (ACC).//4.4e-43:169:51//BACILLUS SUBTILIS.//P49787  
 F-NT2RP3000092//CELL DIVISION CONTROL PROTEIN 1.//0.00016:103:31//SACCHAROMYCES CEREVI-  
 25 SIAE (BAKER'S YEAST).//P40986  
 F-NT2RP3000109//ACYL CARRIER PROTEIN HOMOLOG (ACP).//0.76:83:28//MYCOPLASMA GENITALIUM.//  
 P47529  
 F-NT2RP3000134  
 F-NT2RP3000142//GAR2 PROTEIN.//0.00098:241:20//SCHIZOSACCHAROMYCES POMBE (FISSION  
 30 YEAST).//P41891  
 F-NT2RP3000149//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.0014:33:36//PONGO PYGMAEUS ABE-  
 LI (SUMATRAN ORANGUTAN).//P92694  
 F-NT2RP3000186!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/8.3e-15:36:83//HOMO SAPIENS (HUMAN).//  
 P39188  
 35 F-NT2RP3000197//HYPOTHETICAL 6.0 KD PROTEIN IN TH12 5'REGION.//0.91:21:52//SACCHAROMYCES  
 CEREVISIAE (BAKER'S YEAST).//P53820  
 F-NT2RP3000207//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-  
 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//0.026:209:27//SACCHAROMYCES CEREVISIAE  
 (BAKER'S YEAST).//P08640  
 40 F-NT2RP3000220//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//1.0:26:42//HOMO  
 SAPIENS (HUMAN).//P30808  
 F-NT2RP3000233//RING CANAL PROTEIN (KELCH PROTEIN).//2.1e-42:249:39//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY).//Q04652  
 45 F-NT2RP3000235//HOMEBOX PROTEIN H40 (FRAGMENT).//0.55:45:40//APIS MELLIFERA (HONEYBEE).//  
 P15858  
 F-NT2RP3000247//HYPOTHETICAL PROTEIN KIA0218.//1.7e-82:123:69//HOMO SAPIENS (HUMAN).//  
 Q93075  
 F-NT2RP3000251//SERINE PROTEINASE STUBBLE (EC 3.4.21.-) (STUBBLE-STUBBLOID PROTEIN).//1.0:53:  
 33//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q05319  
 50 F-NT2RP3000252//HYPOTHETICAL 40 KD GTP-BINDING PROTEIN IN RIBOSOMAL PROTEIN GENE CLUS-  
 TER 5'REGION.//2.2e-06:96:32//HALOBACTERIUM CUTIRUBRUM.//P17103  
 F-NT2RP3000255//HISTONE H1.1 (FRAGMENT).//0.95:71:33//BOS TAURUS (BOVINE).//P02253  
 F-NT2RP3000267//HYPOTHETICAL 21.1 KD PROTEIN IN SSR-SERA INTERGENIC REGION (O182).//0.38:77:  
 33//ESCHERICHIA COLI.//P09160  
 55 F-NT2RP3000299//MYOSIN IC HEAVY CHAIN.//1.2e-11:147:34//ACANTHAMOEBA CASTELLANII (AMOEBA).//  
 P10569  
 F-NT2RP3000312//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.64:216:  
 29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

F-NT2RP3000320//TRANSLATION INITIATION FACTOR IF-2.//5.2e-05:184-22//AQUIFEX AEOLICUS.//O67825  
 F-NT2RP3000324//HYPOTHETICAL PROTEIN HI1036.//0.69:64:35//HAEMOPHILUS INFLUENZAE.//P44097  
 F-NT2RP3000333//WIR1A PROTEIN.//0.35:51:41//TRITICUM AESTIVUM (WHEAT).//Q01482  
 F-NT2RP3000341//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.1e-30:57:80//HOMO SAPIENS (HUMAN).//  
 P39189  
 F-NT2RP3000348  
 F-NT2RP3000350//HYPOTHETICAL 40 KD GTP-BINDING PROTEIN IN RIBOSOMAL PROTEIN GENE CLUS-  
 TER 5'REGION.//0.0011:77:35//HALOBACTERIUM CUTIRUBRUM.//P17103  
 F-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//1.2e-97:222:  
 84//BOS TAURUS (BOVINE).//P08760  
 F-NT2RP3000361//PRE-MRNA SPLICING FACTOR PRP6.//2.2e-08:128:28//SACCHAROMYCES CEREVISIAE  
 (BAKER'S YEAST).//P19735  
 F-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.1e-107:206:99//MUS MUSCULUS (MOUSE).//P35293  
 F-NT2RP3000393//HOMEBOX PROTEIN HOX-C4 (HOX-3E) (CP19).//0.0023:36:52//HOMO SAPIENS (HU-  
 MAN).//P09017  
 F-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13).//  
 5.5e-27:116:44//MUS MUSCULUS (MOUSE).//O35286  
 F-NT2RP3000403//PRE-MRNA PROCESSING PROTEIN PRP40.//0.00044:67:34//SACCHAROMYCES CERE-  
 VISIAE (BAKER'S YEAST).//P33203  
 F-NT2RP3000418//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE  
 (EC 2.7.7.49); ENDONUCLEASE].//2.2e-16:228:34//MUS MUSCULUS (MOUSE).//P11369  
 F-NT2RP3000433//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.7e-17:79:55//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//9.8e-10:201:  
 26//ESCHERICHIA COLI.//P37908  
 F-NT2RP3000441//PROTEIN-EXPORT MEMBRANE PROTEIN SECY HOMOLOG.//0.91:48:35//MYCOBACTERI-  
 UM LEPRAE.//P38388  
 F-NT2RP3000449//HOMEBOX PROTEIN HOX-B8 (CHOX-2.4) (FRAGMENT).//1.0:42:33//GALLUS GALLUS  
 (CHICKEN).//P23681  
 F-NT2RP3000451  
 F-NT2RP3000456//COLLAGEN ALPHA 1(I) CHAIN  
 (FRAGMENTS).//0.00018:178:36//RATTUS NORVEGICUS (RAT).//P02454  
 F-NT2RP3000484//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).//0.098:40:27//BOS  
 TAURUS (BOVINE).//P37359  
 F-NT2RP3000487//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.00037:16:81//VOLVOX CART-  
 ERI.//P21997  
 F-NT2RP3000512  
 F-NT2RP3000526//HYPOTHETICAL NIN REGION PROTEIN ORF56.//0.51:37:43//BACTERIOPHAGE LAMB-  
 DA.//P03769  
 F-NT2RP3000527//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.0e-16:234:30//HOMO SA-  
 PIENS (HUMAN).//P51522  
 F-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//3.4e-15:192:30//HOMO SA-  
 PIENS (HUMAN).//P15151  
 F-NT2RP3000542//CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) (FRAGMENT).//0.60:51:39//AS-  
 TERINA PECTINIFERA (STARFISH).//P11958  
 F-NT2RP3000561//HYPOTHETICAL ATP-BINDING PROTEIN MJ0423.//0.79:53:32//METHANOCOCCUS JAN-  
 NASCHIL.//Q57866  
 F-NT2RP3000562//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONAL PEPTIDE B).//0.99:26:34//  
 DROSOPHILA MAURITIANA (FRUIT FLY). AND DROSOPHILA SIMULANS (FRUIT FLY).//O18666  
 F-NT2RP3000578//HYPOTHETICAL 49.8 KD PROTEIN IN RPL14B-GPA1 INTERGENIC REGION.//1.5e-26:127:  
 37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38755  
 F-NT2RP3000582  
 F-NT2RP3000584//METALLOTHIONEIN-II (MT-II).//0.28:27:29//MUS MUSCULUS (MOUSE).//P02798  
 F-NT2RP3000590//UVS-2 PROTEIN.//4.8e-10:113:33//NEUROSPORA CRASSA.//P33288  
 F-NT2RP3000592//TRANSCRIPTION INITIATION FACTOR TFIIID 135 KD SUBUNIT (TAFII-135) (TAFII135)  
 (TAFII-130) (TAFII130).//0.00087:178:31//HOMO SAPIENS (HUMAN).//O00268  
 F-NT2RP3000596//YEMANUCLEIN-ALPHA.//1.8e-05:98:34//DROSOPHILA MELANOGASTER (FRUIT FLY).//  
 P25992

F-NT2RP3000599//SPICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.00095:90:37//HOMO SAPIENS (HUMAN).//Q15428

F-NT2RP3000603//S55 ANTIGEN.//1.0e-09:181:34//RATTUS NORVEGICUS (RAT).//Q63003

5 F-NT2RP3000605//STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 1).//0.00098:76:34//HOMO SAPIENS (HUMAN).//P36956

F-NT2RP3000622//HYPOTHETICAL PROTEIN MG096 HOMOLOG 5 (P02\_ORF427).//0.15:52:36//MYCOPLASMA PNEUMONIAE.//P75277

10 F-NT2RP3000624//HYPOTHETICAL PROTEIN KIAA0256.//5.4e-16:222:31//HOMO SAPIENS (HUMAN).//Q93073

F-NT2RP3000628

F-NT2RP3000632//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).//2.0e-16:52:63//MUS MUSCULUS (MOUSE).//Q61967

15 F-NT2RP3000644/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!6.7e-40:102:79//HOMO SAPIENS (HUMAN).//P39194

F-NT2RP3000661//HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHROMOSOME II.//6.0e-08:83:36//CAENORHABDITIS ELEGANS.//Q09441

F-NT2RP3000665//HOMEODOMAIN PROTEIN PROPHET OF PIT-1 (PROP-1) (PITUITARY SPECIFIC HOMEODOMAIN FACTOR).//0.13:48:35//HOMO SAPIENS (HUMAN).//O75360

20 F-NT2RP3000685//HYPOTHETICAL 33.5 KD PROTEIN IN CAT1 5'REGION (ORFY).//0.26:202:23//CLOSTRIDIUM KLUYVERI.//P38943

F-NT2RP3000690//INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO- HYDROLASE) (PPASE).//0.99:131:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P00817

F-NT2RP3000736//HYPOTHETICAL 28.7 KD PROTEIN IN RNR3-ARC15 INTERGENIC REGION.//3.5e-27:211:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40516

25 F-NT2RP3000739//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I.//6.0e-23:114:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149

F-NT2RP3000742//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III).//6.7e-12:85:36//RATTUS NORVEGICUS (RAT).//P10888

30 F-NT2RP3000753//CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1).//0.00011:208:28//CLOSTRIDIUM THERMOCELLUM.//Q06852

F-NT2RP3000759//ADP-RIBOSYLATION FACTOR 6.//8.1e-28:141:38//GALLUS GALLUS (CHICKEN).//P26990

35 F-NT2RP3000815//CYTOCHROME C-551 (C551) (CYTOCHROME C8).//0.24:45:37//PSEUDOMONAS DENITRIFICANS.//P00103

F-NT2RP3000825//ALPHA-LACTALBUMIN (LACTOSE SYNTHASE B PROTEIN (EC 2.4.1.22)).//0.82:51:39//MACROPUS RUFOGRISEUS (RED-NECKED WALLABY).//P07458

F-NT2RP3000826//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.025:79:37//BOS TAURUS (BOVINE).//P25508

40 F-NT2RP3000836//HYPOTHETICAL PROTEIN IN KSGA 3'REGION (ORF L5) (FRAGMENT).//0.85:36:47//MYCOPLASMA CAPRICOLUM.//P43040

F-NT2RP3000841//UDP-GLUCURONOSYLTRANSFERASE 1-7 PRECURSOR, MICROSMAL (EC 2.4.1.17) (UDPGT) (UGT1\*7) (UGT1-07) (UGT1.7) (UGT1A7) (UGTP4) (FRAGMENT).//1.0:70:34//MUS MUSCULUS (MOUSE).//Q62452

45 F-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//5.2e-72:247:61//HOMO SAPIENS (HUMAN).//P27448

F-NT2RP3000847//HYPOTHETICAL PROTEIN KIAA0161.//0.037:55:30//HOMO SAPIENS (HUMAN).//P50876

F-NT2RP3000850/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!7.4e-31:90:75//HOMO SAPIENS (HUMAN).//P39194

50 F-NT2RP3000852//HYDROPHOBIC SEED PROTEIN (HPS).//0.33:23:69//GLYCINE MAX (SOYBEAN).//P24337

F-NT2RP3000859//IMMEDIATE-EARLY PROTEIN.//3.6e-07:189:25//HERPESVIRUS SA1MIRI (STRAIN 11).//Q01042

F-NT2RP3000865

55 F-NT2RP3000868//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ISOFORM (FRAGMENT).//1.4e-09:232:28//GALLUS GALLUS (CHICKEN).//P29616

F-NT2RP3000869//CUTICLE COLLAGEN 2.//4.5e-08:58:46//CAENORHABDITIS ELEGANS.//P17656

F-NT2RP3000875//HOMEODOMAIN PROTEIN CDX-2 (CAUDAL-TYPE HOMEODOMAIN PROTEIN 2).//0.90:62:37//MUS MUSCULUS (MOUSE).//P43241

F-NT2RP3000901//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//0.99:124:33//BOS TAURUS (BOVINE)//  
 P02453  
 F-NT2RP3000904  
 F-NT2RP3000917//DHP1 PROTEIN//6.5e-60:229:55//SCHIZOSACCHAROMYCES POMBE (FISSION  
 5 YEAST)//P40848  
 F-NT2RP3000918//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I//2.4e-19:159:34//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10149  
 F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//3.7e-48:73:98//HOMO SAPIENS (HUMAN), AND RAT-  
 10 TUS NORVEGICUS (RAT)//P39027  
 F-NT2RP3000980//COPA/INCA PROTEIN (REPA3 PROTEIN)//0.24:19:47//ESCHERICHIA COLI//P13946  
 F-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN//1.4e-10:78:48//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY)//P25159  
 F-NT2RP3001004//HYPOTHETICAL 7.6 KD PROTEIN B0563.8 IN CHROMOSOME X//0.70:50:32//  
 CAENORHABDITIS ELEGANS//Q11084  
 15 F-NT2RP3001007  
 F-NT2RP3001055//N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG//1.3e-05:  
 138:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P36416  
 F-NT2RP3001057//ZINC FINGER PROTEIN 45 (BRC1744)//4.0e-28:141:51//HOMO SAPIENS (HUMAN)//  
 Q02386  
 20 F-NT2RP3001081//HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME III//3.8e-08:144:29//  
 CAENORHABDITIS ELEGANS//P34568  
 F-NT2RP3001084//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT)//3.4e-06:217:32//NEPHILA CLA-  
 VIPES (ORB SPIDER)//P48804  
 F-NT2RP3001096//SYNAPTONEMAL COMPLEX PROTEIN SC65//1.1e-30:244:33//RATTUS NORVEGICUS  
 25 (RAT)//Q64375  
 F-NT2RP3001107//ARYLSULFATASE F (EC 3.1.6.-) (ASF) (FRAGMENT)//0.041:47:44//HOMO SAPIENS (HU-  
 MAN)//P54793  
 F-NT2RP3001109  
 F-NT2RP3001111//MALE SPECIFIC SPERM PROTEIN MST84DC//0.17:28:39//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY)//Q01644  
 30 F-NT2RP3001113//INVOLUCRIN//0.00036:192:23//MUS MUSCULUS (MOUSE)//P48997  
 F-NT2RP3001115  
 F-NT2RP3001116//AMINOPEPTIDASE G (EC 3.4.11.-) (FRAGMENT)//0.99:29:51//STREPTOMYCES LIVI-  
 DANS//Q54340  
 35 F-NT2RP3001119//COLLAGEN ALPHA 4(IV) CHAIN (FRAGMENT)//0.0015:73:39//BOS TAURUS (BOVINE)//  
 Q29442  
 F-NT2RP3001120//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)//1.3e-57:229:52//HOMO SAPIENS (HU-  
 MAN)//P16415  
 F-NT2RP3001126//HYPOTHETICAL 91.2 KD PROTEIN IN RPS4B-SCH9 INTERGENIC REGION//2.8e-07:83:  
 34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38888  
 40 F-NT2RP3001133//CALCIUM BINDING PROTEIN//2.0e-08:171:32//DICTYOSTELIUM DISCOIDEUM (SLIME  
 MOLD)//P35085  
 F-NT2RP3001140//F-SPONDIN PRECURSOR//2.0e-147:244:97//RATTUS NORVEGICUS (RAT)//P35446  
 F-NT2RP3001147//TROPOMYOSIN 2 (TMII)//0.11:159:23//SCHISTOSOMA MANSONI (BLOOD FLUKE)//  
 45 P42638  
 F-NT2RP3001150//OCTAPEPTIDE-REPEAT PROTEIN T2//6.2e-09:163:25//MUS MUSCULUS (MOUSE)//  
 Q06666  
 F-NT2RP3001155//DNA POLYMERASE ALPHA-BINDING PROTEIN (POB1/CTF4 PROTEIN) (CHROMOSOME  
 REPLICATION PROTEIN CHL15)//4.1e-05:244:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//  
 50 Q01454  
 F-NT2RP3001176//LEUKOSIALIN PRECURSOR (LEUCOCYTE SIALOGLYCOPROTEIN) (SIALOPHORIN)  
 (CD43) (LY 48) (B CELL DIFFERENTIATION ANTIGEN LP-3)//0.21:136:26//MUS MUSCULUS (MOUSE)//  
 P15702  
 F-NT2RP3001214//SAP1 PROTEIN//0.058:133:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//  
 55 P39955  
 F-NT2RP3001216//CYCLIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT)//2.1e-08:137:33//HOMO SA-  
 PIENS (HUMAN)//P35663  
 F-NT2RP3001221//GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-

- BUTYROBETAINE HYDROXYLASE).//4.2e-05:131.26//PSEUDOMONAS SP. (STRAIN AK-1).//P80193  
 F-NT2RP3001232//HYPOTHETICAL PROTEIN PRECURSOR IN CS5 3'REGION (FRAGMENT).//0.75:57.31//  
 ESCHERICHIA COLI.//P33792  
 5 F-NT2RP3001236//TRANSFORMING PROTEIN MAF.//0.017:136.30//AVIAN MUSCULOAPONEUROTIC FIB-  
 ROSARCOMA VIRUS AS42.//P23091  
 F-NT2RP3001239//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 1 (FRAGMENT).//4.2e-55:221.49//  
 TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P14400  
 F-NT2RP3001245  
 10 F-NT2RP3001253//TROPOMYOSIN 2, MUSCLE THORACIC ISOFORM (TROPOMYOSIN I).//0.0042:142.24//  
 DROSOPHILA MELANOGASTER (FRUIT FLY).//P09491  
 F-NT2RP3001260//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.//0.0011:89.43//HOMO SAPIENS (HU-  
 MAN).//P53420  
 F-NT2RP3001268//ZINC FINGER PROTEIN 45 (BRC1744).//9.0e-29:194.44//HOMO SAPIENS (HUMAN).//  
 Q02386  
 15 F-NT2RP3001272//HYPOTHETICAL 75.2 KD PROTEIN C13F4.08C IN CHROMOSOME I.//8.2e-17:183.26//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10199  
 F-NT2RP3001274//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOS-  
 PHATASE T) (PPT) (FRAGMENT).//1.7e-09:78.39//MUS MUSCULUS (MOUSE).//Q60676  
 F-NT2RP3001281//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.7e-08:38.71//HOMO SAPIENS (HUMAN).//  
 20 P39188  
 F-NT2RP3001297//HYPOTHETICAL PROTEIN KIAA0281 (HA6725).//2.2e-57:159.70//HOMO SAPIENS (HU-  
 MAN).//Q92556  
 F-NT2RP3001307//SPERM PROTAMINE P1.//0.21:46.39//ORNITHORHYNCHUS ANATINUS (DUCKBILL PLAT-  
 YPUS).//P35307  
 25 F-NT2RP3001318  
 F-NT2RP3001325//ENHANCER OF RUDIMENTARY HOMOLOG.//1.0:73.24//BRACHYDANIO RERIO (ZE-  
 BRAFIN) (ZEBRA DANIO).//Q98874  
 F-NT2RP3001338//ZINC FINGER PROTEIN 29 (ZINC FINGER PROTEIN KOX26) (FRAGMENT).//0.0021:56:  
 35//HOMO SAPIENS (HUMAN).//P17037  
 30 F-NT2RP3001339//CITRON PROTEIN.//3.6e-06:90.33//MUS MUSCULUS (MOUSE).//P49025  
 F-NT2RP3001340//HYPOTHETICAL PROTEIN UL61.//7.2e-11:202.34//HOMO CYTOMEGALOVIRUS  
 (STRAIN AD169).//P16818  
 F-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PRO-  
 TEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN).//7.7e-16:129.33//HOMO SAPIENS (HUMAN).//P53007  
 35 F-NT2RP3001356//RAS-RELATED PROTEIN RABA (FRAGMENT).//0.00041:66.28//DICTYOSTELIUM DISCOI-  
 DEUM (SLIME MOLD).//P34141  
 F-NT2RP3001374  
 F-NT2RP3001383//PTB-ASSOCIATED SPLICING FACTOR (PSF).//2.5e-06:190.32//HOMO SAPIENS (HU-  
 MAN).//P23246  
 40 F-NT2RP3001384//CHORION PROTEIN S15.//0.00079:94.37//DROSOPHILA VIRILIS (FRUIT FLY).//P13424  
 F-NT2RP3001392//VPU PROTEIN (ORF-X PROTEIN) (UPX PROTEIN).//1.0:22.45//CAPRINE ARTHRITIS EN-  
 CEPHALITIS VIRUS (CAEV).//P31834  
 F-NT2RP3001396//HYPOTHETICAL 8.1 KD PROTEIN (ORF4).//1.0:37.32//STRAWBERRY MILD YELLOW  
 EDGE-ASSOCIATED VIRUS (SMYEA).//Q00848  
 45 F-NT2RP3001398//KRUEPPEL-RELATED ZINC FINGER PROTEIN 2 (HKR2 PROTEIN) (FRAGMENT).//1.9e-  
 08:45.37//HOMO SAPIENS (HUMAN).//P10073  
 F-NT2RP3001399//SSU72 PROTEIN.//7.3e-18:84.52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
 P53538  
 50 F-NT2RP3001407//SCY1 PROTEIN.//1.5e-08:143.25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
 P53009  
 F-NT2RP3001420//HYPOTHETICAL 7.9 KD PROTEIN.//0.25:41.26//VACCINIA VIRUS (STRAIN COPENHA-  
 GEN).//P20542  
 F-NT2RP3001426//DNAJ PROTEIN.//7.5e-15:78.43//HAEMOPHILUS INFLUENZAE.//P43735  
 F-NT2RP3001427//WERNER SYNDROME HELICASE.//3.6e-13:159.33//HOMO SAPIENS (HUMAN).//Q14191  
 55 F-NT2RP3001428//NUCLEOPROTEIN TPR.//1.8e-53:117.99//HOMO SAPIENS (HUMAN).//P12270  
 F-NT2RP3001432//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.96:52:  
 21//TARSIVUS SYRICHTA (TARSIER).//Q36151  
 F-NT2RP3001447//HYPOTHETICAL 5.5 KD PROTEIN IN REPLICATION ORIGIN REGION (ORF1).//0.96:45:35//



- ESCHERICHIA COLI //P14505  
F-NT2RP3001449//HOMEBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT) //0.0043:53:43//GALLUS GALLUS (CHICKEN) //P19601
- 5 F-NT2RP3001453//MALE SPECIFIC SPERM PROTEIN MST84DB //0.0048:65:40//DROSOPHILA MELANOGASTER (FRUIT FLY) //Q01643  
F-NT2RP3001457//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS28 //0.055:121:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //Q02767  
F-NT2RP3001459//MYOSIN IC HEAVY CHAIN //0.10:126:34//ACANTHAMOEBA CASTELLANII (AMOEBA) //P10569
- 10 F-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A //3.0e-14:87:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P11632  
F-NT2RP3001490//METALLOTHIONEIN-LIKE PROTEIN LSC54 //1.0:39:35//BRASSICA NAPUS (RAPE) //P43402  
F-NT2RP3001495//UBIQUITIN-PROTEIN LIGASE RSP5 (EC 6.3.2.-) //3.3e-14:148:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P39940
- 15 F-NT2RP3001497//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS) //0.13:44:38//BOS TAURUS (BOVINE) //P25508  
F-NT2RP3001527//SPERM PROTAMINE P1 //0.30:25:37//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONDELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM) //P35305  
20 F-NT2RP3001529//HYPOTHETICAL 43.3 KD GTP-BINDING PROTEIN IN DACB-RPMA INTERGENIC REGION //3.3e-21:125:37//ESCHERICHIA COLI //P42641  
F-NT2RP3001538//HNF3/FH TRANSCRIPTION FACTOR GENESIS (WINGED HELIX PROTEIN CWH-3) //0.13:53:39//GALLUS GALLUS (CHICKEN) //P79772  
F-NT2RP3001554//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 2 (FRAGMENT) //2.3e-48:137:52//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY) //P14401
- 25 F-NT2RP3001580//GERM CELL-LESS PROTEIN //8.2e-18:100:42//DROSOPHILA MELANOGASTER (FRUIT FLY) //Q01820  
F-NT2RP3001587//UBIQUITIN-ACTIVATING ENZYME E1-LIKE (POLYMERASE-INTERACTING PROTEIN 2) //2.0e-47:188:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P52488  
30 F-NT2RP3001589//ALU SUBFAMILY SP WARNING ENTRY //7.4e-41:87:80//HOMO SAPIENS (HUMAN) //P39193  
F-NT2RP3001607//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L) //1.0:49:32//DICENTRARCHUS LABRAX (EUROPEAN SEA BASS) //Q36362  
F-NT2RP3001608//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN) //0.0013:177:25//ZEA MAYS (MAIZE) //P14918
- 35 F-NT2RP3001621//MALE SPECIFIC SPERM PROTEIN MST84DD //0.84:29:37//DROSOPHILA MELANOGASTER (FRUIT FLY) //Q01645  
F-NT2RP3001629//RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 (P21-RAC1) (FRAGMENTS) //0.91:57:24//CAVIA PORCELLUS (GUINEA PIG) //P80236  
40 F-NT2RP3001634//ALU SUBFAMILY SB WARNING ENTRY //8.9e-11:73:54//HOMO SAPIENS (HUMAN) //P39189  
F-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210 //1.1e-12:117:29//HOMO SAPIENS (HUMAN) //Q92609  
F-NT2RP3001646//HYPOTHETICAL 29.3 KD PROTEIN (ORF92) //0.0092:69:34//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV) //O10341
- 45 F-NT2RP3001671//RING CANAL PROTEIN (KELCH PROTEIN) //0.0042:55:41//DROSOPHILA MELANOGASTER (FRUIT FLY) //Q04652  
F-NT2RP3001672  
F-NT2RP3001676//GTP-BINDING PROTEIN LEPA (FRAGMENT) //1.2e-15:56:62//PSEUDOMONAS FLUORESCENS //P26843  
50 F-NT2RP3001678//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT) //0.054:187:31//NEPHILA CLAVIPES (ORB SPIDER) //P46804  
F-NT2RP3001679//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III //1.5e-07:63:44//CAENORHABDITIS ELEGANS //P34679  
F-NT2RP3001688//GLUCOAMYLASE S1 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) (GAI) //1.0:83:28//SACCHAROMYCES DIASTATICUS (YEAST) //P04065
- 55 F-NT2RP3001690//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM //0.021:247:24//HOMO SA-

PIENS (HUMAN).//P12883  
 F-NT2RP3001698  
 F-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR.//7.7e-12:73:43//DROSOPHILA MEL-  
 ANOASTER (FRUIT FLY).//P54356  
 5 F-NT2RP3001712//CEC-1 PROTEIN.//1.9e-07:121:29//CAENORHABDITIS ELEGANS.//P34618  
 F-NT2RP3001716//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.89:54:40//DROSOPHILA SIMULANS  
 (FRUIT FLY).//P13729  
 F-NT2RP3001724//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//7.5e-41:164:48//HO-  
 MO SAPIENS (HUMAN).//O14646  
 10 F-NT2RP3001727//HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III.//1.5e-51:240:41//  
 CAENORHABDITIS ELEGANS.//P34669  
 F-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT).//2.4e-122:267:86//HOMO SAPIENS (HUMAN).//  
 Q14141  
 F-NT2RP3001739//INTESTINAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE  
 15 COTRANSPORTER).//0.99:63:34//RATTUS NORVEGICUS (RAT).//P70545  
 F-NT2RP3001752!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.0e-21:60:85//HOMO SAPIENS (HUMAN).//  
 P39193  
 F-NT2RP3001753//HYPOTHETICAL PROTEIN KIAA0127.//7.9e-12:83:44//HOMO SAPIENS (HUMAN).//  
 Q14140  
 20 F-NT2RP3001764//DUAL SPECIFICITY PROTEIN PHOSPHATASE 6 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPE-  
 CIFICITY PROTEIN PHOSPHATASE PYST1).//7.7e-25:146:36//HOMO SAPIENS (HUMAN).//Q16828  
 F-NT2RP3001777//SERINE/THREONINE-PROTEIN KINASE STE20 HOMOLOG (EC 2.7.1.-).//0.0096:204:25//  
 CANDIDA ALBICANS (YEAST).//Q92212  
 F-NT2RP3001782//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.91:34:44//PONGO PYGMAEUS ABELII  
 25 (SUMATRAN ORANGUTAN).//P92694  
 F-NT2RP3001792//HETEROGENEOUS CELLULAR RIBONUCLEOPROTEIN M (HNRNP M).//1.8e-33:159:53//  
 HOMO SAPIENS (HUMAN).//P52272  
 F-NT2RP3001799//LIGHT-HARVESTING PROTEIN B800/830/1020, ALPHA-2 CHAIN (EHS-ALPHA-2) (ANTEN-  
 NA PIGMENT PROTEIN, ALPHA-2 CHAIN).//0.14:46:28//ECTOTHIORHODOSPIRA HALOCHLORIS.//P80103  
 30 F-NT2RP3001819//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.//0.00030:77:36//HOMO SAPIENS (HU-  
 MAN).//P08123  
 F-NT2RP3001844//OCTAMER-BINDING TRANSCRIPTION FACTOR 1 (OTF-1) (NF-A1) (FRAGMENT).//0.99:  
 43:34//MACROPUS EUGENII (TAMMAR WALLABY).//Q28466  
 F-NT2RP3001854//FIBRINOGEN- AND IG-BINDING PROTEIN PRECURSOR (MRP PROTEIN).//9.3e-10:213:  
 35 24//STREPTOCOCCUS PYOGENES.//P30141  
 F-NT2RP3001855//HOMEBOX PROTEIN PKNOX1 (HOMEBOX PROTEIN PREP-1).//2.6e-61:220:60//HO-  
 MO SAPIENS (HUMAN).//P55347  
 F-NT2RP3001857//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1.//1.0e-13:213:24//PODOSPORA AN-  
 SERINA.//Q00808  
 40 F-NT2RP3001896//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.074:124:34//HOMO SA-  
 PIENS (HUMAN).//Q15428  
 F-NT2RP3001898//REGULATORY PROTEIN E2.//0.36:131:29//CANINE ORAL PAPILLOMAVIRUS (COPV).//  
 Q89420  
 F-NT2RP3001915//CHITIN BIOSYNTHESIS PROTEIN CHS5 (CAL3 PROTEIN).//0.0021:237:23//SACCHARO-  
 MYCES CEREVISIAE (BAKER'S YEAST).//Q12114  
 45 F-NT2RP3001926//HYPOTHETICAL 14.0 KD PROTEIN IN RPL15B-GCR3 INTERGENIC REGION.//1.0:63:34//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03880  
 F-NT2RP3001929!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.4e-14:35:60//HOMO SAPIENS (HUMAN).//  
 P39195  
 50 F-NT2RP3001931//HYPOTHETICAL 59.3 KD PROTEIN IN TAP42-ARP9 INTERGENIC REGION.//0.86:162:24//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q05040  
 F-NT2RP3001938//GLYCOPROTEIN GP50.//0.0036:54:40//PSEUDORABIES VIRUS (STRAIN RICE) (PRV).//  
 P07645  
 F-NT2RP3001943//33.2 KD PROTEIN IN DIND-RPH INTERGENIC REGION (ORF X).//1.0:113:27//ES-  
 CHERICHIA COLI.//P23839  
 55 F-NT2RP3001944//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//4.1e-56:208:47//  
 CAENORHABDITIS ELEGANS.//Q09251  
 F-NT2RP3001969//PUFF II/9-2 PROTEIN PRECURSOR.//0.0078:149:26//SCIARA COPROPHILA (FUNGUS

GNAT).//P22312  
 F-NT2RP3001989//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//1.0.41:31//MUS MUSCULUS (MOUSE).//P02319  
 5 F-NT2RP3002002//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.2e-44:69:79//HOMO SAPIENS (HUMAN).//P39195  
 F-NT2RP3002004//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2).//0.00024:45:40//MUS MUSCULUS (MOUSE).//Q61345  
 F-NT2RP3002007//TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEI) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C).//0.21:115:28//HOMO SAPIENS (HUMAN).//P24821  
 10 F-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//1.7e-25:139:48//CAENORHABDITIS ELEGANS.//Q09232  
 F-NT2RP3002033//ACTIVATOR OF APOPTOSIS HARAKIRI (NEURONAL DEATH PROTEIN DP5).//0.14:65:41//HOMO SAPIENS (HUMAN).//O00198  
 15 F-NT2RP3002045//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//8.1e-108:192:98//MUS MUSCULUS (MOUSE).//P17427  
 F-NT2RP3002054//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.046:176:31//STREPTOMYCES FRADIAE.//P20186  
 20 F-NT2RP3002056//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140).//1.4e-07:245:25//RATTUS NORVEGICUS (RAT).//P41777  
 F-NT2RP3002057//SMALL HYDROPHOBIC PROTEIN.//1.0:12:66//SIMIAN VIRUS 5 (STRAIN W3) (SV5).//P07577  
 F-NT2RP3002062//PROTEASE A INHIBITOR 3 (PROTEINASE INHIBITOR I(A)3).//1.0:49:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P01094  
 25 F-NT2RP3002063//ACYL CARRIER PROTEIN (ACP).//0.99:38:31//HAEMOPHILUS INFLUENZAE.//P43709  
 F-NT2RP3002081//HYPOTHETICAL 100.5 KD PROTEIN C1B9.04 IN CHROMOSOME I.//5.8e-35:253:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10429  
 F-NT2RP3002097//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-CGR2 INTERGENIC REGION.//6.2e-06:99:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40164  
 30 F-NT2RP3002102//HYPOTHETICAL 7.4 KD PROTEIN.//0.68:34:47//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19302  
 F-NT2RP3002108//HYPOTHETICAL 105.5 KD PROTEIN R13F6.10 IN CHROMOSOME III.//7.9e-19:179:34//CAENORHABDITIS ELEGANS.//Q21986  
 35 F-NT2RP3002142//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.6e-17:37:75//HOMO SAPIENS (HUMAN).//P39188  
 F-NT2RP3002146//CUTICLE COLLAGEN 40.//0.00034:90:37//CAENORHABDITIS ELEGANS.//P34804  
 F-NT2RP3002147//SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).//0.011:166:28//HOMO SAPIENS (HUMAN).//P10163  
 40 F-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING PROTEIN GST1-HS).//4.8e-11:60:53//HOMO SAPIENS (HUMAN).//P15170  
 F-NT2RP3002163//TRANSCRIPTION INITIATION FACTOR TFIIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TARII130).//0.028:191:29//HOMO SAPIENS (HUMAN).//O00268  
 F-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP.//2.3e-131:223:91//MUS MUSCULUS (MOUSE).//Q02614  
 45 F-NT2RP3002166//D-ALANYL CARRIER PROTEIN (DCP).//1.0:65:33//LACTOBACILLUS CASEI.//P55153  
 F-NT2RP3002173//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.4e-26:114:62//HOMO SAPIENS (HUMAN).//P39194  
 F-NT2RP3002181//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.25:31:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645  
 50 F-NT2RP3002244//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.069:16:62//OVIS ARIES (SHEEP), AND CAPRA HIRCUS (GOAT).//P04102  
 F-NT2RP3002248//MICROFIBRILLAR-ASSOCIATED PROTEIN 1 (ASSOCIATED MICROFIBRIL PROTEIN) (AMF).//0.0079:187:24//GALLUS GALLUS (CHICKEN).//P55080  
 55 F-NT2RP3002255//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//4.6e-10:168:34//MUS MUSCULUS (MOUSE).//P05143  
 F-NT2RP3002273//SCD6 PROTEIN.//1.5e-11:160:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P45978

- F-NT2RP3002276//PROBABLE E4 PROTEIN./0.91:54:29//HUMAN PAPILLOMAVIRUS TYPE 16.//P06922  
 F-NT2RP3002303//HYPOTHETICAL 30.2 KD PROTEIN C4D7.04C IN CHROMOSOME I.//1.7e-42:191:43//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14171  
 F-NT2RP3002304
- 5 F-NT2RP3002330//NRP-1 PROTEIN./0.52:140:18//MUS MUSCULUS (MOUSE).//P56183  
 F-NT2RP3002343//5E5 ANTIGEN./0.0056:189:30//RATTUS NORVEGICUS (RAT).//Q63003  
 F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.15)  
 / METHENYLtetrahydrofolate cyclohydrolase (EC 3.5.4.9) MITOCHONDRIAL PRECURSOR.//  
 1.0e-66:196:68//HOMO SAPIENS (HUMAN).//P13995
- 10 F-NT2RP3002352//PRESYNAPTIC PROTEIN SAP102 (SYNAPSE-ASSOCIATED PROTEIN 102) (NEUROEN-  
 DOCRINE-DLG) (NE-DLG).//0.79:173:27//HOMO SAPIENS (HUMAN).//Q92796  
 F-NT2RP3002377//PUTATIVE HELICASE YGR271W.//1.0e-56:216:44//SACCHAROMYCES CEREVISIAE  
 (BAKER'S YEAST).//P53327
- 15 F-NT2RP3002399//MINICHROMOSOME MAINTENANCE PROTEIN 6.//1.4e-19:136:31//SACCHAROMYCES  
 CEREVISIAE (BAKER'S YEAST).//P53091  
 F-NT2RP3002402//EBNA-6 NUCLEAR PROTEIN (EBNA-3C) (EBNA-4B).//0.74:107:36//EPSTEIN-BARR VIRUS  
 (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03204  
 F-NT2RP3002455//DNAJ PROTEIN (FRAGMENT).//5.6e-06:57:42//AGROBACTERIUM TUMEFACIENS.//  
 P50018
- 20 F-NT2RP3002484//HYPOTHETICAL 46.5 KD PROTEIN C12B10.04 IN CHROMOSOME I.//0.00032:52:48//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10438  
 F-NT2RP3002501//HYPOTHETICAL 34.9 KD PROTEIN IN FRE2-JEN1 INTERGENIC REGION.//9.4e-42:209:  
 42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36007
- 25 F-NT2RP3002512//HYPOTHETICAL 37.4 KD PROTEIN IN GPM1-MCR1 INTERGENIC REGION.//7.7e-32:162:  
 37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36059  
 F-NT2RP3002529//PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN C2G11.03C.//2.1e-45:  
 241:43//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09805  
 F-NT2RP3002545
- 30 F-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III.//2.8e-41:161:52//  
 CAENORHABDITIS ELEGANS.//Q10010  
 F-NT2RP3002566//IMMEDIATE-EARLY PROTEIN IE180.//0.56:130:24//PSEUDORABIES VIRUS (STRAIN KA-  
 PLAN) (PRV).//P33479  
 F-NT2RP3002587  
 F-NT2RP3002590
- 35 F-NT2RP3002602//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1) (THIOREDOXIN-RE-  
 LATED GLYCOPROTEIN 1).//0.00091:111:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P17967  
 F-NT2RP3002603//HYPOTHETICAL 14.2 KD PROTEIN IN BLAB 3'REGION.//1.0e-65:40//STREPTOMYCES CA-  
 CAO1.//P33654
- 40 F-NT2RP3002628//DNAJ-LIKE PROTEIN SLR0093.//2.4e-17:101:44//SYNECHOCYSTIS SP. (STRAIN PCC  
 6803).//P50027  
 F-NT2RP3002631//METALLOTHIONEIN-IB (MT-1B).//0.092:36:33//HOMO SAPIENS (HUMAN).//P07438  
 F-NT2RP3002650//DUALIN.//3.0e-21:184:37//GALLUS GALLUS (CHICKEN).//Q90830  
 F-NT2RP3002659//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.//0.00016:223:33//HOMO SAPIENS (HU-  
 MAN).//P08123
- 45 F-NT2RP3002660//40S RIBOSOMAL PROTEIN S27A.//0.16:72:31//CAENORHABDITIS ELEGANS.//P37165  
 F-NT2RP3002663//OXYSTEROL-BINDING PROTEIN.//5.4e-23:168:41//HOMO SAPIENS (HUMAN).//P22059  
 F-NT2RP3002671//HYPOTHETICAL 124.5 KD PROTEIN IN SKO1-RPL44A INTERGENIC REGION.//6.0e-38:  
 203:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53893  
 F-NT2RP3002682//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.25:63:31//ARTEMIA  
 SALINA (BRINE SHRIMP).//P19049
- 50 F-NT2RP3002687//HYPOTHETICAL 30.4 KD PROTEIN IN LEF3-IAP2 INTERGENIC REGION.//0.029:60:36//  
 AUTOGRAPH CALIFORNICA NUCLEAR POLYHYDROSIS VIRUS (ACMPNV).//P41469  
 F-NT2RP3002688//KINESIN-LIKE PROTEIN KIF1B.//5.3e-61:130:88//MUS MUSCULUS (MOUSE).//Q60575  
 F-NT2RP3002701//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//7.4e-05:109:33//MUS  
 MUSCULUS (MOUSE).//P15265
- 55 F-NT2RP3002713//PROBABLE ATP-DEPENDENT RNA HELICASE DDX10 (DEAH BOX PROTEIN 10).//0.77:  
 70:32//HOMO SAPIENS (HUMAN).//Q13206  
 F-NT2RP3002763//HYPOTHETICAL 11.3 KD PROTEIN C2C6.07 IN CHROMOSOME I.//6.7e-11:66:40//

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14056  
 F-NT2RP3002770//COLLAGEN ALPHA 1(IX) CHAIN (FRAGMENT).//0.33:87:34//MUS MUSCULUS (MOUSE).//Q05722  
 F-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//9.7e-36:187:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24371  
 F-NT2RP3002799//ALU SUBFAMILY J WARNING ENTRY!!!!//5.6e-08:41:73//HOMO SAPIENS (HUMAN).//P39188  
 F-NT2RP3002810//ALU SUBFAMILY SP WARNING ENTRY!!!!//0.0034:35:65//HOMO SAPIENS (HUMAN).//P39193  
 F-NT2RP3002818//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B).//3.2e-17:148:37//MUS MUSCULUS (MOUSE).//P27790  
 F-NT2RP3002861//HYPOTHETICAL 70.2 KD PROTEIN IN GSH1-CHS6 INTERGENIC REGION.//1.7e-05:95:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42951  
 F-NT2RP3002869//TRYPSIN INHIBITOR II (BDT-II).//0.97:23:39//BRYONIA DIOICA (RED BRYONY).//P11968  
 F-NT2RP3002876//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).//0.00017:140:31//RAT-TUS NORVEGICUS (RAT).//P04474  
 F-NT2RP3002877//ALU SUBFAMILY SQ WARNING ENTRY!!!!//2.5e-06:55:60//HOMO SAPIENS (HUMAN).//P39194  
 F-NT2RP3002909//P53-BINDING PROTEIN 53BP2 (BCL2-BINDING PROTEIN) (BBP).//4.6e-08:129:38//HOMO SAPIENS (HUMAN).//Q13625  
 F-NT2RP3002911//HYPOTHETICAL PROTEIN C18.//0.99:26:50//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//P32217  
 F-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-23:113:47//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652  
 F-NT2RP3002953//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//0.55:116:27//DROSOPHILA MELANOGASTER (FRUIT FLY).//P33450  
 F-NT2RP3002955//HYPOTHETICAL 16.5 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION.//0.87:67:37//BACILLUS SUBTILIS.//P54445  
 F-NT2RP3002969//LONG-CHAIN-FATTY-ACID-COA LIGASE 4 (EC 6.2.1.3) (LONG-CHAIN ACYL-COA SYNTHETASE 4) (LACS 4).//6.7e-56:189:59//HOMO SAPIENS (HUMAN).//Q60488  
 F-NT2RP3002972//HYPOTHETICAL 73.0 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION.//0.0028:147:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48566  
 F-NT2RP3002978//PROBABLE E5 PROTEIN.//0.15:55:36//HUMAN PAPILLOMAVIRUS TYPE 51.//P26553  
 F-NT2RP3002985//METALLOTHIONEIN (MT).//0.0031:49:42//PLEURONECTES PLATESSA (PLAICE).//P07216  
 F-NT2RP3002988//NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR (MOTCH PROTEIN).//1.0:111:29//MUS MUSCULUS (MOUSE).//Q01705  
 F-NT2RP3003008//HYPOTHETICAL 54.7 KD PROTEIN F37A4.1 IN CHROMOSOME III.//0.96:112:25//CAENORHABDITIS ELEGANS.//P41879  
 F-NT2RP3003032  
 F-NT2RP3003059//HYPOTHETICAL 52.3 KD PROTEIN C56F8.06C IN CHROMOSOME I PRECURSOR.//9.7e-27:216:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10254  
 F-NT2RP3003061//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//3.7e-25:167:34//HOMO SAPIENS (HUMAN).//P16157  
 F-NT2RP3003068//SERYL-TRNA SYNTHETASE (EC 6.1.1.11) (SERINE-TRNA LIGASE) (SERRS) (FRAGMENT).//0.074:82:39//SULFOLOBUS SOLFATARICUS.//O33780  
 F-NT2RP3003071//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.0085:128:30//HOMO SAPIENS (HUMAN).//P50552  
 F-NT2RP3003078//SPERM ACROSOMAL PROTEIN FSA-ACR.1 PRECURSOR (FRAGMENT).//0.028:165:31//VULPES VULPES (RED FOX).//P53353  
 F-NT2RP3003101//TETRACYCLINE RESISTANCE PROTEIN, CLASS C (TET(C)).//1.0e-14:243:25//ESCHERICHIA COLI.//P02981  
 F-NT2RP3003121//SUPPRESSOR PROTEIN SRP40.//7.4e-05:143:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583  
 F-NT2RP3003133//65 KD YES-ASSOCIATED PROTEIN (YAP65).//0.024:61:42//GALLUS GALLUS (CHICKEN).//P46936  
 F-NT2RP3003138//KINESIN-LIKE PROTEIN KIF4.//1.1e-118:151:93//MUS MUSCULUS (MOUSE).//P33174  
 F-NT2RP3003139//ATP-BINDING CASSETTE TRANSPORTER ABC1.//1.0:70:30//SCHIZOSACCHAROMYCES

POMBE (FISSION YEAST).//Q92337

F-NT2RP3003145//MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (HMGF) (BREAST EPITHELIAL ANTIGEN BA46) (MFGM).//2.0e-12:121:37//HOMO SAPIENS (HUMAN).//Q08431

F-NT2RP3003150

5 F-NT2RP3003157//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//4.0e-79:260:54//HOMO SAPIENS (HUMAN).//P51522

F-NT2RP3003185//TROPOMYOSIN.//0.077:122:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q02088

F-NT2RP3003193//ZINC FINGER PROTEIN 135.//17.2e-91:239:65//HOMO SAPIENS (HUMAN).//P52742

10 F-NT2RP3003197//HYPOTHETICAL 28.1 KD PROTEIN IN SIPU-PBPC INTERGENIC REGION.//1.3e-07:117:34//BACILLUS SUBTILIS.//P42966

F-NT2RP3003203//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I.//9.9e-23:132:39//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149

F-NT2RP3003204//RAS-LIKE PROTEIN RASB.//0.92:103:27//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P32252

F-NT2RP3003210//VERY HYPOTHETICAL 13.2 KD PROTEIN IN PTC3-SAS3 INTERGENIC REGION.//0.23:106:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38190

F-NT2RP3003212//SUPPRESSOR PROTEIN SRP40.//0.019:171:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583

20 F-NT2RP3003230//CORONIN-LIKE PROTEIN P57.//8.3e-74:183:73//BOS TAURUS (BOVINE).//Q92176

F-NT2RP3003242//STANNIOLCALCIN PRECURSOR.//1.4e-21:127:37//HOMO SAPIENS (HUMAN).//P52823

F-NT2RP3003251//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//3.1e-51:198:52//MUS MUSCULUS (MOUSE).//P15533

F-NT2RP3003264//E6 PROTEIN.//1.0:31:41//HUMAN PAPILLOMAVIRUS TYPE 48.//Q80920

25 F-NT2RP3003278//45.8 KD PROTEIN IN SHM1-MRPL37 INTERGENIC REGION.//8.6e-07:80:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38344

F-NT2RP3003282//DYNAMIN 2 (DYNAMIN UDNM).//8.0e-108:226:88//MUS MUSCULUS (MOUSE).//P39054

F-NT2RP3003290//BIOH PROTEIN.//0.0055:107:30//ESCHERICHIA COLI.//P13001

F-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//1.3e-69:200:55//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//O64948

30 F-NT2RP3003302//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.4e-69:102:66//HOMO SAPIENS (HUMAN).//P08547

F-NT2RP3003311//MYOSIN II HEAVY CHAIN, NON MUSCLE.//0.18:225:26//ACANTHAMOEBA CASTELLANII (AMOEBA).//P05659

35 F-NT2RP3003313//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.0014:142:33//HOMO SAPIENS (HUMAN).//P10162

F-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52).//8.8e-18:94:43//MUS MUSCULUS (MOUSE).//Q62191

F-NT2RP3003330//HYPOTHETICAL PROTEIN KIAA0176 (FRAGMENT).//1.3e-20:123:44//HOMO SAPIENS (HUMAN).//Q14681

40 F-NT2RP3003344//HYPOTHETICAL 8.8 KD PROTEIN IN ICDC-MINE INTERGENIC REGION.//1.0:28:42//ESCHERICHIA COLI.//P75991

F-NT2RP3003346//ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//6.9e-26:74:78//HOMO SAPIENS (HUMAN).//P39191

45 F-NT2RP3003353//HYPOTHETICAL 52.4 KD PROTEIN R08D7.2 IN CHROMOSOME III.//3.7e-10:118:33//CAENORHABDITIS ELEGANS.//P30641

F-NT2RP3003377//PUTATIVE CUTICLE COLLAGEN F09G8.6.//1.5e-05:102:37//CAENORHABDITIS ELEGANS.//P34391

F-NT2RP3003384

50 F-NT2RP3003385//SKD3 PROTEIN.//5.1e-83:210:69//MUS MUSCULUS (MOUSE).//Q60649

F-NT2RP3003403

F-NT2RP3003409//SOX-22 PROTEIN.//0.042:173:28//HOMO SAPIENS (HUMAN).//O15370

F-NT2RP3003411//PROBABLE E3 PROTEIN.//0.17:91:31//BOVINE PAPILLOMAVIRUS TYPE 2.//P11300

F-NT2RP3003427//HOLOTICRIN 3 PRECURSOR.//0.012:36:41//HOLOTICRIN DIOMPHALIA.//Q25055

F-NT2RP3003433

55 F-NT2RP3003464//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.0042:110:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

F-NT2RP3003490

- F-NT2RP3003491//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (HEAT SHOCK 10 KD PROTEIN)//0.99:49:34//LEPTOSPIRA INTERROGANS //P35472
- F-NT2RP3003500//SCY1 PROTEIN//6.8e-14:192:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53009
- 5 F-NT2RP3003543//COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR//0.0026:175:30//HOMO SAPIENS (HUMAN)//P29400
- F-NT2RP3003552//ANNEXIN VII (SYNEXIN) (FRAGMENT)//0.19:21:47//BOS TAURUS (BOVINE)//P20072
- F-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC REGION//7.3e-27:159:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40529
- 10 F-NT2RP3003564//RNA REPLICASE POLYPROTEIN (EC 2.7.7.48)//1.0:99:30//TURNIP YELLOW MOSAIC VIRUS//P10358
- F-NT2RP3003572//PUTATIVE CUTICLE COLLAGEN F09G8.6//0.0:33:128:32//CAENORHABDITIS ELEGANS//P34391
- 15 F-NT2RP3003576//ALU SUBFAMILY SX WARNING ENTRY !!!!!/7.1e-28:58:77//HOMO SAPIENS (HUMAN)//P39195
- F-NT2RP3003589//RAS-RELATED PROTEIN RAB-10//5.4e-54:114:94//CANIS FAMILIARIS (DOG)//P24409
- F-NT2RP3003621//COAGULATION FACTOR XII PRECURSOR (EC 3.4.21.38) (HAGEMAN FACTOR) (HAF)//2.0e-15:89:40//HOMO SAPIENS (HUMAN)//P00748
- F-NT2RP3003625//MALE SPECIFIC SPERM PROTEIN MST84DD//0.0:99:22:50//DROSOPHILA MELANOGASTER (FRUIT FLY)//IQ01645
- 20 F-NT2RP3003656//HOMEBOX PROTEIN OTX3 (ZOTX3)//0.0:30:111:25//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO)//IQ90267
- F-NT2RP3003659//HYPOTHETICAL 49.8 KD PROTEIN IN RPL14B-GPA1 INTERGENIC REGION//1.1e-20:127:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38755
- 25 F-NT2RP3003665//PENAEIDIN-3C PRECURSOR (P3-C)//0.0:34:52:34//PENAEUS VANNAMEI (PENOEID SHRIMP) (EUROPEAN WHITE SHRIMP)//P81060
- F-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7)//8.7e-15:146:42//HOMO SAPIENS (HUMAN)//P14209
- F-NT2RP3003680//HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION//4.3e-25:159:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P43601
- 30 F-NT2RP3003686//NONHISTONE CHROMOSOMAL PROTEIN HMG-17//0.0:67:63:31//GALLUS GALLUS (CHICKEN) (CHICKEN)//P02314
- F-NT2RP3003701//F-SPONDIN PRECURSOR//1.8e-13:193:27//RATTUS NORVEGICUS (RAT)//P35446
- 35 F-NT2RP3003716//SLIT PROTEIN PRECURSOR//1.3e-12:150:34//DROSOPHILA MELANOGASTER (FRUIT FLY)//P24014
- F-NT2RP3003728//INSERTION ELEMENT IS136 HYPOTHETICAL 16.9 KD PROTEIN//0.47:109:28//AGROBACTERIUM TUMEFACIENS //P05680
- F-NT2RP3003746//HYPOTHETICAL 7.7 KD PROTEIN IN FIXX 3'REGION (ORF1)//0.57:34:38//AZORHIZOBIUM CAULINODANS //P26486
- 40 F-NT2RP3003795//ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.3e-10:40:90//HOMO SAPIENS (HUMAN)//P39195
- F-NT2RP3003799//MATING-TYPE PHEROMONE BBP1(3) PRECURSOR//0.75:60:36//SCHIZOPHYLLUM COMMUNE (BRACKET FUNGUS)//P78744
- 45 F-NT2RP3003800//PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC (EC 2.7.1.112) (P60-SRC)//4.2e-51:72:95//GALLUS GALLUS (CHICKEN)//P00523
- F-NT2RP3003805//HYPOTHETICAL 32.1 KD PROTEIN IN DBP7-GCN3 INTERGENIC REGION//0.00069:160:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36121
- F-NT2RP3003809//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENTS)//0.0:28:135:35//GALLUS GALLUS (CHICKEN)//P12105
- 50 F-NT2RP3003819//C-HORDEIN (PCP387) (FRAGMENT)//0.0026:90:33//HORDEUM VULGARE (BARLEY)//P06472
- F-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP)//5.6e-20:174:31//BOS TAURUS (BOVINE) //P02720
- F-NT2RP3003828//ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-INHIBITABLE ADENYLATE CYCLASE) //0.0017:111:38//CANIS FAMILIARIS (DOG)//P30803
- 55 F-NT2RP3003831//ENDONUCLEASE G PRECURSOR (EC 3.1.30.-) (ENDO G)//1.1e-37:187:42//MUS MUSCULUS (MOUSE) //O08600
- F-NT2RP3003833//HYPOTHETICAL 6.4 KD PROTEIN IN INTE-PIN INTERGENIC REGION//1.0:38:39//ES-

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CHERICHA COLI//P75979  
 F-NT2RP3003842  
 F-NT2RP3003846//RETINAL DEGENERATION B PROTEIN (PROBABLE CALCIUM TRANSPORTER RDGB)//  
 0.61:54:35//DROSOPHILA MELANOGASTER (FRUIT FLY)//P43125  
 F-NT2RP3003870//MALE SPECIFIC SPERM PROTEIN MST84DB//0.83:51:37//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY)//Q01643  
 F-NT2RP3003876//PROTEIN TRANSPORT PROTEIN SEC2//0.0017:151:27//SACCHAROMYCES CEREVI-  
 SIAE (BAKER'S YEAST)//P17065  
 F-NT2RP3003914//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-)  
 (DUGT)//3.3e-23:76:64//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q09332  
 F-NT2RP3003918//VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPTOBREVIN BINDING PROTEIN  
 (VAP-33)//5.5e-45:127:69//APLYSIA CALIFORNICA (CALIFORNIA SEA HARE)//Q16943  
 F-NT2RP3003932  
 F-NT2RP3003989//PREPROTEIN TRANSLOCASE SECE SUBUNIT//0.96:46:32//THERMOTOGA MARITIMA//  
 P35874  
 F-NT2RP3003992//NUCLEAR LOCALIZATION SEQUENCE BINDING PROTEIN (P67)//0.0011:170:26//SAC-  
 CHAROMYCES CEREVISIAE (BAKER'S YEAST)//P27476  
 F-NT2RP3004013//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAM-  
 INASE) (RNA EDITING ENZYME 1)//3.6e-21:134:45//RATTUS NORVEGICUS (RAT)//P51400  
 F-NT2RP3004016//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION//0.00021:64:40//  
 AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMPV)//P41479  
 F-NT2RP3004041//SPERM PROTAMINE P1//0.0028:43:46//ORNITHORHYNCHUS ANATINUS (DUCKBILL  
 PLATYPUS)//P35307  
 F-NT2RP3004051//MICROBIAL COLLAGENASE PRECURSOR (EC 3.4.24.3) (120 KD COLLAGENASE)//  
 0.0079:194:24//CLOSTRIDIUM PERFRINGENS//P43153  
 F-NT2RP3004070//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.4e-11:51:72//HOMO SAPIENS (HUMAN)//  
 P39188  
 F-NT2RP3004078//DNA BINDING PROTEIN RFX2//2.7e-114:243:87//MUS MUSCULUS (MOUSE)//P48379  
 F-NT2RP3004093//HYPOTHETICAL 32.3 KD PROTEIN IN RHSE-NARV INTERGENIC REGION (ORFB)//8.0e-  
 13:111:41//ESCHERICHIA COLI//P37757  
 F-NT2RP3004095//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.5e-17:72:65//HOMO SAPIENS (HUMAN)//  
 P39188  
 F-NT2RP3004110//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.6e-10:51:72//HOMO SAPIENS (HUMAN)//  
 P39195  
 F-NT2RP3004125//ZINC FINGER PROTEIN 75//1.1e-28:118:47//HOMO SAPIENS (HUMAN)//P51815  
 F-NT2RP3004145//AEROLYSIN REGULATORY PROTEIN//0.012:45:33//AEROMONAS SOBRIA//P09165  
 F-NT2RP3004148//METALLOTHIONEIN-I (MT-1)//0.055:18:50//COLUMBA LIVIA (DOMESTIC PIGEON)//  
 P15786  
 F-NT2RP3004155//UBIQUINONE BIOSYNTHESIS PROTEIN COQ7 HOMOLOG//1.7e-82:178:89//RATTUS  
 NORVEGICUS (RAT)//Q63619  
 F-NT2RP3004189//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1//1.7e-11:25:24//PODOSPORA AN-  
 SERINA//Q00808  
 F-NT2RP3004206//CROOKED NECK PROTEIN//3.8e-101:241:73//DROSOPHILA MELANOGASTER (FRUIT  
 FLY)//P17886  
 F-NT2RP3004207//CUTICLE COLLAGEN 12 PRECURSOR//0.13:130:33//CAENORHABDITIS ELEGANS//  
 P20630  
 F-NT2RP3004209//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTE-  
 RASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUI-  
 TOS NUCLEAR PROTEIN HOMOLOG)//6.5e-16:207:29//HOMO SAPIENS (HUMAN)//Q13107  
 F-NT2RP3004215//PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT//1.0:69:31//SACCHAROMY-  
 CES CEREVISIAE (BAKER'S YEAST)//P35179  
 F-NT2RP3004242//HYPOTHETICAL 30.2 KD PROTEIN ZK632.12 IN CHROMOSOME III//1.1e-64:191:63//  
 CAENORHABDITIS ELEGANS//P34657  
 F-NT2RP3004246//RING3 PROTEIN (KIAA9001)//0.060:101:28//HOMO SAPIENS (HUMAN)//P25440  
 F-NT2RP3004253//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//1.1e-07:184:35//BOS TAURUS (BOVINE)//  
 P02453  
 F-NT2RP3004258//SUPPRESSOR PROTEIN SRP40//4.9e-08:98:39//SACCHAROMYCES CEREVISIAE (BAK-  
 ER'S YEAST)//P32583



- F-NT2RP3004262//DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40).//1.6e-63:210:61//HOMO SAPIENS (HUMAN).//P25685
- F-NT2RP3004282//HYPOTHETICAL PROTEIN F44G4.1 IN CHROMOSOME II (FRAGMENT).//1.6e-29:177:38//CAENORHABDITIS ELEGANS.//P54073
- 5 F-NT2RP3004332//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//0.030:118:36//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414
- F-NT2RP3004334
- F-NT2RP3004341//ALPHA-INTERNEKIN (ALPHA-INK).//0.91:110:28//MUS MUSCULUS (MOUSE).//P46660
- 10 F-NT2RP3004348//HYPOTHETICAL 105.3 KD PROTEIN C01G6.5 IN CHROMOSOME III.//0.60:198:24//CAENORHABDITIS ELEGANS.//P46012
- F-NT2RP3004349//ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.0e-37:60:76//HOMO SAPIENS (HUMAN).//P39193
- F-NT2RP3004378//HYPOTHETICAL 18.8 KD PROTEIN IN GNT-1 INTERGENIC REGION (O162).//0.0026:76:28//ESCHERICHIA COLI.//P46854
- 15 F-NT2RP3004399//LEUCINE-RICH PRIMARY RESPONSE PROTEIN 1 (FOLLICLE-STIMULATING HORMONE PRIMARY RESPONSE PROTEIN).//4.4e-109:212:96//HOMO SAPIENS (HUMAN).//Q92674
- F-NT2RP3004424//JTV-1 PROTEIN.//4.5e-18:60:70//HOMO SAPIENS (HUMAN).//Q13155 F-NT2RP3004428//METALLOTHIONEIN-A (MTA).//0.0010:36:47//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//P04734
- 20 F-NT2RP3004451//MYOSIN IC HEAVY CHAIN.//0.00072:113:34//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569
- F-NT2RP3004454//VERPROLIN.//3.3e-07:156:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P37370
- F-NT2RP3004466//HYPOTHETICAL PROTEIN F-215.//0.0013:125:32//HUMAN ADENOVIRUS TYPE 2.//P03291
- 25 F-NT2RP3004470//HYPOTHETICAL 15.4 KD PROTEIN C16C10.11 IN CHROMOSOME III.//1.0:33:51//CAENORHABDITIS ELEGANS.//Q09254
- F-NT2RP3004472//GERM CELL-LESS PROTEIN.//7.3e-33:170:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01820
- 30 F-NT2RP3004475//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//8.4e-54:214:46//HOMO SAPIENS (HUMAN).//P98171
- F-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//3.9e-47:199:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P34110
- F-NT2RP3004490//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.0013:121:33//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437
- 35 F-NT2RP3004498//HYPOTHETICAL 43.5 KD PROTEIN IN COTD-KDUD INTERGENIC REGION PRECURSOR.//0.066:87:35//BACILLUS SUBTILIS.//P50840
- F-NT2RP3004503//ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.0e-34:102:69//HOMO SAPIENS (HUMAN).//P39194
- 40 F-NT2RP3004504//SUPPRESSOR PROTEIN SRP40.//0.64:93:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
- F-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).//2.2e-16:90:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40484
- F-NT2RP3004527
- 45 F-NT2RP3004534//S-PHASE ENTRY CYCLIN 6.//0.38:148:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32943
- F-NT2RP3004539//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (IGFBP-1) (BP-1) (IGF-BINDING PROTEIN 1).//0.38:89:38//RATTUS NORVEGICUS (RAT).//P21743
- F-NT2RP3004544//CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 2 (CYTADHERENCE ACCESSORY PROTEIN 2).//0.0024:200:24//MYCOPLASMA PNEUMONIAE.//P75471
- 50 F-NT2RP3004568//GASTRULA ZINC FINGER PROTEIN XLCGF17.1 (FRAGMENT).//4.6e-25:126:43//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18713
- F-NT2RP3004569//ANKYRIN.//8.3e-07:150:28//MUS MUSCULUS (MOUSE).//Q02357
- F-NT2RP3004572//TRANSCRIPTION INITIATION FACTOR TFIID 150 KD SUBUNIT (TAFII-150) (TAFII150).//1.6e-70:247:54//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24325
- 55 F-NT2RP3004578//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//1.5e-10:210:26//HOMO SAPIENS (HUMAN).//Q02224
- F-NT2RP3004594//P54 PROTEIN PRECURSOR.//0.0044:230:24//ENTEROCOCCUS FAECIUM (STREPTO-

COCCUS FAECIUM) //P13692  
 F-NT2RP3004617//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR //1.5e-14;113.34//MUS MUSCULUS (MOUSE) //P15533  
 5 F-NT2RP3004618//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.//4.5e-08;149.30//CAENORHABDITIS ELEGANS //P34681  
 F-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN) //1.0e-24;75.48//DROSOPHILA MELANOGASTER (FRUIT FLY) //P54352  
 F-NT2RP3004670//CUTICLE COLLAGEN 210.00090:159:29//CAENORHABDITIS ELEGANS //P17656  
 10 F-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//4.0e-79;243.62//BOS TAURUS (BOVINE) //P35526  
 F-NT2RP4000023  
 F-NT2RP4000035//ALU SUBFAMILY SQ WARNING ENTRY //3.6e-06;46.67//HOMO SAPIENS (HUMAN) //P39194  
 F-NT2RP4000049//CALDESMON (CDM) //0.41;63.34//GALLUS GALLUS (CHICKEN) //P12957  
 F-NT2RP4000051//DUALIN //2.3e-23;195.37//GALLUS GALLUS (CHICKEN) //Q90830  
 15 F-NT2RP4000078//RING CANAL PROTEIN (KELCH PROTEIN) //1.2e-24;182.31//DROSOPHILA MELANOGASTER (FRUIT FLY) //Q04652  
 F-NT2RP4000102//XPAR7 PROTEIN //1.0;54.33//BACILLUS LICHENIFORMIS //Q99166  
 F-NT2RP4000109//SLIT PROTEIN PRECURSOR //1.9e-60;230.46//DROSOPHILA MELANOGASTER (FRUIT FLY) //P24014  
 20 F-NT2RP4000111//CLEFTAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT) //1.4e-91;157.100//BOS TAURUS (BOVINE) //Q10568  
 F-NT2RP4000129//SE5 ANTIGEN //0.00072;124.37//RATTUS NORVEGICUS (RAT) //Q63003  
 F-NT2RP4000147//ZINC FINGER PROTEIN GCS1 //1.5e-26;119.43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P35197  
 25 F-NT2RP4000150  
 F-NT2RP4000151//HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III.//4.2e-31;180.47//CAENORHABDITIS ELEGANS //P32740  
 F-NT2RP4000159//SPORE COAT PROTEIN SP96 //0.84;107.28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD) //P14328  
 30 F-NT2RP4000167//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC REGION //2.4e-08;133.32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P40164  
 F-NT2RP4000185//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN) //5.4e-05;143.32//HERBES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52) //P28284  
 F-NT2RP4000210//PAIRED AMPHIPATHIC HELIX PROTEIN //1.8e-40;258.35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P22579  
 35 F-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA) //1.4e-20;104.40//APLYSIA CALIFORNICA (CALIFORNIA SEA HARE) //P15287  
 F-NT2RP4000214//FERREDOXIN //1.0;19.42//MOORELLA THERMOACETICA (CLOSTRIDIUM THERMOACETICUM) //P00203  
 40 F-NT2RP4000218//ALU SUBFAMILY J WARNING ENTRY //1.7e-15;48.60//HOMO SAPIENS (HUMAN) //P39188  
 F-NT2RP4000243//DUALIN //5.8e-78;192.70//GALLUS GALLUS (CHICKEN) //Q90830  
 F-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1) //3.1e-83;207.76//MUS MUSCULUS (MOUSE) //Q03173  
 45 F-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9) //5.5e-29;153.43//HELIANTHUS ANNUUS (COMMON SUNFLOWER) //O23968  
 F-NT2RP4000263//ANNEXIN VII (SYNEXIN) (FRAGMENT) //0.98;42.40//BOS TAURUS (BOVINE) //P20072  
 F-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//3.5e-71;209.66//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //P87115  
 50 F-NT2RP4000312//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1) //8.9e-22;166.37//HOMO SAPIENS (HUMAN) //Q15404  
 F-NT2RP4000321//VERPROLIN //0.00018;260.28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P37370  
 F-NT2RP4000323//ANTHOPLEURIN B (TOXIN AP-B) //0.42;15.46//ANTHOPLEURA XANTHOGRAMMICA (GIANT GREEN SEA ANEMONE) //P01531  
 55 F-NT2RP4000355//HYPOTHETICAL 90.9 KD PROTEIN IN GCN20-CMK1 INTERGENIC REGION //0.75;125.29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P43596  
 F-NT2RP4000360//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT) //0.27;92.

33//RATTUS NORVEGICUS (RAT)//P10164  
 F-NT2RP4000367//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION.//0.99:52:32//HUMAN AD-  
 ENOVIRUS TYPE 41.//P23691  
 5 F-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).//4.1e-40:  
 163:52//HOMO SAPIENS (HUMAN).//O75570  
 F-NT2RP4000376//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//4.2e-59:125:80//RATTUS NOR-  
 VEGICUS (RAT).//P54319  
 F-NT2RP4000381//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//  
 0.00058:194:30//MUS MUSCULUS (MOUSE).//P19246  
 10 F-NT2RP4000398//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.2e-45:153:39//HOMO SAPIENS (HUMAN).//  
 Q96676  
 F-NT2RP4000415//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.//  
 0.00066:201:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47179  
 F-NT2RP4000417//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).//  
 1.8e-25:196:40//MUS MUSCULUS (MOUSE).//P39098  
 15 F-NT2RP4000424//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.0e-15:72:61//HOMO SAPIENS (HUMAN).//  
 P39195  
 F-NT2RP4000448//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//7.0e-23:63:82//HOMO SAPIENS (HUMAN).//  
 P39192  
 20 F-NT2RP4000449//REGULATORY PROTEIN SIR2 (SILENT INFORMATION REGULATOR 2).//1.3e-41:102:45//  
 KLUYVEROMYCES LACTIS (YEAST).//P33294  
 F-NT2RP4000455//HOMEBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT).//0.00014:92:30//GALLUS GALLUS  
 (CHICKEN).//P19601  
 F-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 7 (EC 3.1.2.15) (UBIQUITIN THIOLESTE-  
 25 RASE 7) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 7) (DEUBIQUITINATING ENZYME 7) (HERPESVI-  
 RUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE).//1.0e-29:218:38//HOMO SAPIENS (HUMAN).//Q93009  
 F-NT2RP4000480//TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN  
 ALGR3).//0.049:117:29//PSEUDOMONAS AERUGINOSA.//P15276  
 30 F-NT2RP4000481//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//2.3e-05:152:23//  
 CAENORHABDITIS ELEGANS.//Q09475  
 F-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//2.3e-48:172:52//SACCHAROMYCES CEREVISIAE  
 (BAKER'S YEAST).//P40484  
 F-NT2RP4000500//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III.//1.3e-23:165:35//  
 CAENORHABDITIS ELEGANS.//P34535  
 35 F-NT2RP4000515//PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE) (5'-NUCLEOTIDE PHOS-  
 PHODIESTERASE) (FRAGMENT).//1.0:48:37//BOS TAURUS (BOVINE).//P15396  
 F-NT2RP4000517//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//1.0:41:36//VICIA FABA (BROAD BEAN).//  
 Q41657  
 40 F-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.1e-11:93:36//SACCHAROMYCES CEREVI-  
 SIAE (BAKER'S YEAST).//P45818  
 F-NT2RP4000519//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.68:55:40//BOS TAURUS (BOVINE).//  
 P25508  
 F-NT2RP4000524//IGA FC RECEPTOR PRECURSOR (BETA ANTIGEN) (B ANTIGEN).//0.37:187:24//STREP-  
 TOCOCOCCUS AGALACTIAE.//P27951  
 45 F-NT2RP4000528//NPL4 PROTEIN.//2.1e-45:305:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
 P33755  
 F-NT2RP4000541//HOMEBOX PROTEIN CHOX-1 (FRAGMENT).//0.23:28:50//GALLUS GALLUS (CHICK-  
 EN).//P13544  
 F-NT2RP4000556//HYPOTHETICAL 34.1 KD PROTEIN C40H1.4 IN CHROMOSOME III.//4.3e-14:174:34//  
 50 CAENORHABDITIS ELEGANS.//Q03574  
 F-NT2RP4000560//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.//2.1e-19:155:36//  
 CAENORHABDITIS ELEGANS.//P34679  
 F-NT2RP4000588//HYPOTHETICAL PROTEIN E-115.//0.014:64:35//HUMAN ADENOVIRUS TYPE 2.//P03290  
 F-NT2RP4000614//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35)  
 55 (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//2.7e-27:188:44//GALLUS GALLUS (CHICKEN).//P30352  
 F-NT2RP4000638//EARLY NODULIN 55-1 PRECURSOR (N-55-1) (FRAGMENT).//0.55:40:40//GLYCINE MAX  
 (SOYBEAN).//Q05544  
 F-NT2RP4000648//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-06:31:74//HOMO SAPIENS (HUMAN).//

- P39188  
F-NT2RP46000657//HYPOTHETICAL PROTEIN MJ1065./2.5e-40:237:40//METHANOCOCCUS JANNAS-  
CHII./Q58465  
F-NT2RP40000704  
5 F-NT2RP4000713//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556./4.0e-07:134:40//STREP-  
TOMYCES FRADIAE./P20186  
F-NT2RP4000724//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE  
(EC 2.7.7.49); ENDONUCLEASE]./1.1e-62:109:88//HOMO SAPIENS (HUMAN)./P10266  
F-NT2RP4000728//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR./0.0033:190:25//SACCHAROMY-  
CES CEREVISIAE (BAKER'S YEAST)./P32323  
10 F-NT2RP4000737//PTB-ASSOCIATED SPLICING FACTOR (PSF)./1.0e-05:114:34//HOMO SAPIENS (HU-  
MAN)./P23246  
F-NT2RP4000739//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)./1.0:20:50//ANAS PLATYRHYNCHOS  
(DOMESTIC DUCK)./P50655  
15 F-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION./0.0013:67:  
31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)./P53915  
F-NT2RP4000787//POLLEN SPECIFIC PROTEIN SF3./1.3e-13:79:39//HELIANTHUS ANNUUS (COMMON  
SUNFLOWER)./P29675  
F-NT2RP4000817//SUPPRESSOR PROTEIN SRP40./1.3e-05:255:21//SACCHAROMYCES CEREVISIAE  
(BAKER'S YEAST)./P32583  
20 F-NT2RP4000833  
F-NT2RP4000837//MALE SPECIFIC SPERM PROTEIN MSTs4DB./0.18:38:44//DROSOPHILA MELA-  
NOGASTER (FRUIT FLY)./Q01643  
F-NT2RP4000839//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAFII-90)./0.026:38:44//  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)./P38129  
25 F-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMI-  
NOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B)./2.8e-64:229:53//RATTUS NORVEGICUS (RAT)./  
Q09175  
F-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)./3.6e-84:174:54//HOMO SAPIENS (HU-  
MAN)./P16415  
30 F-NT2RP4000878//MYELOID UPREGULATED PROTEIN./8.2e-88:227:74//MUS MUSCULUS (MOUSE)./  
Q35682  
F-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN)./9.1e-55:268:43//HOMO SAPIENS  
(HUMAN)./P22314  
35 F-NT2RP4000907//BDNF / NT-3 GROWTH FACTORS RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKB TYRO-  
SINE KINASE) (GP145-TRKB) (TRK-B)./5.4e-10:220:25//HOMO SAPIENS (HUMAN)./Q16620  
F-NT2RP4000915//80S ACIDIC RIBOSOMAL PROTEIN P2 (FRAGMENT)./0.46:23:60//ARABIDOPSIS THAL-  
IANA (MOUSE-EAR CRESS)./P51407  
40 F-NT2RP4000918//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB./0.00010:148:32//BACILLUS SUBTI-  
LIS./P39217  
F-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN)./3.5e-27:  
220:36//HOMO SAPIENS (HUMAN)./Q06828  
F-NT2RP4000927//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6)./  
0.64:75:37//BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA)./P29128  
45 F-NT2RP4000928//PHOSPHATIDATE CYTIDYLTRANSFERASE (EC 2.7.7.41) (CDP-DIGLYCERIDE SYN-  
THETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS)  
(CTP-PHOSPHATIDATE CYTIDYLTRANSFERASE) (CDP-DAG SYNTHASE)./3.1e-104:263:66//HOMO SA-  
PIENS (HUMAN)./Q92903  
F-NT2RP4000929//HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC REGION./0.93:107:  
28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)./P53288  
50 F-NT2RP4000955//PUTATIVE CUTICLE COLLAGEN F09G8.6./2.0e-05:102:37//CAENORHABDITIS ELE-  
GANS./P34391  
F-NT2RP4000973//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION./2.3e-17:78:56//  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)./P40564  
F-NT2RP4000975//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-  
MENT)./0.0041:142:33//HOMO SAPIENS (HUMAN)./P10162  
55 F-NT2RP4000979//HYPOTHETICAL 14.5 KD PROTEIN./0.77:106:33//VACCINIA VIRUS (STRAIN COPENHA-  
GEN)./P20517

- F-NT2RP4000984//HYPOTHETICAL 124.8 KD PROTEIN C29E4.4 IN CHROMOSOME III.//0.90:94:25//CAENORHABDITIS ELEGANS.//P34343
- F-NT2RP4000989//ANTHOPLEURIN B (TOXIN AP-B).//0.76:41:41//ANTHOPLEURA XANTHOGRAMMICA (GI-ANT GREEN SEA ANEMONE).//P01531
- 5 F-NT2RP4000996//PROTEIN Q300.//0.00024:41:53//MUS MUSCULUS (MOUSE).//Q02722
- F-NT2RP4000997//RNA-DIRECTED RNA POLYMERASE 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (PNA135) (RNA POLYMERASE I 127 KD SUBUNIT).//8.7e-115:261:82//RATTUS NORVEGICUS (RAT).//O54888
- 10 F-NT2RP4001004//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.50:61:34//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q42377
- F-NT2RP4001006//HYPOTHETICAL 43.5 KD PROTEIN IN COTD-KDUD INTERGENIC REGION PRECURSOR.//0.010:152:29//BACILLUS SUBTILIS.//P50840
- F-NT2RP4001010//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.9e-05:247:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
- 15 F-NT2RP4001029//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//1.1e-14:175:31//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13002
- F-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//1.5e-74:272:55//CAENORHABDITIS ELEGANS.//Q09996
- 20 F-NT2RP4001057//HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III.//0.0064:76:38//CAENORHABDITIS ELEGANS.//P34664
- F-NT2RP4001064//DUALIN.//2.5e-24:199:38//GALLUS GALLUS (CHICKEN).//Q90830
- F-NT2RP4001078//TRANSCRIPTION INITIATION FACTOR TFIIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.11:139:38//HOMO SAPIENS (HUMAN).//O00268
- 25 F-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE).//1.5e-22:242:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P13586
- F-NT2RP4001080//POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I).//1.7e-82:178:69//SUS SCROFA (PIG).//Q29099
- 30 F-NT2RP4001086//LEUCINE-RICH ACIDIC NUCLEAR PROTEIN.//0.00039:141:26//RATTUS NORVEGICUS (RAT).//P49911
- F-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//9.9e-07:79:43//HOMO SAPIENS (HUMAN).//P78563
- F-NT2RP4001100//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION.//4.4e-16:207:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032
- 35 F-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//8.1e-115:224:99//RATTUS NORVEGICUS (RAT).//P38378
- F-NT2RP4001122//TIPD PROTEIN.//7.5e-11:129:31//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//O15736
- F-NT2RP4001126//TRICHOHYALIN.//1.4e-19:257:28//OVIS ARIES (SHEEP).//P22793
- 40 F-NT2RP4001138//PUTATIVE F420-DEPENDENT NADP REDUCTASE (EC 1.-.-.-).//0.00010:204:25//METHANOCOCCUS JANNASCHII.//Q58896
- F-NT2RP4001143//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION.//4.5e-34:168:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43616
- 45 F-NT2RP4001148//SOF1 PROTEIN.//2.4e-41:158:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33750
- F-NT2RP4001149//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//1.3e-08:106:41//VOLVOX CARTERI.//P21997
- F-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//3.6e-24:194:32//GALLUS GALLUS (CHICKEN).//P35331
- 50 F-NT2RP4001159//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2).//0.0056:117:25//PLASMODIUM FALCIPARUM (ISOLATE K1 / THAILAND).//Q03643
- F-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//5.9e-24:184:34//BRASSICA OLERACEA (CAULIFLOWER).//P52178
- F-NT2RP4001206//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2).//0.0029:117:26//PLASMODIUM FALCIPARUM (ISOLATE K1 / THAILAND).//Q03643
- 55 F-NT2RP4001207//CHROMOSOME SEGREGATION PROTEIN CSE1.//1.0e-07:144:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33307
- F-NT2RP4001210//DERMOPHIN 1 PRECURSOR [CONTAINS: DELTORPHIN (DERMENKEPHALIN); DER-

MORPHIN].//0.019:130:30//PHYLLIOMEDUSA SAUVAGEI (SAUVAGE'S LEAF FROG).//P05422  
 F-NT2RP4001213//ZINC FINGER PROTEIN 177.//3.2e-28:176:39//HOMO SAPIENS (HUMAN).//Q13360  
 F-NT2RP4001219//DISULFIDE ISOMERASE MPD1 PRECURSOR (EC 5.3.4.1).//2.4e-13:108:37//SACCHARO-  
 MYCES CEREVISIAE (BAKER'S YEAST).//Q12404  
 5 F-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//2.7e-56:242:40//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY).//Q04652  
 F-NT2RP4001235//REGULATORY PROTEIN E2.//0.0080:100:38//HUMAN PAPILLOMAVIRUS TYPE 25.//  
 P36787  
 10 F-NT2RP4001256//CUTICLE COLLAGEN 1.//0.014:104:31//CAENORHABDITIS ELEGANS.//P08124  
 F-NT2RP4001260//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//0.00077:16:68//ESCHERICHIA  
 COLI.//P05834  
 F-NT2RP4001274//HISTONE H1.M6.1.//0.98:65:35//TRYPANOSOMA CRUZI.//P40273  
 F-NT2RP4001276//ELAV PROTEIN.//0.00054:134:33//DROSOPHILA VIRILIS (FRUIT FLY).//P23241  
 15 F-NT2RP4001313//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//  
 0.014:71:35//NICOTIANA TABACUM (COMMON TOBACCO).//P13983  
 F-NT2RP4001315//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.//2.3e-12:190:27//SAC-  
 CHAROMYCES CEREVISIAE (BAKER'S YEAST).//P54787  
 F-NT2RP4001336//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//0.0037:108:31//PODOSPORA AN-  
 SERINA.//Q00808  
 20 F-NT2RP4001339//HYPOTHETICAL PROTEIN MJ0810.//1.2e-09:150:34//METHANOCOCCUS JANNASCHII.//  
 Q58220  
 F-NT2RP4001343//HYPOTHETICAL 85.2 KD PROTEIN F52C9.3 IN CHROMOSOME III.//1.4e-18:244:27//  
 CAENORHABDITIS ELEGANS.//Q10123  
 25 F-NT2RP4001345//PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)  
 (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE)  
 (FRAGMENT).//4.0e-49:212:50//GALLUS GALLUS (CHICKEN).//P53760  
 F-NT2RP4001351//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//5.7e-11:229:26//SACCHARO-  
 MYCES CEREVISIAE (BAKER'S YEAST).//P25386  
 30 F-NT2RP4001353//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//0.00088:84:28//HO-  
 MO SAPIENS (HUMAN).//Q15404  
 F-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN).//1.0e-  
 22:222:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q08180  
 F-NT2RP4001373//OV-17 ANTIGEN PRECURSOR (IMMUNODOMINANT HYPODERMAL ANTIGEN).//0.51:92:  
 26//ONCHOCERCA VOLVULUS.//P36991  
 35 F-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-  
 TEIN KINASE 1).//3.5e-13:146:35//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P18160  
 F-NT2RP4001379//HYPOTHETICAL 64.2 KD PROTEIN IN SLT2-PUT2 INTERGENIC REGION.//1.2e-14:207:  
 28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38767  
 40 F-NT2RP4001389//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAG-  
 MENT).//0.073:112:33//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414  
 F-NT2RP4001407//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//0.0019:233:24//HOMO SAPIENS (HU-  
 MAN).//Q02224  
 F-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//6.2e-89:195:81//HOMO SAPIENS (HUMAN).//Q14141  
 45 F-NT2RP4001433//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.5e-85:216:56//HOMO SAPIENS (HU-  
 MAN).//P28160  
 F-NT2RP4001442//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (VERSION 1).//  
 0.012:107:35//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P18616  
 F-NT2RP4001447//60S ACIDIC RIBOSOMAL PROTEIN P2 (EL12).//0.0046:69:33//ARTEMIA SALINA (BRINE  
 SHRIMP).//P02399  
 50 F-NT2RP4001474//CBP3 PROTEIN PRECURSOR.//0.0011:111:29//SACCHAROMYCES CEREVISIAE (BAK-  
 ER'S YEAST).//P21560  
 F-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (AL-  
 PHA-KETOGLUTARATE DEHYDROGENASE).//6.2e-60:146:61//HOMO SAPIENS (HUMAN).//Q02218  
 F-NT2RP4001498//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//2.3e-24:137:37//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701  
 55 F-NT2RP4001502//HYPOTHETICAL 24.7 KD PROTEIN IN POM152-REC114 INTERGENIC REGION.//6.0e-22:  
 148:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40206  
 F-NT2RP4001507//CUTICLE COLLAGEN 40.//0.00029:166:31//CAENORHABDITIS ELEGANS.//P34804

- F-NT2RP4001524//LACTOCOCCIN A IMMUNITY PROTEIN //0.74-96:30//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS), AND LACTOCOCCUS LACTIS (SUBSP. CREMORIS) (STREPTOCOCCUS CREMORIS) //Q00561
- 5 F-NT2RP4001529//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1) //2.8e-06:79:41//DROSOPHILA MELANOGASTER (FRUIT FLY) //P13002
- F-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENIC REGION //5.4e-34:88:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P25656
- 10 F-NT2RP4001551//CELL DIVISION CONTROL PROTEIN 68 //1.5e-18:243:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P32558
- F-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-) //0.00030:158:24//MYCOBACTERIUM TUBERCULOSIS //P96902
- F-NT2RP4001567//IMPORTIN ALPHA-1 SUBUNIT (KARYOPHERIN ALPHA-1 SUBUNIT) //0.00013:147:29//XENOPUS LAEVIS (AFRICAN CLAWED FROG) //P52170
- 15 F-NT2RP4001568//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT) //8.0e-22:119:42//HOMO SAPIENS (HUMAN) //Q15057
- F-NT2RP4001571//NEUROMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (PP46) (B-50) (PROTEIN F1) (CALMODULIN-BINDING PROTEIN P-57) //0.012:167:28//BOS TAURUS (BOVINE) //P06836
- F-NT2RP4001574//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP) //6.8e-115:208:98//BOS TAURUS (BOVINE) //P53620
- 20 F-NT2RP4001575//M-RELATED PROTEIN PRECURSOR //0.22:184:25//STREPTOCOCCUS PYOGENES //P16946
- F-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS) //7.4e-45:229:39//SYNECHOCYSTIS SP. (STRAIN PCC 6803) //P73505
- 25 F-NT2RP4001610//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII) //0.41:74:28//SUS SCROFA (PIG) //P27917
- F-NT2RP4001614//BASIC PROLINE-RICH PEPTIDE P-E (IB-9) //1.0:29:37//HOMO SAPIENS (HUMAN) //P02811
- F-NT2RP4001634//MYOSIN HEAVY CHAIN, PERINATAL SKELETAL MUSCLE (FRAGMENT) //0.16:233:23//RATTUS NORVEGICUS (RAT) //P04462
- 30 F-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/34/MS19 //4.2e-21:249:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P40469
- F-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK) //4.5e-18:111:44//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD) //P25323
- 35 F-NT2RP4001656//HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II //3.4e-13:175:32//CAENORHABDITIS ELEGANS //Q09600
- F-NT2RP4001677//HYPOTHETICAL 73.6 KD PROTEIN CY49.21 //0.065:66:43//MYCOBACTERIUM TUBERCULOSIS //Q10690
- F-NT2RP4001679//!!! ALU SUBFAMILY SQ WARNING ENTRY !!! //1.3e-36:103:72//HOMO SAPIENS (HUMAN) //P39194
- 40 F-NT2RP4001696//PHOTOSYSTEM II REACTION CENTRE J PROTEIN //0.93:37:37//CHLORELLA VULGARIS //P56338
- F-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT //4.3e-11:128:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //Q10282
- 45 F-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT) //4.1e-22:201:27//DROSOPHILA MELANOGASTER (FRUIT FLY) //Q09332
- F-NT2RP4001739//HOMEBOX PROTEIN HOX-A10 (HOX-1H) (HOX-1.8) (PL) //1.0:67:34//HOMO SAPIENS (HUMAN) //P31260
- 50 F-NT2RP4001753//ZINC FINGER PROTEIN 10 (ZINC FINGER PROTEIN KOX1) (FRAGMENT) //1.2e-19:72:62//HOMO SAPIENS (HUMAN) //P21506
- F-NT2RP4001760//BREAKPOINT CLUSTER REGION PROTEIN //1.8e-13:179:28//HOMO SAPIENS (HUMAN) //P11274
- F-NT2RP4001790//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49) //7.9e-38:147:49//MUS MUSCULUS (MOUSE) //Q07231
- 55 F-NT2RP4001803//CUTICLE COLLAGEN 12 PRECURSOR //0.40:48:39//CAENORHABDITIS ELEGANS //P20630
- F-NT2RP4001822//NOVEL ANTIGEN 2 (NAG-2) //2.7e-27:173:36//HOMO SAPIENS (HUMAN) //O14817
- F-NT2RP4001823//PUTATIVE CUTICLE COLLAGEN F09G8.6 //3.3e-16:152:42//CAENORHABDITIS ELE-

- GANS.//P34391  
 F-NT2RP4001828//HOLIN.//0.99:33:36//BACTERIOPHAGE HP1.//P51727  
 F-NT2RP4001838//METASTASIS-ASSOCIATED PROTEIN MTA1.//1.2e-07:95:31//HOMO SAPIENS (HUMAN).//Q13330
- 5 F-NT2RP4001841//INTESTINAL MUCIN-LIKE PROTEIN (MLP) (FRAGMENT).//0.94:141:22//RATTUS NORVEGICUS (RAT).//P98089  
 F-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1.//5.6e-52:276:45//MUS MUSCULUS (MOUSE).//P55194  
 F-NT2RP4001861//HYPOTHETICAL 10.6 KD PROTEIN IN GALE-PEPT INTERGENIC REGION.//0.92:39:51//BACILLUS SUBTILIS.//P55185
- 10 F-NT2RP4001889//HYPOTHETICAL BHLF1 PROTEIN.//0.32:97:31//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181  
 F-NT2RP4001893//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).//3.6e-07:124:29//MUS MUSCULUS (MOUSE).//Q05921  
 F-NT2RP4001896//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PT1 INTERGENIC REGION.//3.9e-10:210:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42935
- 15 F-NT2RP4001901//ACROSIN PRECURSOR (EC 3.4.21.10).//2.4e-07:53:45//ORYCTOLAGUS CUNICULUS (RABBIT).//P48038  
 F-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//3.1e-19:170:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12024
- 20 F-NT2RP4001938//ZINC FINGER PROTEIN MOK-2.//1.3e-28:72:50//MUS MUSCULUS (MOUSE).//P24399  
 F-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISO-ASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE).//4.8e-14:183:30//TRITICUM AESTIVUM (WHEAT).//Q43209
- 25 F-NT2RP4001950//HYPOTHETICAL PROTEIN ORF-1137.//3.7e-07:115:29//MUS MUSCULUS (MOUSE).//P11260  
 F-NT2RP4001953  
 F-NT2RP4001968//WALL-ASSOCIATED PROTEIN PRECURSOR.//0.13:151:27//BACILLUS SUBTILIS.//Q07833
- 30 F-NT2RP4001975//FIBRIL-FORMING COLLAGEN ALPHA CHAIN.//0.00031:190:31//RIFTIA PACHYPTILA (TUBE WORM).//P30754  
 F-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//3.5e-18:185:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
- 35 F-NT2RP4002047//GTP-BINDING PROTEIN GUF1 (GTPASE GUF1).//4.0e-49:158:65//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P46943  
 F-NT2RP4002052//HYPOTHETICAL 54.3 KD PROTEIN C23D3.03C IN CHROMOSOME 1.//0.0047:148:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09844
- 40 F-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE F56D2.6.//0.057:66:30//CAENORHABDITIS ELEGANS.//Q20875  
 F-NT2RP4002071//VERY HYPOTHETICAL 13.2 KD PROTEIN CY251.09.//0.94:45:46//MYCOBACTERIUM TUBERCULOSIS.//Q10888
- 45 F-NT2RP4002075//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.44:36:38//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18804  
 F-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.6e-19:46:76//HOMO SAPIENS (HUMAN).//Q05481
- 50 F-NT2RP4002081//MHC CLASS II REGULATORY FACTOR RFX1 (RFX) (ENHANCER FACTOR C) (EF-C).//2.8e-05:196:31//HOMO SAPIENS (HUMAN).//P22670  
 F-NT2RP4002083//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//0.0064:29:55//OWENIA FUSIFORMIS.//P21260
- 55 F-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.1e-37:159:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P38938  
 F-NT2RP4002791//30S RIBOSOMAL PROTEIN S20.//1.0:73:26//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//P56027  
 F-NT2RP4002888//HYPOTHETICAL PROTEIN TP0352.//0.98:52:26//TREPONEMA PALLIDUM.//O83371
- F-NT2RP4002905//G2/MITOTIC-SPECIFIC CYCLIN S13-7 (B-LIKE CYCLIN) (FRAGMENT).//5.9e-05:138:27//GLYCINE MAX (SOYBEAN).//P25012  
 F-NT2RP5003459//HOMEBOX PROTEIN HOX-A3 (HOX-1.5) (MO-10).//0.027:40:40//MUS MUSCULUS (MOUSE).//P02831



- F-NT2RP5003461//HYPOTHETICAL PROTEIN C22F3.14C IN CHROMOSOME I (FRAGMENT).//1.1e-12:142:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09779
- F-NT2RP5003477//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1.//5.3e-13:215:28//PODOSPORA ANSERINA.//Q00808
- 5 F-NT2RP5003492//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//0.0055:144:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
- F-NT2RP5003500//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//9.0e-05:103:38//MUS MUSCULUS (MOUSE).//P05142
- 10 F-NT2RP5003506//MALE SPECIFIC SPERM PROTEIN MST87F.//0.53:21:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175
- F-NT2RP5003512//HYPOTHETICAL PROTEIN IN CYCB 3'REGION PRECURSOR (ORF2) (FRAGMENT).//0.92:49:32//PARACOCCLUS DENITRIFICANS.//P29969
- 15 F-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//2.7e-18:165:39//PHASEOLUS AUREUS (MUNG BEAN) (VIGNA RADIATA).//P37116
- F-NT2RP5003524//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//6.0e-08:125:41//RATTUS NORVEGICUS (RAT).//P02454
- F-NT2RP5003534//ATP SYNTHASE, SUBUNIT F (EC 3.6.1.34).//0.88:37:45//HALOBACTERIUM VOLCANII (HALOPHILUS VOLCANII).//Q48331
- 20 F-OVARC1000001//GAR22 PROTEIN.//1.9e-05:41:58//HOMO SAPIENS (HUMAN).//Q99501
- F-OVARC1000004//70 KD EXOCYST COMPLEX PROTEIN.//3.7e-08:186:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P19658
- F-OVARC1000006//HISTONE H2A.1.//4.7e-55:117:98//RATTUS NORVEGICUS (RAT).//P02262
- 25 F-OVARC1000013//WD-REPEAT PROTEIN POP1.//0.00022:126:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87060
- F-OVARC1000014//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//2.3e-05:220:30//GALLUS GALLUS (CHICKEN).//P02457
- 30 F-OVARC1000017//CUTICLE COLLAGEN DPY-13.//2.6e-05:97:30//CAENORHABDITIS ELEGANS.//P17657
- F-OVARC1000035
- F-OVARC1000058//RAS-RELATED PROTEIN RABC.//0.00015:110:24//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34143
- F-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE).//6.8e-09:60:45//LYCOPERSICON ESCULENTUM (TOMATO).//P80022
- 35 F-OVARC1000068//CYTOTOXIN 4 (CARDIOTOXIN V-4).//1.0:27:44//NAJA MOSSAMBICA (MOZAMBIQUE COBRA).//P01452
- F-OVARC1000071//NUCLEAR TRANSPORT FACTOR 2 (NTF-2) (PLACENTAL PROTEIN 15) (PP15).//5.2e-06:115:29//HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT).//P13662
- F-OVARC1000085
- 40 F-OVARC1000087//HISTONE MACRO-H2A.1.//1.2e-13:174:26//RATTUS NORVEGICUS (RAT).//Q02874
- F-OVARC1000091//OCTAPEPTIDE-REPEAT PROTEIN T2.//0.00013:137:32//MUS MUSCULUS (MOUSE).//Q06666
- F-OVARC1000092//MITOCHONDRIAL RIBOSOMAL PROTEIN S7.//0.97:46:39//ACANTHAMOEBA CASTELLANI (AMOEBA).//P46756
- 45 F-OVARC1000106//HYPOTHETICAL 141.5 KD PROTEIN IN YPT53-RHO2 INTERGENIC REGION.//0.0012:165:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53935
- F-OVARC1000109//PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR (FRAGMENT).//0.18:35:34//DAUCUS CAROTA (CARROT).//P06600
- F-OVARC1000113//HYPOTHETICAL PROTEIN C18.//1.0:26:26//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//P32217
- 50 F-OVARC1000114//ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.6e-28:57:63//HOMO SAPIENS (HUMAN).//P39194
- F-OVARC1000133
- F-OVARC1000139//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//1.9e-09:200:29//HOMO SAPIENS (HUMAN).//Q13107
- 55 F-OVARC1000145//HOMEBOX PROTEIN DLX-3.//1.0:65:30//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q01702
- F-OVARC1000148//HYPHAL WALL PROTEIN 1 (CELL ELONGATION PROTEIN 2).//0.12:175:29//CANDIDA AL-

BICANS (YEAST).//P46593  
 F-OVARC1000151//HYPOTHETICAL PROTEIN KIAA0161.//5.6e-20:197:30//HOMO SAPIENS (HUMAN).//  
 P50876  
 5 F-OVARC1000168//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.0030:77:38//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-OVARC1000191//COLANIC ACID BIOSYNTHESIS PROTEIN WCAH.//0.95:56:35//ESCHERICHIA COLI.//  
 P32056  
 F-OVARC1000198//HISTONE H1.C2.//0.96:70:25//TRYPANOSOMA CRUZI.//P40268  
 10 F-OVARC1000208//HYPOTHETICAL 20.9 KD PROTEIN IN PLB1-HXT2 INTERGENIC REGION.//2.5e-33:178:  
 44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03677  
 F-OVARC1000212//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//1.7e-05:66:46//MUS MUSCULUS  
 (MOUSE).//P05142  
 F-OVARC1000240//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.8e-10:41:78//HOMO SAPIENS (HUMAN).//  
 P39193  
 15 F-OVARC1000241//ENDOTHELIAL PAS DOMAIN PROTEIN 1 (EPAS-1) (HIF-1 ALPHA-LIKE FACTOR) (MHLF)  
 (HIF-RELATED FACTOR) (HRF).//7.4e-54:177:54//MUS MUSCULUS (MOUSE).//P97481  
 F-OVARC1000288//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION.//2.9e-20:115:  
 45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38821  
 20 F-OVARC1000302//CORTICOSTEROID-BINDING GLOBULIN PRECURSOR (CBG) (TRANSCORTIN).//1.0:79:  
 25//MUS MUSCULUS (MOUSE).//Q06770  
 F-OVARC1000304//PROTEIN MOV.10.//1.6e-79:181:83//MUS MUSCULUS (MOUSE).//P23249  
 F-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//6.9e-36:156:42//ASHBYA GOSSYPPII (EREMOTH-  
 ECIIUM GOSSYPPII).//Q00063  
 25 F-OVARC1000321//HYPOTHETICAL 28.1 KD PROTEIN C4F8.03 IN CHROMOSOME I.//5.2e-45:159:53//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14179  
 F-OVARC1000326//BASIC PROLINE-RICH PEPTIDE IB-1.//0.036:67:35//HOMO SAPIENS (HUMAN).//P04281  
 F-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//1.2e-16:200:  
 27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40004  
 30 F-OVARC1000347//HYPOTHETICAL 7.6 KD PROTEIN YCF33.//0.69:41:43//ICYANOPHORA PARADOXA.//  
 P48273  
 F-OVARC1000384//ANTIFREEZE PEPTIDE 4 PRECURSOR.//0.98:49:34//PSEUDOPLEURONECTA AMERI-  
 CANUS (WINTER FLOUNDER).//P02734  
 F-OVARC1000408//INTEGUMENTARY MUCIN C.1 (FIM-C.1) (FRAGMENT).//8.1e-05:115:33//XENOPUS LAE-  
 VIS (AFRICAN CLAWED FROG).//Q05049  
 35 F-OVARC1000411//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP-150)  
 (DAP-150) (P150-GLUED).//0.00076:100:29//RATTUS NORVEGICUS (RAT).//P28023  
 F-OVARC1000414//HYPOTHETICAL 7.0 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION.//1.0:46:34//  
 BACILLUS SUBTILIS.//P54431  
 40 F-OVARC1000420//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT).//0.0028:97:  
 37//HOMO SAPIENS (HUMAN).//P25067  
 F-OVARC1000427//HYPOTHETICAL 13.9 KD PROTEIN IN PRFA-SPOIIR INTERGENIC REGION.//0.70:21:47//  
 BACILLUS SUBTILIS.//P39150  
 F-OVARC1000431  
 F-OVARC1000437//TENSIN.//9.2e-42:195:52//GALLUS GALLUS (CHICKEN).//Q04205  
 45 F-OVARC1000440//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//3.4e-31:37:  
 97//HOMO SAPIENS (HUMAN).//P48059  
 F-OVARC1000442  
 F-OVARC1000443//CUTICLE COLLAGEN 2C (FRAGMENT).//0.0056:163:34//HAEMONCHUS CONTORTUS.//  
 P16252  
 50 F-OVARC1000461//FIXU PROTEIN.//0.36:36:44//RHIZOBIUM LEGUMINOSARUM (BIOVAR TRIFOLII).//  
 P42710  
 F-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//2.4e-14:222:26//SACCHAROMYCES CEREVI-  
 SIAE (BAKER'S YEAST).//P11075  
 F-OVARC1000466//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.3e-08:29:93//HOMO SAPIENS (HUMAN).//  
 P39192  
 55 F-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 7 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPE-  
 CIFICITY PROTEIN PHOSPHATASE MKP-X) (FRAGMENT).//2.8e-06:96:36//RATTUS NORVEGICUS (RAT).//  
 Q63340

- F-OVARC1000479//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X (PSI-K).//0.99:48:37//CYANIDIUM CALDARIUM (GALDIERIA SULPHURARIA).//P31567 F-OVARC1000486
- F-OVARC1000493//HYPOTHETICAL PROTEIN MJ1213.//1.0:62:32//METHANOCOCCUS JANNASCHII.//Q58610
- 5 F-OVARC1000520//MEROZOITE SURFACE PROTEIN CMZ-8 (FRAGMENT).//0.0011:66:40//EIMERIA ACERVULINA.//P09125
- F-OVARC1000526//PROTEIN Q300.//1.2e-05:51:43//MUS MUSCULUS (MOUSE).//Q02722
- F-OVARC1000533//NEURONAL PROTEIN 3.1 (P311 PROTEIN).//0.74:43:41//HOMO SAPIENS (HUMAN).//Q16612
- 10 F-OVARC1000543//POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYLGLACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYLGLACTOSAMINYLTRANSFERASE) (GALNAC-T1).//2.3e-23:192:35//HOMO SAPIENS (HUMAN).//Q10472
- F-OVARC1000556
- 15 F-OVARC1000557//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!1.6e-08:80:47//HOMO SAPIENS (HUMAN).//P39188
- F-OVARC1000564//VPX PROTEIN (X ORF PROTEIN) (VIRAL ACCESSORY PROTEIN).//0.45:32:50//HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D194) (HIV-2).//P17760
- F-OVARC1000573
- F-OVARC1000576//BETA-DEFENSIN 1 (BNDB-1).//0.47:29:41//BOS TAURUS (BOVINE).//P46159
- 20 F-OVARC1000578//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.023:96:36//BOS TAURUS (BOVINE).//P02459
- F-OVARC1000588//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3.//0.75:57:29//HOMO SAPIENS (HUMAN).//P09001
- F-OVARC1000605//AUTOLYSIN PRECURSOR (EC 3.4.24.38) (GAMETE LYTIC ENZYME) (GLE).//0.91:134:28//CHLAMYDOMONAS REINHARDTII.//P31178
- 25 F-OVARC1000622//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!2.6e-36:100:80//HOMO SAPIENS (HUMAN).//P39189
- F-OVARC1000640//HYPOTHETICAL 8.5 KD PROTEIN YCF40 (ORF73).//0.96:34:38//ODONTELLA SINENSIS.//P49535
- 30 F-OVARC1000649//ANTHER-SPECIFIC PROTEIN SF18 PRECURSOR (FRAGMENT).//0.0036:64:37//HELIANTHUS ANNUUS (COMMON SUNFLOWER).//P22357
- F-OVARC1000661//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENTS).//0.21:53:47//RATTUS NORVEGICUS (RAT).//P02466
- 35 F-OVARC1000678//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//1.0:17:58//ESCHERICHIA COLI.//P05834
- F-OVARC1000679//DNA-DIRECTED RNA POLYMERASE OMEGA CHAIN (EC 2.7.7.6) (TRANSCRIPTASE OMEGA CHAIN) (RNA POLYMERASE OMEGA SUBUNIT).//0.096:67:29//ESCHERICHIA COLI.//P08374
- F-OVARC1000681//PROTEIN Q300.//0.72:16:43//MUS MUSCULUS (MOUSE).//Q02722
- F-OVARC1000682//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).//7.6e-70:102:99//MUS MUSCULUS (MOUSE).//P39098
- 40 F-OVARC1000689//CADMIUM-METALLOTHIONEIN (CD-MT).//0.032:30:40//HELIX POMATIA (ROMAN SNAIL) (EDIBLE SNAIL).//P33187
- F-OVARC1000700//BRAIN NEURON CYTOPLASMIC PROTEIN 2.//0.17:60:40//RATTUS NORVEGICUS (RAT).//P02684
- 45 F-OVARC1000703//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.57:42:42//HOMO SAPIENS (HUMAN).//P02811
- F-OVARC1000722//N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGALACTOSAMINE (BETA 1-4GT:4)GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT).//1.1e-20:44:70//BOS TAURUS (BOVINE).//P08037
- 50 F-OVARC1000730//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III.//5.2e-29:224:36//CAENORHABDITIS ELEGANS.//Q18262
- F-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN.//6.2e-12:78:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25159
- F-OVARC1000769
- 55 F-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.1e-46:121:79//HOMO SAPIENS (HUMAN), AND CANIS FAMILIARIS (DOG).//P08886
- F-OVARC1000781//HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEBOX PROTEIN 2).//0.81:36:52//HOMO SAPIENS (HUMAN).//P52951

F-OVARC1000787//40S RIBOSOMAL PROTEIN S14 (FRAGMENT).//0.96:37:48//SUS SCROFA (PIG).//Q29303  
 F-OVARC1000800//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.5e-31:47:82//HOMO SAPIENS (HUMAN).//  
 P39189  
 5 F-OVARC1000802//HYPOTHETICAL 8.8 KD PROTEIN B0302.2 IN CHROMOSOME X.//0.16:55:40//  
 CAENORHABDITIS ELEGANS.//Q10926  
 F-OVARC1000834//SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA (EC 2.7.1.-) (P68-PAK) (P21- ACTI-  
 VATED KINASE) (ALPHA-PAK) (PROTEIN KINASE MUK2).//0.87:140:31//RATTUS NORVEGICUS (RAT).//  
 P35465  
 10 F-OVARC1000846//NUCLEOLIN (PROTEIN C23).//7.0e-07:109:30//MESOCRICETUS AURATUS (GOLDEN  
 HAMSTER).//P08199  
 F-OVARC1000850//HYPOTHETICAL 56.2 KD PROTEIN IN ERG8-UBP8 INTERGENIC REGION.//6.9e-09:180:  
 28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04991  
 F-OVARC1000862//UBIQUITIN-CONJUGATING ENZYME E2-17.5 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN  
 LIGASE) (UBIQUITIN CARRIER PROTEIN).//0.0020:74:28//SACCHAROMYCES CEREVISIAE (BAKER'S  
 15 YEAST).//P52490  
 F-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).//9.8e-39:154:55//SACCHAROMYCES CEREVISIAE  
 (BAKER'S YEAST).//P40484  
 F-OVARC1000883//METALLOTHIONEIN-I.//0.87:38:36//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLA-  
 BRATA).//P15113  
 20 F-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.-.-).//2.8e-18:170:34//ESCHERICHIA COLI.//P37440  
 F-OVARC1000886//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//0.00033:60:45//BOS TAURUS (BOVINE).//  
 P02465  
 F-OVARC1000890//PROBABLE E5 PROTEIN.//0.92:7:71//HUMAN PAPILLOMAVIRUS TYPE 70.//P50774  
 F-OVARC1000891//HYPOTHETICAL 8.3 KD PROTEIN (ORF5).//1.0:36:36//PARAMECIUM TETRAURELIA.//  
 25 P15606  
 F-OVARC1000897//HYPOTHETICAL 6.1 KD PROTEIN PRECURSOR (ORF87).//1.0:34:44//ORGYIA PSEU-  
 DOTUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10337  
 F-OVARC1000912//PUTATIVE CUTICLE COLLAGEN C09G5.4.//4.0e-07:98:35//CAENORHABDITIS ELE-  
 GANS.//Q09455  
 30 F-OVARC1000915//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//1.7e-47:115:76//HOMO SAPIENS (HU-  
 MAN).//P56524  
 F-OVARC1000924//CYTOCHROME B (EC 1.10.2.2) (FRAGMENT).//0.99:54:24//BOA CONSTRICTOR (BOA).//  
 P92848  
 35 F-OVARC1000936//HYPOTHETICAL 7.5 KD PROTEIN IN INAA-GLPQ INTERGENIC REGION.//1.0:48:33//ES-  
 CHERICHIA COLI.//P45505  
 F-OVARC1000937//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//1.0:135:31//HOMO SAPIENS (HU-  
 MAN).//P02452  
 F-OVARC1000945//EARLY E1A 11 KD PROTEIN.//0.087:81:24//MOUSE ADENOVIRUS TYPE 1 (MAV-1).//  
 P12533  
 40 F-OVARC1000948  
 F-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//0.99:67:28//METHANOCOCCUS JANNASCHII.//  
 Q58343  
 F-OVARC1000960//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.8e-32:56:75//HOMO SAPIENS (HUMAN).//  
 P39193  
 45 F-OVARC1000964//MAMBIN (GLYCOPROTEIN IIB-IA ANTAGONIST) (PLATELET AGGREGATION INHIBITOR)  
 (DENDROASPIN).//1.0:30:36//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S MAMBA).//  
 P28375  
 F-OVARC1000971  
 F-OVARC1000984//HYPOTHETICAL 52.3 KD PROTEIN IN MRPL10-ERG24 INTERGENIC REGION PRECUR-  
 50 SOR.//0.093:36:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53832  
 F-OVARC1000996//MO25 PROTEIN.//1.9e-39:80:95//MUS MUSCULUS (MOUSE).//Q06138  
 F-OVARC1000999//BRAIN-SPECIFIC HOMEBOX/POU DOMAIN PROTEIN 1 (BRN-1 PROTEIN).//0.00020:50:  
 40//HOMO SAPIENS (HUMAN).//P20264  
 F-OVARC1001000//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.4e-16:43:90//HOMO SAPIENS (HUMAN).//  
 55 P39195  
 F-OVARC1001004//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.95:33:42//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY).//Q01642  
 F-OVARC1001010//HYPOTHETICAL PROTEIN MJ0926.//0.50:71:23//METHANOCOCCUS JANNASCHII.//

Q58336

F-OVARC1001011//CORTISTATIN PRECURSOR.//0.81:45:37//RATTUS NORVEGICUS (RAT).//Q62949  
 F-OVARC1001032//FERREDOXIN LIKE PROTEIN.//1.0:26:46//RHIZOBIUM LEGUMINOSARUM (BIOVAR PHASEOL) //Q05561

5 F-OVARC1001034//METALLOTHIONEIN-IG (MT-1G).//0.14:9:77//HOMO SAPIENS (HUMAN).//P13640  
 F-OVARC1001038//NUCLEOLIN (PROTEIN C23).//3.2e-07:36:80//HOMO SAPIENS (HUMAN).//P19338  
 F-OVARC1001040//ALU SUBFAMILY SQ WARNING ENTRY !!!!!1.5e-18:45:60//HOMO SAPIENS (HUMAN).//P39194

10 F-OVARC1001044//BIS(5'-NUCLEOSYL)-TETRAPHOSPHATASE (SYMMETRICAL) (EC 3.6.1.41) (DIADENOSINE TETRAPHOSPHATASE).//0.88:43:39//ESCHERICHIA COLI.//P05637  
 F-OVARC1001051//SERINE PROTEINASE STUBBLE (EC 3.4.21.-) (STUBBLE-STUBBLOID PROTEIN).//0.34:117:25//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q05319  
 F-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSOR.//1.6e-33:43:97//HOMO SAPIENS (HUMAN).//P43490

15 F-OVARC1001062  
 F-OVARC1001065//METHIONYL-TRNA SYNTHETASE (EC 6.1.1.10) (METHIONINE-TRNA LIGASE) (METRS).//0.79:76:39//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//Q44951  
 F-OVARC1001068//GTP-BINDING PROTEIN ERA HOMOLOG (FRAGMENT).//5.3e-15:100:44//BRADYRHIZOBIUM JAPONICUM.//O69162

20 F-OVARC1001072//ALU SUBFAMILY J WARNING ENTRY !!!!!0.0076:41:56//HOMO SAPIENS (HUMAN).//P39188  
 F-OVARC1001074//60S RIBOSOMAL PROTEIN L38.//1.0:32:40//LYCOPERSICON ESCULENTUM (TOMATO).//P46291  
 F-OVARC1001085//HYPOTHETICAL 126.5 KD PROTEIN C13F4.06 IN CHROMOSOME 1.//0.73:135:25//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10197

25 F-OVARC1001092//HYPOTHETICAL 51.2 KD PROTEIN IN PET54-DIE2 INTERGENIC REGION.//5.6e-05:30:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P50079  
 F-OVARC1001107//SHK1 KINASE-BINDING PROTEIN 1.//1.8e-08:52:51//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P78963

30 F-OVARC1001113//DIAPHANOUS PROTEIN.//1.9e-33:218:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48608  
 F-OVARC1001117//GENE 7 PROTEIN.//0.68:12:50//SPIROPLASMA VIRUS 4 (SPV4).//P11339  
 F-OVARC1001118  
 F-OVARC1001129//30S RIBOSOMAL PROTEIN S17.//0.15:57:22//AQUIFEX AEOLICUS.//O66439

35 F-OVARC1001154//GRANULINS PRECURSOR (ACROGRANIN).//2.3e-95:99:77//MUS MUSCULUS (MOUSE).//P28798  
 F-OVARC1001161//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//0.17:87:34//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P49177  
 F-OVARC1001162

40 F-OVARC1001167//TRBD PROTEIN.//0.92:24:45//ESCHERICHIA COLI.//P41070  
 F-OVARC1001169//FRUCTOSE-1,6-BISPHOSPHATASE (EC 3.1.3.11) (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) (FRAGMENT).//0.82:35:40//MUS MUSCULUS (MOUSE).//P97323  
 F-OVARC1001170//PROLINE-RICH PEPTIDE P-B.//0.17:27:37//HOMO SAPIENS (HUMAN).//P02814  
 F-OVARC1001171//ALU SUBFAMILY J WARNING ENTRY !!!!!0.00023:28:75//HOMO SAPIENS (HUMAN).//P39188

45 F-OVARC1001173  
 F-OVARC1001176//HYPOTHETICAL BHLF1 PROTEIN.//2.7e-05:158:31//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181  
 F-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2.//1.4e-12:208:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48510

50 F-OVARC1001188//HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//3.3e-31:129:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53215  
 F-OVARC1001200//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION.//0.018:148:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47057

55 F-OVARC1001232//HYPOTHETICAL PROTEIN MJ1236.//2.5e-27:141:39//METHANOCOCCUS JANNASCHII.//Q58633  
 F-OVARC1001240  
 F-OVARC1001243

- F-OVARC1001244//RING3 PROTEIN (KIAA9001)//1.7e-13:37:91//HOMO SAPIENS (HUMAN)//P25440  
 F-OVARC1001261//OCTAPEPTIDE-REPEAT PROTEIN T2//1.3e-07:109:35//MUS MUSCULUS (MOUSE)//Q06666
- 5 F-OVARC1001268//HYPOTHETICAL 57.4 KD PROTEIN IN PILT REGION (ORF4)//0.71:43:41//PSEUDOMONAS AERUGINOSA//P24563  
 F-OVARC1001270//HYPOTHETICAL 9.0 KD PROTEIN IN UVSW-UVSY INTERGENIC REGION//1.0:44:29//BACTERIOPHAGE T4//P32281  
 F-OVARC1001271//HYPOTHETICAL 104.7 KD PROTEIN F23F12.8 IN CHROMOSOME III PRECURSOR//0.00015:188:23//CAENORHABDITIS ELEGANS//P46504
- 10 F-OVARC1001282  
 F-OVARC1001296//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31)//0.022:101:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38968  
 F-OVARC1001306//HYPOTHETICAL 52.9 KD SERINE-RICH PROTEIN C11G7.01 IN CHROMOSOME I//0.023:134:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O13695
- 15 F-OVARC1001329//CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)//1.3e-14:150:28//ZEA MAYS (MAIZE)//P49133  
 F-OVARC1001330  
 F-OVARC1001339//RIBONUCLEOPROTEIN RB97D//0.0013:55:38//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q02926
- 20 F-OVARC1001341//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION//4.9e-17:110:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40032  
 F-OVARC1001342  
 F-OVARC1001344//PREPROTEIN TRANSLOCASE SECE SUBUNIT//0.99:39:23//STAPHYLOCOCCUS CARINOSUS//P36253
- 25 F-OVARC1001357//METALLOTHIONEIN//0.99:28:42//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//Q05890  
 F-OVARC1001360//LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)//0.86:109:31//HOMO SAPIENS (HUMAN)//P48634  
 F-OVARC1001369//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT)//6.7e-05:124:36//BOS TAURUS (BOVINE)//P02465
- 30 F-OVARC1001372//HYPOTHETICAL 34.5 KD PROTEIN IN CLCB-CLCD INTERGENIC REGION PRECURSOR//0.75:33:48//PSEUDOMONAS PUTIDA, AND PSEUDOMONAS SP. (STRAIN B13)//Q47100  
 F-OVARC1001376//ALU SUBFAMILY J WARNING ENTRY !!!!!//2.8e-24:96:61//HOMO SAPIENS (HUMAN)//P39188
- 35 F-OVARC1001381//MEMBRANE-ASSOCIATED ATPASE EPSILON CHAIN (EC 3.6.1.34) (SUL-ATPASE EPSILON)//0.96:46:39//SULFOLOBUS ACIDOCALDARIUS//P23039  
 F-OVARC1001391//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT)//0.00024:189:29//HOMO SAPIENS (HUMAN)//P10162  
 F-OVARC1001399//ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.062:18:77//HOMO SAPIENS (HUMAN)//P39195
- 40 F-OVARC1001417//HYPOTHETICAL 157.0 KD PROTEIN C38C10.5 IN CHROMOSOME III//0.010:185:23//CAENORHABDITIS ELEGANS//Q03570  
 F-OVARC1001419//A-TYPE INCLUSION PROTEIN (AT)//0.50:135:28//CAMELOPOX VIRUS (STRAIN CP-1)//Q05482
- 45 F-OVARC1001425//COLLAGEN ALPHA 1(X) CHAIN PRECURSOR//0.43:85:40//HOMO SAPIENS (HUMAN)//Q03692  
 F-OVARC1001436//HYPOTHETICAL 11.4 KD PROTEIN (C4 PROTEIN)//0.031:100:30//TOMATO YELLOW LEAF CURL VIRUS (STRAIN AUSTRALIA) (TYLCV)//P36283  
 F-OVARC1001442//HOMEBOX PROTEIN HTR-A2 (FRAGMENT)//1.0:32:34//HELOBDELLA TRISERIALIS (LEECH)//P17138
- 50 F-OVARC1001453//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF)//0.74:19:47//MUS MUSCULUS (MOUSE)//P28184  
 F-OVARC1001476//GTP-BINDING PROTEIN GTR2//3.0e-12:114:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53290
- 55 F-OVARC1001480//COLLAGEN ALPHA 2(VI) CHAIN PRECURSOR//0.00019:134:32//MUS MUSCULUS (MOUSE)//Q02788  
 F-OVARC1001489//HYPOTHETICAL PROTEIN HI1270//0.98:30:43//HAEMOPHILUS INFLUENZAE//P44149  
 F-OVARC1001496//C-TERMINAL BINDING PROTEIN 2//4.0e-65:132:100//HOMO SAPIENS (HUMAN)//

P56545  
 F-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE  
 PROTEIN 1) //3.2e-70:159:94//HOMO SAPIENS (HUMAN) //P98161  
 5 F-OVARC1001525//FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 14 (FIN14) //1.0:36:33//MUS MUS-  
 CULUS (MOUSE) //Q61077  
 F-OVARC1001542//SMALL PROLINE-RICH PROTEIN 2B (SPR-2B) //0.69:57:33//HOMO SAPIENS (HUMAN) //  
 P35325  
 F-OVARC1001547  
 10 F-OVARC1001555//NGG1-INTERACTING FACTOR 3 //7.6e-16:148:34//SACCHAROMYCES CEREVISIAE  
 (BAKER'S YEAST) //P53081  
 F-OVARC1001577//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35)  
 (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN) //8.8e-38:94:81//GALLUS GALLUS (CHICKEN) //P30352  
 F-OVARC1001600//GENE 7 PROTEIN //0.80:38:39//SPIROPLASMA VIRUS SPV1-R8A2 B. //P15898  
 15 F-OVARC1001610//DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE (EC 2.7.8.2) (SN-1,2- DIACYLG-  
 LYCEROL CHOLINEPHOSPHOTRANSFERASE) (CHOPT) //1.6e-22:122:39//SACCHAROMYCES CEREVI-  
 SIAE (BAKER'S YEAST) //P17898  
 F-OVARC1001611  
 F-OVARC1001615//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X. //0.30:43:34//  
 CAENORHABDITIS ELEGANS //Q11116  
 20 F-OVARC1001668//ALU SUBFAMILY SC WARNING ENTRY !!!!! //1.0e-19:45:82//HOMO SAPIENS (HUMAN) //  
 P39192  
 F-OVARC1001702//SOX-20 PROTEIN //2.4e-28:71:83//HOMO SAPIENS (HUMAN) //Q60248  
 F-OVARC1001703//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-  
 BINDING PROTEIN 1) (INTERFERON-GAMMA INDUCIBLE PROTEIN MAG-1) //0.00018:88:36//MUS MUSCU-  
 25 LUS (MOUSE) //Q01514  
 F-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B) //2.7e-05:98:32//  
 MUS MUSCULUS (MOUSE) //Q62267  
 F-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM  
 BINDING INHIBITOR) (MA-DBI) //4.5e-20:46:67//BOS TAURUS (BOVINE) //P07106  
 30 F-OVARC1001726//ALPHA-AMYLASE INHIBITOR PAIM I (PIG PANCREATIC ALPHA-AMYLASE INHIBITOR OF  
 MICROBES I) //0.59:23:56//STREPTOMYCES OLIVACEOVIRIDIS (STREPTOMYCES CORCHORUSII) //  
 P09921  
 F-OVARC1001731//TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE //2.1e-75:176:87//XENOPUS LAEVIS  
 (AFRICAN CLAWED FROG) //Q01173  
 35 F-OVARC1001745//GENE 11 PROTEIN //0.31:36:52//SPIROPLASMA VIRUS SPV1-R8A2 B. //P15902  
 F-OVARC1001762//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMI-  
 NO, ACETYLTRANSFERASE 1) //2.8e-23:197:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P12945  
 F-OVARC1001766//FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE)  
 (PIPAE) (EC 5.2.1.8) (PROLINE ROTAMASE) (NUCLEOLAR PROLINE ISOMERASE) (FKBP-70) //2.2e-06:99:  
 40 40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P38911  
 F-OVARC1001767//33.2 KD PROTEIN IN DIND-RPH INTERGENIC REGION (ORF X) //0.99:113:27//ES-  
 CHERICHIA COLI //P23839  
 F-OVARC1001768  
 45 F-OVARC1001791//HYPOTHETICAL 63.3 KD PROTEIN IN MPT5-SAE2 INTERGENIC REGION //0.090:75:32//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P46945  
 F-OVARC1001795//HYPOTHETICAL 7.5 KD PROTEIN IN RPBA-GP46 INTERGENIC REGION //0.81:21:38//  
 BACTERIOPHAGE T4 //P07878  
 F-OVARC1001802//PLECTOXIN VIII (PLT-VIII) (PLTVIII) //0.41:19:36//PLECTREURYS TRISTIS (SPIDER) //P36984  
 50 F-OVARC1001805//60S RIBOSOMAL PROTEIN L40 (CEP52) //0.67:24:58//SACCHAROMYCES CEREVISIAE  
 (BAKER'S YEAST) //P14796  
 F-OVARC1001809//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS) //0.23:111:31//RATTUS NORVEGICUS  
 (RAT) //P02454  
 55 F-OVARC1001812//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L) //0.99:28:42//HALICHOERUS GRYPUS  
 (GRAY SEAL) //P38592  
 F-OVARC1001813//HYPOTHETICAL 9.9 KD PROTEIN //0.41:36:30//VACCINIA VIRUS (STRAIN COPENHA-  
 GEN) //P20562

F-OVARC1001820//HYPOTHETICAL PROTEIN ORF-1137 //0.80:58:29//MUS MUSCULUS (MOUSE).//P11260  
 F-OVARC1001828  
 F-OVARC1001846  
 5 F-OVARC1001861//METALLOTHIONEIN (MT).//0.18:11:54//PLEURONECTES PLATESSA (PLAICE).//P07216  
 F-OVARC1001873  
 F-OVARC1001879//HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME II.//2.3e-05:73:31//  
 CAENORHABDITIS ELEGANS.//Q09296  
 F-OVARC1001880//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC  
 PEPTIDE P-F] (FRAGMENT).//2.4e-11:203:32//HOMO SAPIENS (HUMAN).//P02812  
 10 F-OVARC1001883//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.3e-16:86:59//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-OVARC1001900//HYPOTHETICAL 105.9 KD PROTEIN F22B7.5 IN CHROMOSOME III.//0.0053:48:47//  
 CAENORHABDITIS ELEGANS.//P34408  
 F-OVARC1001901  
 15 F-OVARC1001911//40S RIBOSOMAL PROTEIN S28.//1.0:33:36//ARABIDOPSIS THALIANA (MOUSE-EAR  
 CRESS).//P34789  
 F-OVARC1001916//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-  
 CIOGENITAL DYSPLASIA PROTEIN).//0.00082:114:27//HOMO SAPIENS (HUMAN).//P98174  
 F-OVARC1001928//FERREDOXIN III (FDIII).//1.0:64:29//ANABAENA VARIABILIS.//P46050  
 20 F-OVARC1001942//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMI-  
 NO, ACETYLTRANSFERASE 1).//3.0e-07:93:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
 P12945  
 F-OVARC1001943//HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III.//1.7e-23:147:43//  
 CAENORHABDITIS ELEGANS.//P34664  
 25 F-OVARC1001949//ZINC FINGER PROTEIN 177.//2.0e-23:56:66//HOMO SAPIENS (HUMAN).//Q13360  
 F-OVARC1001950//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.011:57:47//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-OVARC1001987//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.39:14:64//MUS MUSCULUS  
 (MOUSE).//P02319  
 30 F-OVARC1001989//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-13:55:72//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-OVARC1002044  
 F-OVARC1002050//UTROPHIN (DYSTROPHIN-RELATED PROTEIN 1) (DRP1) (DRP).//3.6e-12:221:25//HOMO  
 SAPIENS (HUMAN).//P46939  
 35 F-OVARC1002066  
 F-OVARC1002082  
 F-OVARC1002107//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.99:149:24//SACCHARO-  
 MYCES CEREVISIAE (BAKER'S YEAST).//P25386  
 F-OVARC1002112//HISTONE MACRO-H2A.1.//2.8e-64:133:98//RATTUS NORVEGICUS (RAT).//Q02874  
 40 F-OVARC1002127//60S RIBOSOMAL PROTEIN L22.//0.0023:95:35//DROSOPHILA MELANOGASTER (FRUIT  
 FLY).//P50887  
 F-OVARC1002138//PROBABLE 26S PROTEASE SUBUNIT YTA6 (TAT-BINDING HOMOLOG 6).//6.4e-51:198:  
 56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40328  
 F-OVARC1002143  
 45 F-OVARC1002158//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.00010:64:  
 34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53915  
 F-OVARC1002158//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//8.2e-07:119:35//  
 AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMPNV).//P41479  
 F-OVARC1002165//EBNA-6 NUCLEAR PROTEIN (EBNA-3C) (EBNA-4B).//0.00023:90:45//EPSTEIN-BARR VI-  
 50 RUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03204  
 F-OVARC1002182//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHRO-  
 MOSOME II.//1.3e-34:165:35//CAENORHABDITIS ELEGANS.//Q18964  
 F-PLACE1000004//HYPOTHETICAL 180.2 KD PROTEIN C31A2.05C IN CHROMOSOME I.//8.8e-05:148:25//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09725  
 55 F-PLACE1000005//PROTEIN Q300.//0.30:10:100//MUS MUSCULUS (MOUSE).//Q02722  
 F-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15)  
 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-  
 ZYME).//2.3e-39:134:62//CAENORHABDITIS ELEGANS.//P34547



F-PLACE1000014//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//  
 0.00036:63:39//HOMO SAPIENS (HUMAN).//P19474  
 F-PLACE1000031  
 5 F-PLACE1000040//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.4e-12:97:41//HOMO SAPIENS (HUMAN).//  
 P39194  
 F-PLACE1000048//50S RIBOSOMAL PROTEIN L15 (FRAGMENT).//0.98:31:38//BACILLUS SP. (STRAIN C-  
 125).//P38373  
 F-PLACE1000050//COLLAGEN ALPHA 1(III) CHAIN.//0.00062:190:33//BOS TAURUS (BOVINE).//P04258  
 10 F-PLACE1000061//60S RIBOSOMAL PROTEIN L37A.//6.4e-19:51:86//GALLUS GALLUS (CHICKEN).//P32046  
 F-PLACE1000066//SSU72 PROTEIN.//2.3e-39:165:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
 P53538  
 F-PLACE1000078//BAD PROTEIN (BCL-2 BINDING COMPONENT 6).//1.7e-06:21:95//HOMO SAPIENS (HU-  
 MAN).//Q92934  
 15 F-PLACE1000081//HOMEBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3).//0.0053:146:33//MUS MUSCULUS  
 (MOUSE).//P08798  
 F-PLACE1000094  
 F-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//  
 1.8e-62:158:81//HOMO SAPIENS (HUMAN).//P20290  
 20 F-PLACE1000142//ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR (EC 4.2.1.17) (SHORT CHAIN  
 ENOYL-COA HYDRATASE) (SCEH) (ENOYL-COA HYDRATASE 1).//9.8e-12:104:34//HOMO SAPIENS (HU-  
 MAN).//P30084  
 F-PLACE1000184//AC PROTEIN.//0.44:31:29//BACTERIOPHAGE T4.//P18924  
 F-PLACE1000185//HYPOTHETICAL GLYCINE-RICH 49.6 KD PROTEIN CY130.10C PRECURSOR.//0.11:48:  
 33//MYCOBACTERIUM TUBERCULOSIS.//Q10637  
 25 F-PLACE1000213//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-  
 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//3.4e-05:194:26//SACCHAROMYCES CEREVISIAE  
 (BAKER'S YEAST).//P08640  
 F-PLACE1000214  
 F-PLACE1000236//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//0.027:63:34//GALLUS GALLUS  
 30 (CHICKEN).//P02457  
 F-PLACE1000246//TEGUMENT PROTEIN (GENE 11 PROTEIN).//0.78:100:26//EQUINE HERPESVIRUS TYPE  
 4 (STRAIN 1942) (EHV-4) (EQUINE HERPESVIRUS TYPE 1 SUBTYPE 2).//Q00039  
 F-PLACE1000292  
 35 F-PLACE1000308//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT).//0.049:28:42//MEDICAGO SATIVA  
 (ALFALFA).//P11728  
 F-PLACE1000332  
 F-PLACE1000347//HYPOTHETICAL PROTEIN TP0420.//0.15:24:54//TREPONEMA PALLIDUM.//O83435  
 F-PLACE1000374//LYSOZYME C (EC 3.2.1.17) (1,4-BETA-N-ACETYLMURAMIDASE C).//1.0:63:25//ORYC-  
 40 TOLAGUS CUNICULUS (RABBIT).//P16973  
 F-PLACE1000380//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1) (PROTEIN KINASE  
 A INTERFERENCE PROTEIN).//0.018:169:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36027  
 F-PLACE1000383//MYOTUBULARIN.//1.2e-65:215:57//HOMO SAPIENS (HUMAN).//Q13496  
 F-PLACE1000401//ELASTIN PRECURSOR (TROPELASTIN).//0.00023:145:30//MUS MUSCULUS  
 45 (MOUSE).//P54320  
 F-PLACE1000406//54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)).//3.4e-27:90:63//HOMO SAPIENS  
 (HUMAN).//Q15233  
 F-PLACE1000420//7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE).//4.7e-  
 07:134:29//MUS MUSCULUS (MOUSE).//P53368  
 50 F-PLACE1000421//HYPOTHETICAL 8.8 KD PROTEIN C11D3.01C IN CHROMOSOME I.//0.48:72:27//  
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10080  
 F-PLACE1000424  
 F-PLACE1000435  
 F-PLACE1000444//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.0e-31:129:63//HOMO SAPIENS (HU-  
 MAN).//P39195  
 55 F-PLACE1000453//PROTEIN Q300.//0.013:16:68//MUS MUSCULUS (MOUSE).//Q02722  
 F-PLACE1000481//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.14:63:36//HOMO SAPIENS (HU-  
 MAN).//P08547  
 F-PLACE1000492//BASP1 PROTEIN.//0.17:114:28//HOMO SAPIENS (HUMAN).//P80723

F-PLACE1000540  
 F-PLACE1000547//MANNOSYL-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSYL-1-PHOSPHATE GUANYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//1.8e-21:87:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41940  
 5 F-PLACE1000562//HYPOTHETICAL PROTEIN MJ0562.//1.0:35:34//METHANOCOCCUS JANNASCHII.//Q57992  
 F-PLACE1000564//ADRENAL SPECIFIC 30 KD PROTEIN (CLONE PG2).//0.13:66:37//HOMO SAPIENS (HUMAN).//P15803  
 10 F-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.0e-45:192:47//HOMO SAPIENS (HUMAN).//P51522  
 F-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1).//5.3e-63:122:88//HOMO SAPIENS (HUMAN).//P32455  
 F-PLACE1000596//RING CANAL PROTEIN (KELCH PROTEIN).//2.6e-12:120:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04852  
 15 F-PLACE1000599//EARLY E3B 12.7 KD PROTEIN PRECURSOR.//0.83:53:32//HUMAN ADENOVIRUS TYPE 12.//P36707  
 F-PLACE1000610  
 F-PLACE1000611//HYPOTHETICAL 33.6 KD PROTEIN IN MCK1-RPS19B INTERGENIC REGION.//9.4e-07:64:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48558  
 20 F-PLACE1000636//MALE STERILITY PROTEIN 2.//3.7e-09:83:43//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q08891  
 F-PLACE1000653//PUTATIVE PHOSPHOACETYLGLUCOSAMINE MUTASE (EC 5.4.2.3) (ACETYLGLUCOSAMINE PHOSPHOMUTASE) (N-ACETYLGLUCOSAMINE-PHOSPHATE MUTASE).//1.9e-30:203:41//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09687  
 25 F-PLACE1000656//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.0029:75:33//NICOTIANA TABACUM (COMMON TOBACCO).//P13983  
 F-PLACE1000706//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).//1.1e-38:180:42//HOMO SAPIENS (HUMAN).//Q13263  
 F-PLACE1000712//VERY HYPOTHETICAL 8.9 KD PROTEIN CY44.1.05 PRECURSOR.//0.93:49:34//MYCOBACTERIUM TUBERCULOSIS.//P71934  
 30 F-PLACE1000716  
 F-PLACE1000748//HYPOTHETICAL 10.4 KD PROTEIN IN SPAT 3'REGION (ORF-11).//0.90:53:37//SHIGELLA FLEXNERI.//P55794  
 F-PLACE1000749//HYPOTHETICAL PROTEIN MG148.//0.0014:142:27//MYCOPLASMA GENITALIUM.//P47394  
 35 F-PLACE1000755//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//1.1e-15:98:48//CAENORHABDITIS ELEGANS.//P34529  
 F-PLACE1000769//VIGILIN.//0.51:60:33//GALLUS GALLUS (CHICKEN).//P81021  
 40 F-PLACE1000785//PROBABLE COLD SHOCK PROTEIN CY15C10.04.//1.0:22:45//MYCOBACTERIUM TUBERCULOSIS.//Q06360  
 F-PLACE1000786//HYPOTHETICAL 30.2 KD PROTEIN ZK632.12 IN CHROMOSOME III.//2.6e-38:159:51//CAENORHABDITIS ELEGANS.//P34657  
 F-PLACE1000793//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.0097:128:30//HOMO SAPIENS (HUMAN).//P50552  
 45 F-PLACE1000798!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.4e-07:47:61//HOMO SAPIENS (HUMAN).//P39188  
 F-PLACE1000841  
 F-PLACE1000849//ELAV PROTEIN.//3.5e-05:140:35//DROSOPHILA VIRILIS (FRUIT FLY).//P23241  
 50 F-PLACE1000856//HYPOTHETICAL PROTEIN MJ0008.//0.95:100:23//METHANOCOCCUS JANNASCHII.//Q60319  
 F-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR148W.//2.3e-46:172:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32899  
 F-PLACE1000909//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//0.00022:105:35//HOMO SAPIENS (HUMAN).//P16157  
 55 F-PLACE1000931//KILLER TOXIN HM-1.//0.95:24:33//WILLIOPSIS MRKII (YEAST) (HANSENULA MRKII).//P10410  
 F-PLACE1000948//SL CYTOKINE PRECURSOR (FLT3 LIGAND).//0.97:52:40//HOMO SAPIENS (HUMAN).//P49771

- F-PLACE1000972//MYOSIN ID HEAVY CHAIN.//1.9e-06:79:43//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34109
- F-PLACE1000977//HYPOTHETICAL 94.2 KD PROTEIN C38D4.5 IN CHROMOSOME III.//2.5e-23:105:41//CAENORHABDITIS ELEGANS.//P46941
- 5 F-PLACE1000979//ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4) (ZINC FINGER PROTEIN HF. 16).//0.91:83:30//HOMO SAPIENS (HUMAN).//P17097
- F-PLACE1000987//HYPOTHETICAL 111.5 KD PROTEIN C22G7.02 IN CHROMOSOME I.//0.10:128:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09796
- F-PLACE1001000
- 10 F-PLACE1001007//ZYXIN.//2.2e-05:135:30//GALLUS GALLUS (CHICKEN).//Q04584
- F-PLACE1001010//BETA-1 BUNGAROTOXIN B CHAIN, MAJOR COMPONENT PRECURSOR (BUNGAROTOXIN, B1 CHAIN).//1.0:30:40//BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT).//P00987
- F-PLACE1001015
- F-PLACE1001024
- 15 F-PLACE1001036
- F-PLACE1001054//HOLOTRICIN 3 PRECURSOR.//0.0044:56:39//HOLOTRICIA DIOMPHALIA.//Q25055
- F-PLACE1001062//SACCHAROPINE DEHYDROGENASE [NADP+, L-GLUTAMATE FORMING] (EC 1.5.1.10).//0.0013:38:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38999
- F-PLACE1001076
- 20 F-PLACE1001088//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT).//0.95:32:50//MEDICAGO SATIVA (ALFALFA).//P11728
- F-PLACE1001092//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION.//0.0026:81:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47057
- F-PLACE1001104//HYPOTHETICAL 131.5 KD PROTEIN C02F12.7 IN CHROMOSOME X.//0.0063:125:32//CAENORHABDITIS ELEGANS.//Q11102
- 25 F-PLACE1001118//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46).//2.6e-77:209:63//MUS MUSCULUS (MOUSE).//Q03309
- F-PLACE1001136//ALPHA-N-ACETYL GALACTOSAMINIDASE PRECURSOR (EC 3.2.1.49) (ALPHA- GALACTOSIDASE B).//0.99:107:30//HOMO SAPIENS (HUMAN).//P17050
- 30 F-PLACE1001168
- F-PLACE1001171//RETROVIRUS-RELATED POLYPROTEIN (FRAGMENT).//0.00012:37:59//HOMO SAPIENS (HUMAN).//P12895
- F-PLACE1001185//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//3.6e-12:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867
- 35 F-PLACE1001238
- F-PLACE1001241//METALLOTHIONEIN B (MTB) (FRAGMENT).//0.13:30:53//COLINUS VIRGINIANUS (BOBWHITE QUAIL) (COMMON BOBWHITE).//P27087
- F-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.1e-24:125:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
- 40 F-PLACE1001272//HYPOTHETICAL PROTEIN IN KSGA 3'REGION (ORF L5) (FRAGMENT).//1.0:24:45//MYCOPLASMA CAPRICOLUM.//P43040
- F-PLACE1001279//CYTOTOXIN 3 (CYTOTOXIN V-II-3).//0.98:31:41//NAJA MOSSAMBICA (MOZAMBIQUE COBRA).//P01470
- F-PLACE1001280//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].//0.0051:156:32//MUS MUSCULUS (MOUSE).//P28481
- 45 F-PLACE1001294//GAMETOGENESIS EXPRESSED PROTEIN GEG-154.//3.7e-56:109:93//MUS MUSCULUS (MOUSE).//P50636
- F-PLACE1001304//ZINC FINGER PROTEIN 35 (ZFP-35).//3.2e-30:75:57//MUS MUSCULUS (MOUSE).//P15620
- F-PLACE1001311//ALU SUBFAMILY SB WARNING ENTRY.//2.7e-31:66:66//HOMO SAPIENS (HUMAN).//P39189
- 50 F-PLACE1001323
- F-PLACE1001351//REV PROTEIN (ANTI-REPRESSION TRANSACTIVATOR PROTEIN) (ART/TRS).//0.11:66:27//SIMIAN IMMUNODEFICIENCY VIRUS (AGM155 ISOLATE) (SIV-AGM).//P27971
- F-PLACE1001366//SHORT NEUROTOXIN 2 (TOXIN CM-14) (TOXIN V-N-12).//0.070:18:33//NAJA HAJE ANNULIFERA (BANDED EGYPTIAN COBRA).//P01422
- 55 F-PLACE1001377//DISINTEGRIN TRIGRAMIN BETA (PLATELET AGGREGATION ACTIVATION INHIBITOR).//4.9e-06:50:46//TRIMERESURUS GRAMINEUS (INDIAN GREEN TREE VIPER) (GREEN HABU SNAKE).//P17495

- F-PLACE1001383//M PROTEIN, SEROTYPE 49 PRECURSOR.//0.080:136:24//STREPTOCOCCUS PYOGENES.//P16947  
F-PLACE1001384  
F-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//1.9e-22:142:39//HOMO SAPIENS (HUMAN).//Q12929  
5 F-PLACE1001395//HYPOTHETICAL 8.5 KD PROTEIN IN ASIA-MOTA INTERGENIC REGION.//0.98:67:34//BACTERIOPHAGE T4.//P22917  
F-PLACE1001399//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.1e-32:47:74//HOMO SAPIENS (HUMAN).//P39194  
10 F-PLACE1001412//GLYCOPHORIN C (PAS-2') (GLYCOPROTEIN BETA) (GLPC) (GLYCOCONNECTIN) (SIALOGLYCOPROTEIN D) (GLYCOPHORIN D) (GPD).//0.00021:125:36//HOMO SAPIENS (HUMAN).//P04921  
F-PLACE1001414//CHYMOTRYPSIN/ELASTASE ISOINHIBITORS 2 TO 5.//0.99:37:35//ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P07852  
F-PLACE1001440//PROLINE-RICH PEPTIDE P-B.//0.35:16:50//HOMO SAPIENS (HUMAN).//P02814  
15 F-PLACE1001456//RELAXIN.//0.48:38:36//BALAENOPTERA ACUTOROSTRATA (MINKE WHALE) (LESSER RORQUAL).//P11184  
F-PLACE1001468//HYPOTHETICAL PROTEIN MJ0602.//0.10:86:32//METHANOCOCCUS JANNASCHII.//Q58019  
F-PLACE1001484//HYPOTHETICAL 7.5 KD PROTEIN IN DNAC-RPLI INTERGENIC REGION.//1.0:47:34//BACILLUS SUBTILIS.//P37480  
20 F-PLACE1001502//COLLAGEN 1(X) CHAIN PRECURSOR.//0.00029:118:34//BOS TAURUS (BOVINE).//P23206  
F-PLACE1001503//HYPOTHETICAL 77.3 KD PROTEIN T05G5.8 IN CHROMOSOME III.//2.2e-07:107:30//CAENORHABDITIS ELEGANS.//P34561  
F-PLACE1001517//SMALL PROTEIN INHIBITOR OF INSECT ALPHA-AMYLASES 2 (SI ALPHA-2).//0.56:22:45//SORGHUM BICOLOR MILO (SORGHUM).//P21924  
25 F-PLACE1001534//PUTATIVE GENE PROTEIN 54.//0.43:44:40//BACTERIOPHAGE SP01.//O48408  
F-PLACE1001545//HYPOTHETICAL 7.9 KD PROTEIN IN CELF-KATE INTERGENIC REGION.//0.99:70:32//ESCHERICHIA COLI.//P37795  
F-PLACE1001551//CHLOROPLAST 50S RIBOSOMAL PROTEIN L32.//1.0:66:28//MARCHANTIA POLYMRPHA (LIVERWORT).//P12196  
30 F-PLACE1001570//SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN).//0.024:120:27//HOMO SAPIENS (HUMAN).//Q15431  
F-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.1e-30:90:78//MUS MUSCULUS (MOUSE).//Q60809  
35 F-PLACE1001603//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.054:77:33//RATTUS NORVEGICUS (RAT).//P10164  
F-PLACE1001608  
F-PLACE1001610//PROBABLE E4 PROTEIN.//0.90:58:29//HUMAN PAPILLOMAVIRUS TYPE 28.//P51896  
F-PLACE1001611//METALLOTHIONEIN-H (MT-1G).//0.35:30:40//HOMO SAPIENS (HUMAN).//P13640  
40 F-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.6e-28:144:43//HOMO SAPIENS (HUMAN).//P51523  
F-PLACE1001634//PHOTOSYSTEM II REACTION CENTRE N PROTEIN.//1.0:36:41//CYANIDIUM CALDARIUM (GALDIERIA SULPHURARIA).//O19926  
F-PLACE1001640//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.24:47:38//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18804  
45 F-PLACE1001672//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.0:27:66//HOMO SAPIENS (HUMAN).//P39188  
F-PLACE1001691//HYPOTHETICAL 15.5 KD PROTEIN IN PIK1-POL2 INTERGENIC REGION.//0.40:81:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53842  
50 F-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//8.3e-41:103:55//RATTUS NORVEGICUS (RAT).//P08635  
F-PLACE1001705  
F-PLACE1001716//HYPOTHETICAL 138.5 KD PROTEIN C17H9.01 IN CHROMOSOME L.//6.1e-07:157:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13798  
55 F-PLACE1001720  
F-PLACE1001729//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//6.5e-05:196:32//MUS MUSCULUS (MOUSE).//P05143  
F-PLACE1001739//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//

0.00050:213:23//RATTUS NORVEGICUS (RAT)//P12839  
 F-PLACE1001740//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.4e-17:90:56//HOMO SAPIENS (HUMAN)//  
 P39188  
 5 F-PLACE1001745//HYPOTHETICAL PROTEIN KIAA0125.//0.96:38:36//HOMO SAPIENS (HUMAN)//Q14138  
 F-PLACE1001746//CONGLUTIN DELTA-2 SMALL CHAIN.//0.98:23:43//LUPINUS ANGUSTIFOLIUS (NARROW-  
 LEAVED BLUE LUPINE)//P09930  
 F-PLACE1001748//HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17.//2.9e-28:167:38//SCHIZOSACCHARO-  
 MYCES POMBE (FISSION YEAST)//O42908  
 10 F-PLACE1001756//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/9.2e-43:126:77//HOMO SAPIENS (HU-  
 MAN)//P39189  
 F-PLACE1001761//50S RIBOSOMAL PROTEIN L35.//0.26:42:38//HELI COBACTER PYLORI (CAMPYLO-  
 BACTER PYLORI)//P56057  
 F-PLACE1001771//TRANSIENT-RECEPTOR-POTENTIAL LIKE PROTEIN.//4.8e-35:223:40//DROSOPHILA  
 MELANOGASTER (FRUIT FLY)//P48994  
 15 F-PLACE1001781//HYPOTHETICAL 71.1 KD PROTEIN IN DSK2-CAT8 INTERGENIC REGION.//9.5e-41:194:  
 46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q03262  
 F-PLACE1001799  
 F-PLACE1001810  
 20 F-PLACE1001817//SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUC-  
 CINYLYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//2.8e-40:115:61//NEOCALLIMASTIX FRONTALIS (RU-  
 MEN FUNGUS)//P53587  
 F-PLACE1001821  
 F-PLACE1001844//IG KAPPA CHAIN V-I REGION (HAU).//0.59:89:35//HOMO SAPIENS (HUMAN)//P01600  
 F-PLACE1001845  
 25 F-PLACE1001869//MPA43 PROTEIN.//3.5e-14:153:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//  
 P53583  
 F-PLACE1001897//LIGATOXIN A.//1.0:43:27//PHORADENDRON LIGA (ARGENTINE MISTLETOE)//P01540  
 F-PLACE1001912//LONG NEUROTOXIN 2 (TOXIN C).//0.57:44:45//ASTROTIA STOKESI (STOKES'S SEA  
 SNAKE) (DSTEIRA STOKESI).//P01381  
 30 F-PLACE1001920//LATE GENES ACTIVATOR (EARLY PROTEIN GP4) (GPF).//0.89:75:29//BACTERIOPHAGE  
 NF.//P09877  
 F-PLACE1001928  
 F-PLACE1001983//IMMEDIATE-EARLY PROTEIN IE180.//0.0049:51:45//PSEUDORABIES VIRUS (STRAIN KA-  
 PLAN) (PRV).//P33479  
 35 F-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//8.9e-08:125:36//MORAXELLA CATARRHALIS.//Q49091  
 F-PLACE1002004  
 F-PLACE1002046//LIGATIN (FRAGMENT).//1.6e-84:191:84//MUS MUSCULUS (MOUSE).//Q61211  
 F-PLACE1002052  
 F-PLACE1002066  
 40 F-PLACE1002072//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.//0.16:77:31//ARABIDOP-  
 SIS THALIANA (MOUSE-EAR CRESS).//P40602  
 F-PLACE1002073//HYPOTHETICAL 118.2 KD PROTEIN F43C1.1 IN CHROMOSOME III.//4.0e-11:174:28//  
 CAENORHABDITIS ELEGANS.//Q09564  
 F-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).//2.8e-57:112:99//HOMO SA-  
 PIENS (HUMAN).//O76094  
 45 F-PLACE1002115//P8 MTCP-1 PROTEIN (MATURE T-CELL PROLIFERATION-1 TYPE A) (MTCP-1 TYPE A)  
 (PBMTCP1).//1.0:49:30//MUS MUSCULUS (MOUSE).//Q61908  
 F-PLACE1002119//T-LYMPHOCYTE ACTIVATED PROTEIN (CYCLOHEXIMIDE-INDUCED) (CHX1) (IMMEDI-  
 ATE EARLY RESPONSE 2 PROTEIN).//2.7e-11:118:36//MUS MUSCULUS (MOUSE).//P17950  
 50 F-PLACE1002140//HYPOTHETICAL 12.3 KD PROTEIN IN MOBL 3'REGION (ORF 4).//0.0086:39:46//THIOBA-  
 CILLUS FERROOXIDANS.//P20068  
 F-PLACE1002150  
 F-PLACE1002157//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.4e-34:56:82//HOMO SAPIENS (HUMAN)//  
 P39189  
 55 F-PLACE1002163//NEUROTOXIN 1.//1.0:17:52//CENTRUROIDES SCULPTURATUS (BARK SCORPION).//  
 P01492  
 F-PLACE1002170  
 F-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX COMPONENT

SWI3) (TRANSCRIPTION FACTOR  
 TYE2).//0.00023:179:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32591  
 F-PLACE1002205//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION.//0.77:21:47//  
 5 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40490  
 F-PLACE1002213//HISTONE H4 (FRAGMENT).//0.62:31:32//BLEPHARISMA JAPONICUM.//P80738  
 F-PLACE1002227//HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION.//0.41:49:36//RHIZOBIUM LEGUMI-  
 NOSARUM.//P14310  
 F-PLACE1002256//CYTOCHROME B (EC 1.10.2.2).//0.61:95:29//CAENORHABDITIS ELEGANS.//P24890  
 10 F-PLACE1002259//HYPOTHETICAL 9.2 KD PROTEIN IN SP81-QCR7 INTERGENIC REGION.//0.99:22:45//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P56508  
 F-PLACE1002319//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//0.91:18:72//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867  
 F-PLACE1002342//HYPOTHETICAL PROTEIN C16.//1.0:53:32//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//  
 P32219  
 15 F-PLACE1002395//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//6.4e-05:127:37//PLASMODIUM  
 VIVAX.//P08677  
 F-PLACE1002399  
 F-PLACE1002433//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP-150)  
 (DAP-150) (P150-GLUED).//0.00094:182:25//RATTUS NORVEGICUS (RAT).//P28023  
 20 F-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.5e-19:62:77//MUS MUSCULUS  
 (MOUSE).//P41233  
 F-PLACE1002438//HYPOTHETICAL 141.5 KD ZINC FINGER PROTEIN IN TUB1-CPR3 INTERGENIC RE-  
 GION.//0.014:63:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04545  
 F-PLACE1002450//OOCYTE ZINC FINGER PROTEIN XLCOF6 (FRAGMENT).//3.9e-28:159:38//XENOPUS  
 25 LAEVIS (AFRICAN CLAWED FROG).//P18749  
 F-PLACE1002465//LARIAT DEBRANCHING ENZYME (EC 3.1.-.-).//0.0014:148:28//SCHIZOSACCHAROMY-  
 CES POMBE (FISSION YEAST).//O13765  
 F-PLACE1002474//FIBRILLIN 2 PRECURSOR.//2.1e-24:203:33//MUS MUSCULUS (MOUSE).//Q61555  
 30 F-PLACE1002477//ALU SUBFAMILY SP WARNING ENTRY.//0.15:65:41//HOMO SAPIENS (HUMAN).//  
 P39193  
 F-PLACE1002493//SEMNOGELIN II PRECURSOR (SGII).//1.0:72:31//MACACA MULATTA (RHESUS  
 MACAQUE).//Q95196  
 F-PLACE1002499//HYPOTHETICAL 39.3 KD PROTEIN C02B8.6 IN CHROMOSOME X.//2.9e-11:67:35//  
 CAENORHABDITIS ELEGANS.//Q11096  
 35 F-PLACE1002500//COBALT-ZINC-CADMIUM RESISTANCE PROTEIN CZCD (CATION EFFLUX SYSTEM PRO-  
 TEIN CZCD).//8.4e-11:143:32//ALCALIGENES EUTROPHUS.//P13512  
 F-PLACE1002514//HYPOTHETICAL 8.1 KD PROTEIN IN SPEA-METK INTERGENIC REGION (O71).//1.0:15:  
 60//ESCHERICHIA COLI.//P46878  
 F-PLACE1002529  
 40 F-PLACE1002532//HOMEBOX PROTEIN DLX-5.//1.1e-76:183:81//MUS MUSCULUS (MOUSE).//P70396  
 F-PLACE1002537//ALU SUBFAMILY SX WARNING ENTRY.//2.6e-18:51:86//HOMO SAPIENS (HUMAN).//  
 P39195  
 F-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//6.0e-56:140:47//DROSOPHILA MELANOGASTER (FRUIT  
 FLY).//P45890  
 45 F-PLACE1002578  
 F-PLACE1002583  
 F-PLACE1002591//CORONIN-LIKE PROTEIN P57.//5.5e-26:78:69//BOS TAURUS (BOVINE).//Q92176  
 F-PLACE1002598  
 F-PLACE1002604  
 50 F-PLACE1002626//HYPOTHETICAL 180.2 KD PROTEIN IN FAA4-HOR7 INTERGENIC REGION.//6.4e-08:193:  
 23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04781  
 F-PLACE1002655//ADSEVERIN (GELSOLIN-LIKE PROTEIN).//7.1e-100:210:89//MUS MUSCULUS (MOUSE).//  
 Q60604  
 F-PLACE1002665//MOBILIZATION PROTEIN MOBS.//0.35:60:30//THIOBACILLUS FERROOXIDANS.//P20086  
 55 F-PLACE1002685//ACTIN BINDING PROTEIN.//0.052:115:29//SACCHAROMYCES EXIGUUS (YEAST).//  
 P38479  
 F-PLACE1002714//CIS-GOLGI MATRIX PROTEIN GM130.//1.8e-06:214:30//RATTUS NORVEGICUS (RAT).//  
 Q62839

F-PLACE1002722//THROMBIN RECEPTOR PRECURSOR.//2.0e-19:134:38//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P47749

F-PLACE1002768//FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) (FRAGMENT).//0.43:40:35//MUS MUSCULUS (MOUSE).//P35378

5 F-PLACE1002772

F-PLACE1002775//CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5 (CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5).//4.8e-07:96:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14007

10 F-PLACE1002782//COBALT-ZINC-CADMIUM RESISTANCE PROTEIN CZCD (CATION EFFLUX SYSTEM PROTEIN CZCD).//1.1e-07:114:35//ALCALIGENES EUTROPHUS.//P13512

F-PLACE1002794//CUTICLE COLLAGEN 12 PRECURSOR.//0.0068:98:39//CAENORHABDITIS ELEGANS.//P20630

F-PLACE1002811//CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT KINASE 4 INHIBITOR C) (P18-INK4C).//1.1e-09:137:34//MUS MUSCULUS (MOUSE).//Q60772

15 F-PLACE1002815//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.46:35:42//HORDEUM VULGARE (BARLEY).//P17991

F-PLACE1002816//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//1.0e-86:201:74//HOMO SAPIENS (HUMAN).//P56524

F-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.6e-30:54:96//HOMO SAPIENS (HUMAN).//P51522

20 F-PLACE1002839//METALLOTHIONEIN-I (MT-I).//1.0:43:37//MUS MUSCULUS (MOUSE).//P02802

F-PLACE1002851//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (VAI).//0.77:35:37//VICIA ANGUSTIFOLIA (COMMON VETCH).//P01065

F-PLACE1002853//HYPOTHETICAL 7.9 KD PROTEIN IN PE 5'REGION (ORF1).//1.0:18:55//LYMANTRIA DISPAR MULTICAPSID NUCLEAR POLYHEDROSIS VIRUS (LDMNPV).//P36866

25 F-PLACE1002881!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.1e-27:91:70//HOMO SAPIENS (HUMAN).//P39188

F-PLACE1002908//HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III.//2.0e-31:148:46//CAENORHABDITIS ELEGANS.//P34548

30 F-PLACE1002941!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.6e-11:40:85//HOMO SAPIENS (HUMAN).//P39195

F-PLACE1002962//ENDOTHELIN-1 PRECURSOR (ET-1) (FRAGMENT).//0.90:38:36//CANIS FAMILIARIS (DOG).//P13206

F-PLACE1002968//TOXIN IV-5 PRECURSOR (TITYUSTOXIN) (FRAGMENT).//0.97:26:38//TITYUS SERRULATUS (BRAZILIAN SCORPION).//P01496

35 F-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4).//3.3e-20:120:41//METHANOCOCCUS JANNASCHII.//Q58560

F-PLACE1002993//HYPOTHETICAL 17.8 KD PROTEIN IN SMPA-SMPB INTERGENIC REGION (F158).//0.00045:93:23//ESCHERICHIA COLI.//P52121

40 F-PLACE1002996//PUTATIVE REGULATORY PROTEIN TSC-22 (TGFB STIMULATED CLONE 22 HOMOLOG).//0.17:91:29//GALLUS GALLUS (CHICKEN).//Q91012

F-PLACE1003025//SUPPRESSOR PROTEIN SRP40.//0.0079:214:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583

45 F-PLACE1003027//HYPOTHETICAL 128.6 KD PROTEIN ZK1098.10 IN CHROMOSOME III.//1.3e-49:167:63//CAENORHABDITIS ELEGANS.//P34609

F-PLACE1003044//SPORE COAT PROTEIN D.//0.97:24:45//BACILLUS SUBTILIS.//P07791

F-PLACE1003045

F-PLACE1003092

F-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//3.9e-51:188:57//HOMO SAPIENS (HUMAN).//Q13268

50 F-PLACE1003108

F-PLACE1003136

F-PLACE1003145//BUTYROPHILIN PRECURSOR (BT).//0.00024:170:24//BOS TAURUS (BOVINE).//P18892

F-PLACE1003153//HUNCHBACK PROTEIN (FRAGMENT).//1.0:32:37//LOCUSTA MIGRATORIA (MIGRATORY LOCUST).//Q01777

55 F-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//6.3e-05:54:38//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P42743

F-PLACE1003176//HYPOTHETICAL 62.3 KD PROTEIN IN PCS60-ABD1 INTERGENIC REGION.//0.24:74:36//

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38319  
 F-PLACE1003190//SOF1 PROTEIN.//1.0e-52:158:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//  
 P33750  
 F-PLACE1003200  
 5 F-PLACE1003205//SPERM PROTAMINE P1.//0.074:20:45//CAENOLESTES FULIGINOSUS.//P42131  
 F-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//0.013:20:55//HOMO SAPIENS  
 (HUMAN).//Q15391  
 F-PLACE1003249//HYPOTHETICAL PROTEIN KIAA0125.//0.98:48:37//HOMO SAPIENS (HUMAN).//Q14138  
 10 F-PLACE1003256//OMEGA-CONOTOXINS GVIA, GVIB AND GVIC PRECURSOR (SHAKER PEPTIDE).//0.84:  
 53:30//CONUS GEOGRAPHUS (GEOGRAPHY CONE).//P01522  
 F-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN.//4.1e-18:70:47//CAENORHABDITIS ELE-  
 GANS.//P21541  
 F-PLACE1003296//SPECTRIN BETA CHAIN, ERYTHROCYTE.//0.063:160:24//HOMO SAPIENS (HUMAN).//  
 P11277  
 15 F-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//9.4e-69:84:94//HOMO SAPI-  
 ENS (HUMAN).//P51522  
 F-PLACE1003334//NUCLEOBINDIN PRECURSOR (NUCB1) (BONE 63 KD CALCIUM-BINDING PROTEIN).//  
 0.029:125:24//RATTUS NORVEGICUS (RAT).//Q63083  
 F-PLACE1003342//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.97:44:40//DROSOPHILA MELA-  
 20 NOGASTER (FRUIT FLY).//Q01643  
 F-PLACE1003343//GENE 11 PROTEIN.//1.0:37:37//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15902  
 F-PLACE1003353//SH2/SH3 ADAPTOR CRK (ADAPTER MOLECULE CRK) (CRK2).//6.4e-65:69:40//XENOPUS  
 LAEVIS (AFRICAN CLAWED FROG).//P87378  
 F-PLACE1003361/////ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.6e-23:66:75//HOMO SAPIENS (HUMAN).//  
 25 P39192  
 F-PLACE1003366//SMALL PROLINE-RICH PROTEIN 2-1.//0.62:19:57//HOMO SAPIENS (HUMAN).//P35326  
 F-PLACE1003369//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//4.3e-06:102:42//SACCHAROMY-  
 CES CEREVISIAE (BAKER'S YEAST).//P32323  
 F-PLACE1003373//PROTEIN Q300.//0.042:29:37//MUS MUSCULUS (MOUSE).//Q02722  
 30 F-PLACE1003375//OLFACTORY RECEPTOR 11 (M49) (FRAGMENT).//0.99:46:34//MUS MUSCULUS  
 (MOUSE).//Q60890  
 F-PLACE1003383  
 F-PLACE1003394//RAS-RELATED PROTEIN RAB-14.//2.8e-80:166:89//RATTUS NORVEGICUS (RAT).//  
 P35287  
 35 F-PLACE1003401  
 F-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//8.1e-17:138:37//SACCHAROMYCES  
 CEREVISIAE (BAKER'S YEAST).//P40556  
 F-PLACE1003454  
 F-PLACE1003478  
 40 F-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSOR.//3.4e-11:123:32//HOMO SAPIENS (HU-  
 MAN).//Q13201  
 F-PLACE1003516//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.0e-32:68:76//HOMO SAPIENS (HU-  
 MAN).//P08547  
 F-PLACE1003519/////ALU SUBFAMILY J WARNING ENTRY !!!!!/9.2e-17:77:50//HOMO SAPIENS (HUMAN).//  
 45 P39188  
 F-PLACE1003521//HYPOTHETICAL BAMHI-ORF9 PROTEIN.//1.0:38:42//FOWLPOX VIRUS (ISOLATE HP-438  
 [MUNICH]).//P14366  
 F-PLACE1003528//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.96:32:40//XENOPUS LAEVIS (AFRI-  
 CAN CLAWED FROG).//P03931  
 50 F-PLACE1003537//CEF PROTEIN.//0.92:47:29//BACTERIOPHAGE T4.//Q01436  
 F-PLACE1003553  
 F-PLACE1003566//HYPOTHETICAL BAMHI-ORF9 PROTEIN.//1.0:32:34//FOWLPOX VIRUS (ISOLATE HP-438  
 [MUNICH]).//P14366  
 F-PLACE1003575  
 55 F-PLACE1003583//PROBABLE E5 PROTEIN.//0.16:64:31//HUMAN PAPILLOMAVIRUS TYPE 35.//P27226  
 F-PLACE1003584  
 F-PLACE1003592//EXCISIONASE.//0.26:19:52//BACTERIOPHAGE PHI-80.//P05998  
 F-PLACE1003593//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:42:30//OVIS ARIES (SHEEP).//



O78751

F-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.//6.3e-87:238.67//CAENORHABDITIS ELEGANS.//P46975

F-PLACE1003602//HYPOTHETICAL 11.0 KD PROTEIN IN FAA3-MAS3 INTERGENIC REGION.//8.4e-17:98.42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40554

F-PLACE1003605//HAP5 TRANSCRIPTIONAL ACTIVATOR.//2.0e-09:82.35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q02516

F-PLACE1003611//PANCREATIC SECRETORY TRYPSIN INHIBITOR.//0.99:32.43//CANIS FAMILIARIS (DOG).//P04542

F-PLACE1003618//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.7e-65:229.58//HOMO SAPIENS (HUMAN).//P08547

F-PLACE1003625//30S RIBOSOMAL PROTEIN S20 (FRAGMENT).//1.0:56.26//PROTEUS MIRABILIS.//P42275

F-PLACE1003638//PROTEIN Q300.//0.079:41.39//MUS MUSCULUS (MOUSE).//Q02722

F-PLACE1003669//TRICHOHYALIN.//2.9e-07:180.30//OVIS ARIES (SHEEP).//P22793

F-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//3.3e-16:98.40//HOMO SAPIENS (HUMAN).//Q08170

F-PLACE1003709//HYPOTHETICAL 59.5 KD PROTEIN IN CCT3-CCT8 INTERGENIC REGION.//2.8e-07:128.27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47074

F-PLACE1003711//ALPHA/BETA-GLIADIN PRECURSOR (PROLAMIN) (CLASS A-IV).//5.0e-05:88.30//TRITICUM AESTIVUM (WHEAT).//P04724

F-PLACE1003723//TYROSINE-PROTEIN KINASE SRM (EC 2.7.1.112) (PTK70).//6.0e-06:98.36//MUS MUSCULUS (MOUSE).//Q62270

F-PLACE1003738//OOCYTE ZINC FINGER PROTEIN XLCOF6 (FRAGMENT).//2.5e-45:147.46//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18749

F-PLACE1003760//CYTOCHROME B (EC 1.10.2.2).//0.91:49:34//TRYPA NOSOMA BRUCEI BRUCEI.//P00164

F-PLACE1003762//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//0.98:28.32//MALUS DOMESTICA (APPLE) (MALUS SYLVESTRIS).//Q24058

F-PLACE1003768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//8.5e-19:123.37//HOMO SAPIENS (HUMAN).//P08547

F-PLACE1003771

F-PLACE1003783//SRY-RELATED PROTEIN ADW2 (FRAGMENT).//1.0:29:37//ALLIGATOR MISSISSIPPIENSIS (AMERICAN ALLIGATOR).//P40634

F-PLACE1003784//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC REGION.//1.2e-13:199.28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40164

F-PLACE1003795//EC PROTEIN I/II (ZINC-METALLOTHIONEIN CLASS II).//0.67:53.30//TRITICUM AESTIVUM (WHEAT).//P30569

F-PLACE1003833//METHIONYL-TRNA FORMYLTRANSFERASE (EC 2.1.2.9).//0.99:158.28//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P43523

F-PLACE1003850

F-PLACE1003858//HUNCHBACK PROTEIN (FRAGMENT).//0.37:28.42//LITHOBIUS FORFICATUS.//Q02030

F-PLACE1003864//OUTER MEMBRANE LIPOPROTEIN L0LB PRECURSOR.//0.0046:116.31//ACTINOBACILLUS ACTINOMYCETEMCOMITANS (HAEMOPHILUS ACTINOMYCETEMCOMITANS).//O52727

F-PLACE1003870

F-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) (FRAGMENT).//1.6e-92:166.75//HOMO SAPIENS (HUMAN).//P51003

F-PLACE1003886//IMMEDIATE-EARLY PROTEIN IE180.//0.54:96.34//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675

F-PLACE1003888//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).//8.8e-54:260.46//BOS TAURUS (BOVINE).//P10895

F-PLACE1003892//PROBABLE E5 PROTEIN.//1.0:13:61//HUMAN PAPILLOMAVIRUS TYPE 18.//P06792

F-PLACE1003900//BETA-FRUCTOFURANOSIDASE, SOLUBLE ISOENZYME I (EC 3.2.1.26) (SUCROSE-6-PHOSPHATE HYDROLASE) (INVERTASE) (FRAGMENTS).//0.58:49:36//DAUCUS CAROTA (CARROT).//P80065

F-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP-AMMONIA LIGASE) (CTP SYNTHETASE).//3.8e-52:92.85//HOMO SAPIENS (HUMAN).//P17812

F-PLACE1003915//PROBABLE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19) (ARGININE-TRNA LIGASE) (ARGRS).//2.6e-26:202.36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q05506

- F-PLACE1003923//HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE-TRNA LIGASE) (HISRS).//0.94:65:29//STREPTOCOCCUS EQUESTRIS.//P30053
- 5 F-PLACE1003932//HYPOTHETICAL 17.3 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.//0.098:79:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53074
- F-PLACE1003936
- F-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN).//4.7e-68:164:78//RATTUS NORVEGICUS (RAT).//P80385
- 10 F-PLACE1004103//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.9e-14:60:73//HOMO SAPIENS (HUMAN).//P39192
- F-PLACE1004104//EXOCYST COMPLEX COMPONENT SEC5.//0.020:202:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P89102
- F-PLACE1004114//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.1e-15:69:60//HOMO SAPIENS (HUMAN).//P39188
- 15 F-PLACE1004118//REGULATORY PROTEIN E2.//0.73:58:36//CANINE ORAL PAPILLOMAVIRUS (COPV).//Q89420
- F-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA CHAIN 4).//7.7e-62:108:100//MUS MUSCULUS (MOUSE).//P29387
- F-PLACE1004149//PROBABLE NUCLEAR ANTIGEN.//0.0011:73:42//PSEUDORABIES VIRUS (STRAIN KAP-LAN) (PRV).//P33485
- 20 F-PLACE1004155//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//0.00061:39:48//OWENIA FUSIFORMIS.//P21260
- F-PLACE1004161//PLASMINOGEN-BINDING PROTEIN PAM PRECURSOR (FRAGMENT).//0.033:108:27//STREPTOCOCCUS PYOGENES.//P49054
- F-PLACE1004183//HYPOTHETICAL 64.3 KD PROTEIN IN CDC12-ERP5 INTERGENIC REGION.//4.0e-07:146:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38817
- 25 F-PLACE1004197//BUTYROPHILIN PRECURSOR (BT).//5.9e-11:208:27//MUS MUSCULUS (MOUSE).//Q62556
- F-PLACE1004203//PROTEIN A39.//8.5e-18:139:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P21062
- F-PLACE1004242//PHOTOSYSTEM II REACTION CENTRE J PROTEIN.//1.0:28:42//PISUM SATIVUM (GARDEN PEA).//P13555
- 30 F-PLACE1004256//MYOSIN HEAVY CHAIN D (MHC D).//0.73:134:25//CAENORHABDITIS ELEGANS.//P02567
- F-PLACE1004257//HYPOTHETICAL PROTEIN H10490.//0.13:75:29//HAEMOPHILUS INFLUENZAE.//P44006
- F-PLACE1004258//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT).//0.027:128:35//HOMO SAPIENS (HUMAN).//P25067
- 35 F-PLACE1004270//LARGE TEGUMENT PROTEIN.//1.8e-10:100:44//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03186
- F-PLACE1004274//HYPOTHETICAL PROTEIN E-95.//0.44:61:42//HUMAN ADENOVIRUS TYPE 2.//P03286
- F-PLACE1004277//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.0013:55:38//BOS TAURUS (BOVINE).//P25508
- 40 F-PLACE1004284//77 KD PROTEIN (ORF 4).//1.0:63:23//CHRYSANTHEMUM VIRUS B (CVB).//P37990
- F-PLACE1004289//SPERM PROTAMINE P3.//0.00057:22:77//MUS MUSCULUS (MOUSE).//Q62100
- F-PLACE1004302//SERINE/THREONINE PROTEIN KINASE AFSK (EC 2.7.1.-).//0.0065:148:29//STREPTOMYCES COELICOLOR.//P54741
- 45 F-PLACE1004316//AUTOPHAGY PROTEIN APG5.//8.8e-06:117:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12380
- F-PLACE1004336//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.//0.0027:83:36//HOMO SAPIENS (HUMAN).//P53420
- F-PLACE1004358//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//2.9e-05:200:33//GALLUS GALLUS (CHICKEN).//P02457
- 50 F-PLACE1004376//AXONEME-ASSOCIATED PROTEIN MST101(2).//2.4e-05:179:29//DROSOPHILA HYDEI (FRUIT FLY).//Q08696
- F-PLACE1004384//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.6e-28:46:76//HOMO SAPIENS (HUMAN).//P39194
- F-PLACE1004388//HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION.//5.7e-34:202:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39722
- 55 F-PLACE1004405//NEURAMINYLACTOSE-BINDING HEMAGGLUTININ (N-ACETYLNEURAMINYLLACTOSE-BINDING FIBRILLAR HEMAGGLUTININ RECEPTOR-BINDING SUBUNIT) (NLBH) (FLAGELLAR SHEATH ADHESIN) (ADHESIN A) (FRAGMENT).//0.93:74:33//HELICOBACTER ACINONYX.//Q47947

- F-PLACE1004425//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.81:70:42//HOMO SAPIENS (HUMAN).//P39195
- F-PLACE1004428//PRISTANOLYL-COA OXIDASE (EC 1.3.3.-)/1.9e-31:203:39//RATTUS NORVEGICUS (RAT).//Q63448
- 5 F-PLACE1004437//ISOCITRATE DEHYDROGENASE [NAD], MITOCHONDRIAL SUBUNIT BETA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD<sup>+</sup>-SPECIFIC ICDH) (FRAGMENT).//4.2e-93:140:100//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//Q28479
- F-PLACE1004451//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.0001340:62//HOMO SAPIENS (HUMAN).//P39188
- 10 F-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0066:218:23//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25823
- F-PLACE1004467//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/7.8e-10:33:87//HOMO SAPIENS (HUMAN).//P39193
- 15 F-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.0e-56:92:58//HOMO SAPIENS (HUMAN).//P51522
- F-PLACE1004473//HYPOTHETICAL 54.3 KD PROTEIN C23D3.03C IN CHROMOSOME I.//0.019:136:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09844
- F-PLACE1004491//LYSIS PROTEIN.//0.95:53:30//BACTERIOPHAGE FR.//P19903
- F-PLACE1004506//AUTOIMMUNOGENIC CANCER/TESTIS ANTIGEN NY-ESO-1 (LAGE-1).//0.58:66:34//HOMO SAPIENS (HUMAN).//P78358
- 20 F-PLACE1004510//TRANSCRIPTION INITIATION FACTOR TFIID 150 KD SUBUNIT (TAFII-150) (TAFII150).//3.0e-07:63:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24325
- F-PLACE1004516//HYPOTHETICAL PROTEIN 5' TO ASP-RICH AND HIS-RICH PROTEINS (FRAGMENT).//0.95:62:29//PLASMODIUM FALCIPARUM (ISOLATE FCM17 / SENEGAL).//P14587
- 25 F-PLACE1004518//METALLOTHIONEIN 10-III (MT-10-III).//0.91:28:42//MYTILUS EDULIS (BLUE MUSSEL).//P80248
- F-PLACE1004548//DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT.//0.94:75:32//ORYCTOLAGUS CUNICULUS (RABBIT).//P19518
- 30 F-PLACE1004550//CUTICLE COLLAGEN 2.//0.90:155:31//CAENORHABDITIS ELEGANS.//P17656
- F-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//3.2e-70:121:100//BOS TAURUS (BOVINE).//Q10568
- F-PLACE1004629//PROTEIN OS-9 PRECURSOR.//1.7e-10:132:36//HOMO SAPIENS (HUMAN).//Q13438
- F-PLACE1004645//TRANSCRIPTION INITIATION FACTOR IIB HOMOLOG (TFIIB).//0.00036:100:30//PYROCOCCUS FURIOSUS.//Q51731
- 35 F-PLACE1004646//PROBABLE UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9).//0.91:58:29//KLEBSIELLA PNEUMONIAE.//Q48481
- F-PLACE1004658//GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 4 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2D) (NR2D) (NMDAR2D).//0.031:134:32//MUS MUSCULUS (MOUSE).//Q03391
- 40 F-PLACE1004664//HYPOTHETICAL 180.2 KD PROTEIN IN FAA4-HOR7 INTERGENIC REGION.//0.025:125:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04781
- F-PLACE1004672//HYPOTHETICAL 36.7 KD PROTEIN C2F7:14C IN CHROMOSOME I.//7.6e-52:158:56//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09704
- F-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//1.4e-88:144:93//MUS MUSCULUS (MOUSE).//P12815
- 45 F-PLACE1004681//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.0e-34:70:100//MUS MUSCULUS (MOUSE).//Q60809
- F-PLACE1004686//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.4e-08:48:62//HOMO SAPIENS (HUMAN).//P39192
- 50 F-PLACE1004691//METALLOTHIONEIN (MT).//0.064:24:45//ARIANTA ARBUSTORUM.//P55946
- F-PLACE1004693
- F-PLACE1004716//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:27:37//PAN PANISCUS (PYGMY CHIMPANZEE) (BONOBO).//Q35587
- F-PLACE1004722//HYPOTHETICAL 61.5 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION.//0.95:53:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48565
- 55 F-PLACE1004736//NEURONAL AXONAL MEMBRANE PROTEIN NAP-22.//0.014:163:30//RATTUS NORVEGICUS (RAT).//Q05175
- F-PLACE1004740//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.9e-09:37:70//HOMO SAPIENS (HUMAN).//

P39194

F-PLACE1004743//HYPOTHETICAL 12.6 KD PROTEIN IN ALGR3 3'REGION.//0.99:72:33//PSEUDOMONAS AERUGINOSA.//P21484

F-PLACE1004751//CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (EC 2.4.99.-)(BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE)(ST3GALIII)(ALPHA 2,3-ST)(GAL-NAC6S)(STZ)(SIAT4-C)(SAT-3)(ST-4).//2.2e-08:90:38//HOMO SAPIENS (HUMAN).//Q11206

F-PLACE1004773//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//3.2e-25:233:32//HOMO SAPIENS (HUMAN).//P16157

F-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//8.1e-26:210:30//RATTUS NORVEGICUS (RAT).//P30337

F-PLACE1004793//ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36].//0.00062:106:25//MOUSE MAMMARY TUMOR VIRUS (STRAIN BR6).//P10259

F-PLACE1004804

F-PLACE1004813//HYPOTHETICAL PROTEIN UL12.//1.0:22:40//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16777

F-PLACE1004814//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//2.8e-06:136:25//CAENORHABDITIS ELEGANS.//Q09217

F-PLACE1004815

F-PLACE1004824//HYPOTHETICAL 106.7 KD PROTEIN IN MUP1-SPR3 INTERGENIC REGION.//2.3e-09:70:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53236

F-PLACE1004827//HYPOTHETICAL 9.4 KD PROTEIN IN FLAL 3'REGION (ORF3).//0.54:25:56//BACILLUS LICHENIFORMIS.//P22754

F-PLACE1004836//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.0066:12:66//BOS TAURUS (BOVINE).//P20072

F-PLACE1004838

F-PLACE1004840

F-PLACE1004868//MALE STERILITY PROTEIN 2.//4.0e-16:172:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q08891

F-PLACE1004885

F-PLACE1004900//MAST CELL DEGRANULATING PEPTIDE PRECURSOR (MCDP) (MCD) (PEPTIDE 401).//1.0:23:47//APIS MELLIFERA (HONEYBEE).//P01499

F-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//7.3e-15:94:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O42643

F-PLACE1004913//HYPOTHETICAL 7.2 KD PROTEIN IN BC5A-DEGR INTERGENIC REGION.//1.0:42:33//BACILLUS SUBTILIS.//P54165

F-PLACE1004918//HYPOTHETICAL 12.4 KD PROTEIN IN RPS21B-MRS3 INTERGENIC REGION.//0.98:50:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47012

F-PLACE1004930//HYPOTHETICAL PROTEIN MJ0562.//0.82:44:36//METHANOCOCCUS JANNASCHII.//Q57982

F-PLACE1004934

F-PLACE1004937//HYPOTHETICAL 67.1 KD TRP-ASP REPEATS CONTAINING PROTEIN C57A10.05C IN CHROMOSOME I.//9.0e-10:87:33//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87053

F-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//4.0e-14:184:25//CAENORHABDITIS ELEGANS.//Q11073

F-PLACE1004972//BROMELAIN INHIBITOR 2 (BI-II) (BROMELAIN INHIBITOR VI) (BI-VI).//1.0:35:37//ANANAS COMOSUS (PINEAPPLE).//P27478

F-PLACE1004979//ALU SUBFAMILY SC WARNING ENTRY !!!!!/5.3e-30:55:72//HOMO SAPIENS (HUMAN).//P39192

F-PLACE1004982//M PROTEIN, SEROTYPE 12 PRECURSOR (FRAGMENT).//0.00049:124:27//STREPTOCOCCUS PYOGENES.//P19401

F-PLACE1004985//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:26:34//LUMBRICUS TERRESTRIS (COMMON EARTHWORM).//Q34942

F-PLACE1005026//TELOMERE-BINDING PROTEIN HOMOLOG.//0.0011:179:27//EUPLOTES CRASSUS.//Q06183

F-PLACE1005027

F-PLACE1005046//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.082:44:36//BOS TAURUS (BOVINE).//P20072

F-PLACE1005052//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.38:36:44//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645

F-PLACE1005055

- F-PLACE1005068//RING CANAL PROTEIN (KELCH PROTEIN).//2.9e-38:194:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652  
F-PLACE1005077
- 5 F-PLACE1005085//INSECT TOXIN 1 (BOT IT1).//0.85:36:33//BUTHUS OCCITANUS TUNETANUS (COMMON EUROPEAN SCORPION).//P55902  
F-PLACE1005086/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!//8.5e-38:93:76//HOMO SAPIENS (HUMAN).//P39194  
F-PLACE1005101//HYPOTHETICAL PROTEIN ZAP128 (FRAGMENT).//1.6e-11:35:100//HOMO SAPIENS (HUMAN).//P49753
- 10 F-PLACE1005102//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//3.0e-14:110:38//MUS MUSCULUS (MOUSE).//Q60821  
F-PLACE1005108//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).//0.41:35:34//BOS TAURUS (BOVINE).//P37359  
F-PLACE1005111//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L) (CHARGERIN II).//1.0:29:41//RATTUS NORVEGICUS (RAT).//P11608
- 15 F-PLACE1005128//RABPHILIN-3A (FRAGMENT).//5.9e-05:95:36//MUS MUSCULUS (MOUSE).//P47708  
F-PLACE1005146//FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 15 (FIN15).//0.17:48:35//MUS MUSCULUS (MOUSE).//Q61075  
F-PLACE1005162/////ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.0e-31:60:76//HOMO SAPIENS (HUMAN).//P39189
- 20 F-PLACE1005176  
F-PLACE1005181//HYPOTHETICAL 7 KD PROTEIN.//1.0:31:45//MEASLES VIRUS (STRAIN HALLE) (SUBCUTICULAR SCLEROSE PANENCEPHALITIS VIRUS).//P06831  
F-PLACE1005187//GLUCAN SYNTHASE-1 (EC 2.4.1.34) (1,3-BETA-GLUCAN SYNTHASE) (UDP-GLUCOSE-1,3-BETA-D-GLUCAN GLUCOSYLTRANSFERASE).//0.0025:58:34//NEUROSPORA CRASSA.//P38678
- 25 F-PLACE1005206//HYPOTHETICAL 10.7 KD PROTEIN.//0.34:57:42//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20511  
F-PLACE1005232//AMELOGENIN, Y ISOFORM PRECURSOR.//0.70:60:35//HOMO SAPIENS (HUMAN).//Q99218
- 30 F-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//0.0017:114:27//PHYCOMYCES BLAKESLEEANUS.//Q01577  
F-PLACE1005261//HYPOTHETICAL 90.8 KD PROTEIN T05H10.7 IN CHROMOSOME II.//1.2e-38:206:41//CAENORHABDITIS ELEGANS.//Q10003  
F-PLACE1005266
- 35 F-PLACE1005277//PROTEIN GURKEN PRECURSOR.//0.58:95:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//P42287  
F-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.0e-12:21:29//GALLUS GALLUS (CHICKEN).//P53352
- 40 F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//1.8e-78:205:78//BOS TAURUS (BOVINE).//P08760  
F-PLACE1005308//WOUND-INDUCED BASIC PROTEIN.//0.99:40:40//PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).//Q09020  
F-PLACE1005313//HYPOTHETICAL 8.7 KD PROTEIN IN LEUX-FECE INTERGENIC REGION (O67).//0.15:36:41//ESCHERICHIA COLI.//P39355
- 45 F-PLACE1005327//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//1.0:19:52//HOMO SAPIENS (HUMAN).//P30808  
F-PLACE1005331//BREAKPOINT CLUSTER REGION PROTEIN.//0.00021:98:35//HOMO SAPIENS (HUMAN).//P11274  
F-PLACE1005335//IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-3.//0.37:98:33//MUS MUSCULUS (MOUSE).//P81067
- 50 F-PLACE1005373//PSEUDOURIDYLATE SYNTHASE 4 (EC 4.2.1.70) (PSEUDOURIDINE SYNTHASE 4) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLASE).//0.010:96:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48567  
F-PLACE1005374  
F-PLACE1005409
- 55 F-PLACE1005453//LICHENASE PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3,4 GLUCANASE).//1.0:50:32//NICOTIANA PLUMBAGINIFOLIA (LEADWORT-LEAVED TOBACCO).//P07979  
F-PLACE1005467//KERATIN, FEATHER (F-KER).//0.0095:42:35//LARUS NOVAE-HOLLANDIAE (SILVER

- GULL).//P02451  
 F-PLACE1005471//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.23:49:32//PHYTOPHTHORA INFESTANS (POTATO LATE BLIGHT FUNGUS).//Q37598  
 5 F-PLACE1005477//HYPOTHETICAL PROTEIN ORF-1137.//9.6e-13:115:38//MUS MUSCULUS (MOUSE).//P11260  
 F-PLACE1005480//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.97:33:30//HORDEUM VULGARE (BARLEY).//P17991  
 F-PLACE1005481//HUNCHBACK PROTEIN (FRAGMENT).//0.30:52:38//APIS MELLIFERA (HONEYBEE).//P31504  
 10 F-PLACE1005494//TRANSIENT-RECEPTOR-POTENTIAL PROTEIN.//3.9e-05:87:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//P19334  
 F-PLACE1005502  
 F-PLACE1005526//IMMEDIATE-EARLY PROTEIN IE180.//4.6e-05:132:32//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479  
 15 F-PLACE1005528//ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.4e-09:31:74//HOMO SAPIENS (HUMAN).//P39195  
 F-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//9.7e-50:148:58//CAENORHABDITIS ELEGANS.//Q09251  
 F-PLACE1005550//HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III.//3.0e-21:127:37//CAENORHABDITIS ELEGANS.//P34524  
 20 F-PLACE1005554//CYTOCHROME B (EC 1.10.2.2) (FRAGMENT).//0.84:38:31//DIPDOMYS CALIFORNICUS (KANGAROO RAT).//P16359  
 F-PLACE1005557//60S RIBOSOMAL PROTEIN L27.//4.8e-09:60:48//CRYPTOCOCCUS NEOFORMANS (FILOBASIDIELLA NEOFORMANS).//P46288  
 25 F-PLACE1005574//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.89:44:29//BOS TAURUS (BOVINE).//P03929  
 F-PLACE1005584//MALE SPECIFIC SPERM PROTEIN MST87F.//0.00030:33:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175  
 F-PLACE1005595//IMMEDIATE-EARLY PROTEIN IE180.//0.00048:162:30//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675  
 30 F-PLACE1005603//HIGH-MOBILITY-GROUP PROTEIN (NONHISTONE CHROMOSOMAL PROTEIN).//0.00034:83:30//TETRAHYMENA PYRIFORMIS.//P40625  
 F-PLACE1005611//DNAJ PROTEIN.//8.6e-20:108:48//CLOSTRIDIUM ACETOBUTYLICUM.//P30725  
 F-PLACE1005623//EXTRACELLULAR SIGNAL-REGULATED KINASE 5 (EC 2.7.1.-) (ERK5) (ERK4) (BMK1 KINASE).//0.80:116:31//HOMO SAPIENS (HUMAN).//Q13164  
 35 F-PLACE1005630//INTERLEUKIN-14 PRECURSOR (IL-14) (HIGH MOLECULAR WEIGHT B-CELL GROWTH FACTOR) (HMW-BCGF).//0.0024:74:39//HOMO SAPIENS (HUMAN).//P40222  
 F-PLACE1005639//EXTRACELLULAR MATRIX PROTEIN 1 (SECRETORY COMPONENT P85) (FRAGMENT).//0.72:18:61//RATTUS NORVEGICUS (RAT).//Q62894  
 40 F-PLACE1005646//RNA HELICASE-LIKE PROTEIN DB10.//4.8e-29:172:45//NICOTIANA SYLVESTRIS (WOOD TOBACCO).//P46942  
 F-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE).//3.7e-64:133:75//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//Q060561  
 45 F-PLACE1005666//CHLOROPLAST 50S RIBOSOMAL PROTEIN L28.//0.57:36:41//PORPHYRA PURPUREA.//P51224  
 F-PLACE1005698//HYPOTHETICAL PROTEIN IN SIGD 3'REGION (ORFC) (FRAGMENT).//0.50:61:29//BACILLUS SUBTILIS.//P40405  
 F-PLACE1005727//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT).//0.46:27:51//BRASSICA NAPUS (RAPE).//P40603  
 50 F-PLACE1005730//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).//0.95:21:52//ORYCTOLAGUS CUNICULUS (RABBIT).//P02456  
 F-PLACE1005739//INTERFERON-GAMMA INDUCIBLE PROTEIN MG11.//3.4e-46:111:53//MUS MUSCULUS (MOUSE).//Q60710  
 F-PLACE1005755//HYPOTHETICAL 70.2 KD PROTEIN IN GSH1-CHS6 INTERGENIC REGION.//2.6e-12:66:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42951  
 55 F-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//1.5e-26:69:57//RATTUS NORVEGICUS (RAT).//P08635  
 F-PLACE1005799//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.028:96:32//HOMO

SAPIENS (HUMAN).//P26371  
 F-PLACE1005802//PROTEIN PROSPERO.//0.86:64:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//  
 P29617  
 5 F-PLACE1005803//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//1.0:95:25//MUS  
 MUSCULUS (MOUSE).//P17564  
 F-PLACE1005804//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).//  
 2.8e-73:198:73//MUS MUSCULUS (MOUSE).//P39098  
 F-PLACE1005813//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION.//0.022:78:38//  
 10 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47057  
 F-PLACE1005828!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.8e-23:56:76//HOMO SAPIENS (HUMAN).//  
 P39195  
 F-PLACE1005834//LATE CONTROL GENE B PROTEIN (GPB).//0.97:33:39//BACTERIOPHAGE 186.//P08711  
 F-PLACE1005845  
 15 F-PLACE1005850!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//5.5e-28:96:73//HOMO SAPIENS (HUMAN).//  
 P39194  
 F-PLACE1005851  
 F-PLACE1005876//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100  
 KD SUBUNIT).//2.2e-99:155:95//BOS TAURUS (BOVINE).//Q10568  
 F-PLACE1005884  
 20 F-PLACE1005890//BEM46 PROTEIN (FRAGMENT).//1.8e-33:137:49//SCHIZOSACCHAROMYCES POMBE  
 (FISSION YEAST).//P54069  
 F-PLACE1005898//NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3)  
 (COMPLEX I-MLRQ) (CI-MLRQ).//0.77:58:34//HOMO SAPIENS (HUMAN).//Q00483  
 F-PLACE1005921//AIG1 PROTEIN.//1.4e-23:165:38//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//  
 25 P54120  
 F-PLACE1005923//HYPOTHETICAL 22.4 KD PROTEIN (ORF16).//0.90:118:28//PARAMECIUM TETRAURE-  
 LIA.//P15617  
 F-PLACE1005925//HYPOTHETICAL GENE 30 PROTEIN.//0.94:57:29//HERPESVIRUS SAIMIRI (STRAIN 11).//  
 Q01010  
 30 F-PLACE1005932//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//  
 0.42:128:32//NICOTIANA TABACUM (COMMON TOBACCO).//P13983  
 F-PLACE1005934//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6)(RPB1) (FRAG-  
 MENT).//0.40:76:35//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414  
 F-PLACE1005936//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.50:15:66//HUMAN IMMUNO-  
 35 NODEFICIENCY VIRUS TYPE 1 (CLONE 12) (HIV-1).//P04326  
 F-PLACE1005951//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//  
 0.0025:135:32//NICOTIANA TABACUM (COMMON TOBACCO).//P13983  
 F-PLACE1005953//HIGH POTENTIAL IRON-SULFUR PROTEIN (HIPIP).//0.64:57:33//RHODOPHAX FER-  
 40 MENTANS.//P80882  
 F-PLACE1005955//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION.//1.0e-32:110:  
 50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38821  
 F-PLACE1005966//TACHYPLEUS II PRECURSOR.//0.97:31:35//TACHYPLEUS TRIDENTATUS (JAPANESE  
 HORSESHOE CRAB).//P14214  
 F-PLACE1005968//GATA FACTOR SREP.//0.17:52:40//PENICILLIUM CHRYSOGENUM.//Q92259  
 45 F-PLACE1005990//CELL PATTERN FORMATION-ASSOCIATED PROTEIN.//0.36:55:36//EMERICELLA NIDU-  
 LANS (ASPERGILLUS NIDULANS).//P36011  
 F-PLACE1006002!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.5e-36:102:75//HOMO SAPIENS (HU-  
 MAN).//P39192  
 F-PLACE1006003//HYPOTHETICAL 6.8 KD PROTEIN IN COX3-NAD1 INTERGENIC REGION (ORF 61).//1.0:  
 50 22:40//MARCHANTIA POLYMORPHA (LIVERWORT).//P38473  
 F-PLACE1006011//POLY [ADP-RIBOSE] POLYMERASE (EC 2.4.2.30) (PARP) (ADPRT) (NAD+) ADP-RIBO-  
 SYLTRANSFERASE) (POLY[ADP-RIBOSE] SYNTHETASE).//2.8e-21:163:36//ARABIDOPSIS THALIANA  
 (MOUSE-EAR CRESS).//Q11207  
 F-PLACE1006017!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.1e-10:43:67//HOMO SAPIENS (HUMAN).//  
 55 P39192  
 F-PLACE1006037//VITELLOGENIN I PRECURSOR (VTG I) [CONTAINS: LIPOVITELLIN 1 (LV1); PHOSVITIN  
 (PV); LIPOVITELLIN 2 (LV2)].//0.00019:123:37//FUNDULUS HETEROCLOTUS (KILLIFISH) (MUMMICHOG).//  
 Q90508

F-PLACE1006040//CAMP-REGULATED PHOSPHOPROTEIN 19 (ARPP-19) //3.2e-40:110:76//HOMO SAPIENS (HUMAN) //P56211

F-PLACE1006076//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR A-II //0.99:30:40//ARACHIS HYPOGAEA (PEANUT) //P01066

5 F-PLACE1006119//IMPORTIN BETA-3 SUBUNIT (KARYOPHERIN BETA-3 SUBUNIT) (RAN-BINDING PROTEIN 5) //8.8e-94:218:76//HOMO SAPIENS (HUMAN) //Q00410

F-PLACE1006129//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR //0.00092:228:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P32323

10 F-PLACE1006139//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION //5.9e-55:128:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P43616

F-PLACE1006143//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! //1.4e-25:107:63//HOMO SAPIENS (HUMAN) //P39194

F-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAME2) (CD62E) //1.3e-21:168:32//SUS SCROFA (PIG) //P98110

15 F-PLACE1006159//COLD SHOCK INDUCED PROTEIN TIR1 PRECURSOR (SERINE-RICH PROTEIN 1) //0.46:98:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P10863

F-PLACE1006164//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3) //0.70:28:42//ARTEMIA SALINA (BRINE SHRIMP) //P19049

20 F-PLACE1006167//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) //8.9e-05:167:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P08640

F-PLACE1006170//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) //1.1e-67:157:88//MUS MUSCULUS (MOUSE) //P17427

25 F-PLACE1006187//G1/S-SPECIFIC CYCLIN E //5.6e-75:224:62//HOMO SAPIENS (HUMAN) //P24864

F-PLACE1006195//T-RELATED PROTEIN (TRP) (BRACHYENTERON PROTEIN) //0.99:177:29//DROSOPHILA MELANOGASTER (FRUIT FLY) //P55965

F-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06 //2.0e-33:183:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //Q09747

30 F-PLACE1006205

F-PLACE1006223//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS) //0.00015:22:50//MUS MUSCULUS (MOUSE) //P15265

F-PLACE1006225//VIRION INFECTIVITY FACTOR (SOR PROTEIN) //1.0:63:34//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1) //P18805

35 F-PLACE1006236

F-PLACE1006239//60S ACIDIC RIBOSOMAL PROTEIN P2 (FRAGMENT) //0.48:23:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS) //P51407

40 F-PLACE1006246//CMP-SIALIC ACID TRANSPORTER (CMP-SIA-TR) //0.012:84:30//MUS MUSCULUS (MOUSE) //Q61420

F-PLACE1006248//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140) //0.017:203:22//RATTUS NORVEGICUS (RAT) //P41777

F-PLACE1006262//L-FUCULOSE PHOSPHATE ALDOLASE (EC 4.1.2.17) //0.84:25:52//HAEMOPHILUS INFLUENZAE //P44777

45 F-PLACE1006288

F-PLACE1006318//CYSTEINE-RICH ANTIFUNGAL PROTEIN 1 (AFP1) (M1) //1.0:29:48//SINAPIS ALBA (WHITE MUSTARD) (BRASSICA HIRTA) //P30231

F-PLACE1006325//CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR P57) (P57KIP2) //0.99:97:32//HOMO SAPIENS (HUMAN) //P49918

50 F-PLACE1006335//PROLINE-RICH PEPTIDE P-B //0.56:19:52//HOMO SAPIENS (HUMAN) //P02814

F-PLACE1006357

F-PLACE1006360

F-PLACE1006368//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110) //0.0057:122:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P32380

55 F-PLACE1006371//ARS BINDING PROTEIN 1 //0.00030:142:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //P49777

F-PLACE1006382//NEUROTOXIN V //0.85:28:39//ANDROCTONUS MAURETANICUS MAURETANICUS (SCORPION) //P01482



- F-PLACE1006385//HYPOTHETICAL 45.1 KD PROTEIN IN RPSS-ZMS1 INTERGENIC REGION.//3.1e-35:165:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160  
F-PLACE1006412//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.3e-08:40:47//HOMO SAPIENS (HUMAN).//P08547
- 5 F-PLACE1006414//FORKHEAD-RELATED TRANSCRIPTION FACTOR 4 (FREAC-4).//3.8e-05:123:39//HOMO SAPIENS (HUMAN).//Q16676  
F-PLACE1006438//ZINC FINGER PROTEIN 165.//2.8e-21:76:64//HOMO SAPIENS (HUMAN).//P49910  
F-PLACE1006445//SUPPRESSOR OF HAIRY WING PROTEIN.//0.058:99:29//DROSOPHILA VIRILIS (FRUIT FLY).//Q08876
- 10 F-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.8e-64:177:50//ESCHERICHIA COLI.//P27550  
F-PLACE1006470  
F-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//2.0e-47:120:85//GALLUS GALLUS (CHICKEN).//Q90595
- 15 F-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.8e-85:173:95//CANIS FAMILIARIS (DOG).//Q00004  
F-PLACE1006492//VERY HYPOTHETICAL 11.2 KD PROTEIN C56F8.13 IN CHROMOSOME I.//0.75:32:56//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10261  
F-PLACE1006506  
F-PLACE1006521
- 20 F-PLACE1006531//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.//1.3e-53:167:61//CAENORHABDITIS ELEGANS.//P34681  
F-PLACE1006534  
F-PLACE1006540
- 25 F-PLACE1006552//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//1.3e-07:242:23//HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS).//P39922  
F-PLACE1006598//ALU SUBFAMILY SB1 WARNING ENTRY !!!!!0.17:43:51//HOMO SAPIENS (HUMAN).//P39190  
F-PLACE1006615//ACROSIN PRECURSOR (EC 3.4.21.10).//3.6e-05:66:43//ORYCTOLAGUS CUNICULUS (RABBIT).//P48038
- 30 F-PLACE1006617//HYPOTHETICAL 14.6 KD PROTEIN (READING FRAME C) (REPUCATION).//1.0:74:29//STAPHYLOCOCCUS AUREUS.//P03861  
F-PLACE1006626//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//2.9e:10:73:46//CAENORHABDITIS ELEGANS.//P34529
- 35 F-PLACE1006629//HYPOTHETICAL PROTEIN BB0410.//1.0:23:43//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//O51371  
F-PLACE1006640  
F-PLACE1006673  
F-PLACE1006678//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).//1.0:36:41//ORYCTOLAGUS CUNICULUS (RABBIT).//P02456
- 40 F-PLACE1006704//BROAD-COMPLEX CORE-TNT1-Q1-Z1 PROTEIN (BRCORE-TNT1-Q1-Z1) [CONTAINS: BROAD-COMPLEX CORE-Q1-Z1 PROTEIN].//0.0062:157:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01295  
F-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//1.3e-07:127:36//CORYNEBACTERIUM AMMONIAGENES (BREVI BACTERIUM AMMONIAGENES).//Q59263
- 45 F-PLACE1006754//CARCINOEMBRYONIC ANTIGEN CGM1 PRECURSOR (CD66D ANTIGEN).//1.9e-19:78:53//HOMO SAPIENS (HUMAN).//P40198  
F-PLACE1006760//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.21:107:30//RATTUS NORVEGICUS (RAT).//P13941
- 50 F-PLACE1006779//CYTOTOXIN 5 (CTXV).//1.0:20:30//NAJA MOSSAMBICA (MOZAMBIQUE COBRA).//P25517  
F-PLACE1006782//ZINC FINGER PROTEIN 1.//0.00052:178:28//CANDIDA ALBICANS (YEAST).//P28875  
F-PLACE1006792  
F-PLACE1006795//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN SHAW (SHAW2).//1.0:80:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P17972
- 55 F-PLACE1006800//HYPOTHETICAL 9.4 KD PROTEIN.//0.99:62:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20569  
F-PLACE1006805

- F-PLACE1006815//HYPOTHETICAL PROTEIN UL61.//0.038:146:32//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818
- F-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.3e-98:239:76//HOMO SAPIENS (HUMAN).//P08547
- 5 F-PLACE1006878//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//0.061:34:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P50102
- F-PLACE1006860
- F-PLACE1006867
- 10 F-PLACE1006878//HYPOTHETICAL 8.2 KD PROTEIN IN MOBL 3'REGION (ORF 3).//0.85:27:37//THIOBACILLUS FERROOXIDANS.//P20087
- F-PLACE1006883//VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).//0.78:51:37//MUS MUSCULUS (MOUSE).//P48281
- F-PLACE1006901//HYPOTHETICAL 8.1 KD PROTEIN.//0.99:55:23//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20567
- 15 F-PLACE1006904//MATING-TYPE LOCUS ALLELE B1 PROTEIN.//0.95:86:26//USTILAGO MAYDIS (SMUT FUNGUS).//P22015
- F-PLACE1006917//HYPOTHETICAL 40.9 KD PROTEIN C08B11.5 IN CHROMOSOME II.//6.9e-15:101:45//CAENORHABDITIS ELEGANS.//Q09442
- 20 F-PLACE1006932//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//0.089:28:39//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251
- F-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III.//0.93:35:48//CAENORHABDITIS ELEGANS.//Q10000
- F-PLACE1006956//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.00079:122:36//HOMO SAPIENS (HUMAN).//Q00268
- 25 F-PLACE1006958//OSMOTIC STRESS PROTEIN 94 (HEAT SHOCK 70-RELATED PROTEIN APG-1).//8.8e-70:140:98//MUS MUSCULUS (MOUSE).//P48722
- F-PLACE1006961
- F-PLACE1006962//APOLIPOPROTEIN C-I PRECURSOR (APO-C1).//1.0:25:40//PAPIO HAMADRYAS (HAMADRYAS BABOON).//P34929
- 30 F-PLACE1006966//HYPOTHETICAL 49.1 KD PROTEIN IN SSB2-SPX18 INTERGENIC REGION.//1.6e-47:221:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40160
- F-PLACE1006989//HYPOTHETICAL 13.1 KD HIT-LIKE PROTEIN IN P37 5'REGION.//0.15:46:32//MYCOPLASMA HYORHINIS.//P32083
- 35 F-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12) (DER12).//3.4e-09:120:29//HOMO SAPIENS (HUMAN).//Q14542
- F-PLACE1007021//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00046:42:59//HOMO SAPIENS (HUMAN).//P39188
- 40 F-PLACE1007045//HYPOTHETICAL PROTEIN ORF-1137.//8.1e-14:115:35//MUS MUSCULUS (MOUSE).//P11260
- F-PLACE1007053//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.038:48:39//HOMO SAPIENS (HUMAN).//P22531
- F-PLACE1007068//PROTEIN-LYSINE 6-OXIDASE PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE).//0.0040:113:39//GALLUS GALLUS (CHICKEN).//Q05063
- 45 F-PLACE1007097//HYPOTHETICAL 6.8 KD PROTEIN IN HE65-PK2 INTERGENIC REGION.//0.97:47:29//AUTOGRAPH A CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41663
- F-PLACE1007105//HYPOTHETICAL 83.6 KD PROTEIN C15A10.10 IN CHROMOSOME L/2.9e-33:219:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13730
- F-PLACE1007111
- 50 F-PLACE1007112//HYPOTHETICAL 9.2 KD PROTEIN.//0.47:75:28//ESCHERICHIA COLI.//P03853
- F-PLACE1007132//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.8e-11:56:57//HOMO SAPIENS (HUMAN).//P39188
- F-PLACE1007140//GAR2 PROTEIN.//0.72:185:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891
- 55 F-PLACE1007178//HYPOTHETICAL 8.5 KD PROTEIN CY274.40C.//0.97:79:30//MYCOBACTERIUM TUBERCULOSIS.//Q10826
- F-PLACE1007228//HYPOTHETICAL 42.6 KD PROTEIN IN GSHB-ANSB INTERGENIC REGION (O378).//1.9e-15:123:32//ESCHERICHIA COLI.//P52062

F-PLACE1007238//MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL)//5.5e-10:98.44//ACANTHAMOEBA CASTELLANII (AMOEBA)//P19706

F-PLACE1007239//TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A)//3.9e-19:96.57//HOMO SAPIENS (HUMAN)//P23193

5 F-PLACE1007242//GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM B (RALGEF)//1.0:132:30//RATTUS NORVEGICUS (RAT)//Q03386

F-PLACE1007243//HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION//0.04:114:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P39981

10 F-PLACE1007257//DIAPHANOUS PROTEIN//1.3e-42:205.46//DROSOPHILA MELANOGASTER (FRUIT FLY)//P48608

F-PLACE1007274//CADMIUM-METALLOTHIONEIN (CD-MT)//0.054:60:30//HELI POMATIA (ROMAN SNAIL) (EDIBLE SNAIL)//P33187

F-PLACE1007276//BETA-DEFENSIN 1 PRECURSOR (RHB0-1) (DEFENSIN, BETA 1)//1.0:42:28//SUS SCROFA (PIG)//O62697

15 F-PLACE1007282//OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8]//0.070:126:27//HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN ST. THOMAS 3)//P11200

F-PLACE1007286

20 F-PLACE1007301//HYPOTHETICAL PROTEIN KIAA0168//0.042:61:39//HOMO SAPIENS (HUMAN)//P50749

F-PLACE1007317

F-PLACE1007342//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT 1-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1)//1.7e-06:77:36//DROSOPHILA MELANOGASTER (FRUIT FLY)//P13002

F-PLACE1007346//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (KRAB-A INTERACTING PROTEIN) (KRIP-1)//0.0026:147:27//MUS MUSCULUS (MOUSE)//Q62318

25 F-PLACE1007367//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.3e-37:110:76//HOMO SAPIENS (HUMAN)//P39189

F-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13//4.7e-07:71:39//CAENORHABDITIS ELEGANS//P27715

30 F-PLACE1007386//HYPOTHETICAL 7.6 KD PROTEIN IN FLO1-PHO11 INTERGENIC REGION//0.74:48:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P39561

F-PLACE1007402//TRANSCRIPTIONAL REGULATORY PROTEIN ENTR (ENTERICIDIN R)//0.99:63:36//CITROBACTER FREUNDII//O69280

35 F-PLACE1007409//WHITE PROTEIN//7.9e-38:179.41//DROSOPHILA MELANOGASTER (FRUIT FLY)//P10090

F-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP)//0.031:159:23//HOMO SAPIENS (HUMAN)//P27487

40 F-PLACE1007450//ZINC FINGER PROTEIN 39 (ZINC FINGER PROTEIN K0X27) (FRAGMENT)//0.023:36:50//HOMO SAPIENS (HUMAN)//P17038

F-PLACE1007452//HYPOTHETICAL 22.1 KD PROTEIN IN CCP1-MET1 INTERGENIC REGION//2.2e-18:85:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36149

F-PLACE1007454//PHOTOSYSTEM II REACTION CENTRE N PROTEIN//0.66:13:53//CHLAMYDOMONAS REINHARDTII//Q06480

45 F-PLACE1007460//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.93:45:33//SUS SCROFA (PIG)//Q35914

F-PLACE1007478//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE]//5.3e-08:50:56//MUS MUSCULUS (MOUSE)//P11369

F-PLACE1007484//HYPOTHETICAL 6.8 KD PROTEIN IN REPLICATION ORIGIN REGION//0.87:43:37//ESCHERICHIA COLI//P03849

50 F-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-CIOGENITAL DYSPLASIA PROTEIN)//1.2e-25:202:31//HOMO SAPIENS (HUMAN)//P98174

F-PLACE1007507//HYPOTHETICAL 16.0 KD PROTEIN IN TAF60-G4P1 INTERGENIC REGION//0.12:128:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53139

55 F-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19)//2.1e-45:209:48//BOS TAURUS (BOVINE)//P08728

F-PLACE1007524//HYPOTHETICAL 9.2 KD PROTEIN//0.74:80:30//VACCINIA VIRUS (STRAIN COPENHAGEN)//P20550

F-PLACE1007525

F-PLACE1007537//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).//0.045:92:30//MUS MUSCULUS (MOUSE). AND RATTUS NORVEGICUS (RAT).//P80144

F-PLACE1007544//IMMEDIATE-EARLY PROTEIN IE180.//1.5e-07:59:50//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479

5 F-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//2.5e-16:188:34//CAENORHABDITIS ELEGANS.//P34537

F-PLACE1007557

F-PLACE1007583//PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR (FRAGMENT).//0.98:72:33//DAUCUS CAROTA (CARROT).//P06600

10 F-PLACE1007598//ZINC FINGER PROTEIN 92 (ZINC FINGER PROTEIN HTF12) (FRAGMENT).//1.7e-11:88:43//HOMO SAPIENS (HUMAN).//Q03936

F-PLACE1007618//ANION EXCHANGE PROTEIN 2 (NON-ERYTHROID BAND 3-LIKE PROTEIN) (B3RP).//0.19:109:27//MUS MUSCULUS (MOUSE).//P13808

15 F-PLACE1007621//PHOSPHATE REGULON SENSOR PROTEIN PHOR (EC 2.7.3.-) (FRAGMENT).//0.98:34:41//PSEUDOMONAS AERUGINOSA.//P23621

F-PLACE1007632//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//0.70:110:34//BOS TAURUS (BOVINE).//P02465

F-PLACE1007645//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:20:45//STRUTHIO CAMELUS (OSTRICH).//O21401

20 F-PLACE1007649//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.1e-06:197:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

F-PLACE1007677//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.0:47:46//HOMO SAPIENS (HUMAN).//P39192

25 F-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//2.7e-06:116:28//AEDES ALBOPICTUS (FOREST DAY MOSQUITO).//Q26457

F-PLACE1007690//SPERM PROTAMINE P1.//0.12:26:50//TACHYGLOSSUS ACULEATUS ACULEATUS (AUSTRALIAN ECHIDNA).//P35311

30 F-PLACE1007697//SPERM PROTAMINE P1.//0.19:34:52//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM). AND MONDELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM).//P35305

F-PLACE1007705//BIOH PROTEIN.//0.015:97:29//ESCHERICHIA COLI.//P13001

F-PLACE1007706//HYPOTHETICAL 112.2 KD PROTEIN IN TIF35-NPL3 INTERGENIC REGION (ORF 1).//5.3e-55:190:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32898

35 F-PLACE1007725

F-PLACE1007729//PROTEASE (EC 3.4.23.-).//1.8e-21:136:42//MOUSE MAMMARY TUMOR VIRUS (STRAIN BR6).//P10271

F-PLACE1007730//SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).//0.0031:77:40//HOMO SAPIENS (HUMAN).//P81489

40 F-PLACE1007737//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.78:39:56//HOMO SAPIENS (HUMAN).//P39195

F-PLACE1007743

F-PLACE1007746//RRP5 PROTEIN HOMOLOG (KIAA0185) (FRAGMENT).//0.0066:168:25//HOMO SAPIENS (HUMAN).//Q14690

45 F-PLACE1007791//KRUEPPEL PROTEIN (FRAGMENT).//0.62:17:41//LITHOBIUS FORFICATUS.//Q01872

F-PLACE1007807//HYPOTHETICAL 6.4 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION.//1.0:40:30//BACILLUS SUBTILIS.//P54446

F-PLACE1007810//ANTHOPLEURIN A (TOXIN AP-A).//0.79:28:46//ANTHOPLEURA XANTHOGRAMMICA (GIANT GREEN SEA ANEMONE).//P01530

50 F-PLACE1007829//SPORE COAT PROTEIN G.//1.0:65:38//BACILLUS SUBTILIS.//P39801

F-PLACE1007843

F-PLACE1007846//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-32:37:94//HOMO SAPIENS (HUMAN).//P08547

F-PLACE1007852//RHO-RELATED GTP-BINDING PROTEIN RHOH (GTP-BINDING PROTEIN TTF).//8.7e-05:138:30//HOMO SAPIENS (HUMAN).//Q15669

55 F-PLACE1007858//ANAPHASE SPINDLE ELONGATION PROTEIN.//0.0039:127:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P50275

F-PLACE1007866

F-PLACE1007877

- F-PLACE1007897//CD44 ANTIGEN PRECURSOR (PHAGOCYTIC GLYCOPROTEIN I) (PGP-1) (HUTCH-I) (EX-  
TRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP90 LYMPHOCYTE HOMING/ADHESION RECEPTOR)  
(HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (HAM1 ANTI-  
GEN) //0.44:128:28//MESOCRICETUS AURATUS (GOLDEN HAMSTER) //Q60522
- 5 F-PLACE1007908//ALU SUBFAMILY SC WARNING ENTRY !!!!!/5.5e-28:61:65//HOMO SAPIENS (HUMAN) //P39192
- F-PLACE1007946//HYPOTHETICAL MERCURIC RESISTANCE PROTEIN MERC. //0.84:48:37//PSEU-  
DOMONAS AERUGINOSA //P04139
- 10 F-PLACE1007954//HYPOTHETICAL 45.5 KD PROTEIN IN FIG1-GIP1 INTERGENIC REGION //0.00070:96:29//  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P38226
- F-PLACE1007955//HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II //0.00027:255:23//  
CAENORHABDITIS ELEGANS //Q09625
- F-PLACE1007958//HIGH-AFFINITY CAMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE (EC 3.1.4.17) //1.7e-09:127:30//MUS MUSCULUS (MOUSE) //P70453
- 15 F-PLACE1007969//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION //2.4e-05:104:37//  
AUTOGRAPH CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMPV) //P41479
- F-PLACE1007990//SPERM PROTAMINE P1 //0.78:36:47//ORNITHORHYNCHUS ANATINUS (DUCKBILL PLAT-  
YPU) //P35307
- 20 F-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSIN-110) (SYNAPTIC DEN-  
SITY PROTEIN PSD-93) //1.2e-16:128:39//RATTUS NORVEGICUS (RAT) //Q63622
- F-PLACE1008002
- F-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NU-  
CLEOPORIN) (P105) //3.9e-106:208:93//RATTUS NORVEGICUS (RAT) //P52599
- 25 F-PLACE1008045//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS) //3.9e-09:49:53//BOS TAURUS (BO-  
VINE) //P25508
- F-PLACE1008080//RNA REPLICASE POLYPROTEIN (EC 2.7.7.48) //0.00025:100:27//EGGPLANT MOSAIC VI-  
RUS //P20126
- F-PLACE1008095//PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4) (PPO) //0.90:74:25//MYCOBACTERIUM  
TUBERCULOSIS //O53230
- 30 F-PLACE1008111//HYPOTHETICAL PROTEIN MJCS12 //0.30:38:42//METHANOCOCCUS JANNASCHII //Q60311
- F-PLACE1008122//PEA2 PROTEIN (PPF2 PROTEIN) //0.0085:117:34//SACCHAROMYCES CEREVISIAE  
(BAKER'S YEAST) //P40091
- F-PLACE1008129//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS) //1.8e-06:154:36//GAL-  
LUS GALLUS (CHICKEN) //P02467
- 35 F-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III //1.4e-13:227:36//  
CAENORHABDITIS ELEGANS //Q09531
- F-PLACE1008177//TRICHOHYALIN //2.7e-10:230:26//OVIS ARIES (SHEEP) //P22793
- F-PLACE1008181
- 40 F-PLACE1008198//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN) //0.00044:121:34//  
XENOPUS LAEVIS (AFRICAN CLAWED FROG) //P17437
- F-PLACE1008201//ZINC FINGER PROTEIN ZFMSA12A //3.0e-05:82:37//MICROPTERUS SALMOIDES  
(LARGEMOUTH BASS) //P38621
- F-PLACE1008209//METALLOTHIONEIN-I (MT-I) //0.95:39:35//CERCOPITHECUS AETHIOPS (GREEN MON-  
KEY) (GRIVET) //P02797
- 45 F-PLACE1008231//PROCYCLIC FORM SPECIFIC POLYPEPTIDE B1-ALPHA PRECURSOR (PROCYCLIN)  
(PARP) //0.028:23:52//TRYPANOSOMA BRUCEI BRUCEI //P08469
- F-PLACE1008244//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1 //2.2e-23:148:38//PODOSPORA AN-  
SERINA //Q00808
- 50 F-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP) //1.1e-97:222:  
81//BOS TAURUS (BOVINE) //P53620
- F-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-) //5.8e-20:161:37//SACCHAROMYCES CEREVI-  
SIAE (BAKER'S YEAST) //P12689
- F-PLACE1008280//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //6.1e-23:124:42//HOMO SAPIENS (HU-  
MAN) //P08547
- 55 F-PLACE1008309//HYPOTHETICAL 98.3 KD PROTEIN C9G1.06C IN CHROMOSOME I //0.47:99:37//  
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //O14302
- F-PLACE1008329//PUTATIVE Z PROTEIN //0.73:52:28//OVIS ARIES (SHEEP) //P08105

- F-PLACE1008330//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.0e-37:75:81//HOMO SAPIENS (HUMAN).//P39194
- F-PLACE1008331//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.1e-08:70:50//HOMO SAPIENS (HUMAN).//P39188
- 5 F-PLACE1008356//FRUIT PROTEIN PKIW1501//0.0037:148:29//ACTINIDIA CHINENSIS (KIWI) (YANGTAO).//P43393
- F-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//3.5e-18:205:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
- F-PLACE1008369
- 10 F-PLACE1008392
- F-PLACE1008398//GENE 33 POLYPEPTIDE.//1.5e-102:225:84//RATTUS NORVEGICUS (RAT).//P05432
- F-PLACE1008401//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//2.9e-08:186:34//MUS MUSCULUS (MOUSE).//P05143
- F-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED PROTEIN) (TAP).//9.4e-105:207:98//BOS TAURUS (BOVINE).//P14154
- 15 F-PLACE1008405
- F-PLACE1008424//PROTEIN UL56.//1.0:65:33//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN HFEM).//P36297
- F-PLACE1008426//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//4.4e-05:185:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q99323
- 20 F-PLACE1008429//NEURONAL AXONAL MEMBRANE PROTEIN NAP-22.//0.00054:172:25//RATTUS NORVEGICUS (RAT).//Q05175
- F-PLACE1008437//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.//1.9e-23:226:34//CAENORHABDITIS ELEGANS.//P34681
- F-PLACE1008455//DNA-BINDING PROTEIN (AGNOPROTEIN).//0.97:23:52//BUDGERIGAR FLEDGLING DISEASE VIRUS (BFDV).//P13893
- 25 F-PLACE1008457//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.1e-12:89:47//HOMO SAPIENS (HUMAN).//P39188
- F-PLACE1008465//ZINC FINGER PROTEIN 31 (ZINC FINGER PROTEIN KOX29) (FRAGMENT).//0.00017:23:43//HOMO SAPIENS (HUMAN).//P17040
- 30 F-PLACE1008488//HYPOTHETICAL PROTEIN UL61.//9.1e-05:204:30//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818
- F-PLACE1008524//HOMEBOX PROTEIN HLX1 (HOMEBOX PROTEIN HB24).//0.95:74:36//HOMO SAPIENS (HUMAN).//Q14774
- F-PLACE1008531//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.1e-05:86:45//HOMO SAPIENS (HUMAN).//P39192
- 35 F-PLACE1008532//HYPOTHETICAL 36.4 KD PROTEIN IN SMP1-MBA1 INTERGENIC REGION.//3.9e-21:62:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38298
- F-PLACE1008533//HYPOTHETICAL 86.2 KD PROTEIN C4G8.04 IN CHROMOSOME I.//3.5e-06:118:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09830
- 40 F-PLACE1008568//NEURONATIN.//0.046:34:52//HOMO SAPIENS (HUMAN).//Q16517
- F-PLACE1008584//HUNCHBACK PROTEIN (FRAGMENT).//0.94:30:43//LITHOBIUS FORFICATUS.//Q02030
- F-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//3.9e-123:224:96//RATTUS NORVEGICUS (RAT).//P37199
- F-PLACE1008621//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//5.0e-05:31:67//HOMO SAPIENS (HUMAN).//P20931
- 45 F-PLACE1008625//DISAGREGIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).//0.87:17:52//ORNITHODOROS MOUBATA (SOFT TICK).//P36235
- F-PLACE1008626//METALLOTHIONEIN-I (MT-I).//0.77:33:36//SCYLLA SERRATA (MUD CRAB).//P02805
- F-PLACE1008627//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF) (GIFB).//0.14:44:31//HOMO SAPIENS (HUMAN).//P25713
- 50 F-PLACE1008629
- F-PLACE1008630//PROTAMINE Z3 (SCYLLIORHININE Z3).//0.78:33:36//SCYLLIORHINUS CANICULA (SPOTTED DOGFISH) (SPOTTED CATSHARK).//P30258
- F-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR (ITI HEAVY CHAIN H4) (INTER-ALPHA-TRYPSIN INHIBITOR FAMILY HEAVY CHAIN-RELATED PROTEIN) (PLASMA KALLIKREIN SENSITIVE GLYCOPROTEIN 120) (PK-120).//1.7e-30:220:41//HOMO SAPIENS (HUMAN).//Q14624
- 55 F-PLACE1008650//PP1/PP2A PHOSPHATASES PLEIOTROPIC REGULATOR PRL1.//2.5e-10:106:31//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q42384

F-PLACE1008693//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (MSTI).//1.0:36:38//MEDICAGO SCUTEL-  
LATA (SNAIL MEDIC).//P80321

5 F-PLACE1008696//NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC  
1.6.99.3) (COMPLEX I-23KD) (CI-23KD) (TYKY SUBUNIT).//4.8e-14:47:80//HOMO SAPIENS (HUMAN).//  
O00217

F-PLACE1008715//HYPOTHETICAL 13.4 KD PROTEIN IN ACT5-YCK1 INTERGENIC REGION.//0.66:105:24//  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38834

F-PLACE1008748//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.10:178:  
26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

10 F-PLACE1008757//HYPOTHETICAL 10.1 KD PROTEIN IN RHSD-GCL INTERGENIC REGION (ORFD3).//0.60:  
44:34//ESCHERICHIA COLI.//P33669

F-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBUNIT) (IMPORTIN ALPHA  
S2).//3.0e-69:191:80//MUS MUSCULUS (MOUSE).//O35345

15 F-PLACE1008798//BACTERIOCIN LACTOBIN A.//1.0:34:41//LACTOBACILLUS AMYLOVORUS.//P80696

F-PLACE1008807//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.91:77:36//HOMO SAPIENS (HU-  
MAN).//P08547

F-PLACE1008808//REC1 PROTEIN.//0.45:39:30//USTILAGO MAYDIS (SMUT FUNGUS).//P14746

F-PLACE1008813

20 F-PLACE1008851//VERY HYPOTHETICAL 11.8 KD PROTEIN IN KTR3-DUR1,2 INTERGENIC REGION.//1.0:  
62:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38309

F-PLACE1008854//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.//1.0:82:26//  
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170

F-PLACE1008867//PATATIN T5 PRECURSOR (POTATO TUBER PROTEIN).//0.65:61:36//SOLANUM TUBERO-  
SUM (POTATO).//P15478

25 F-PLACE1008887//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-56:180:54//NYCTICEBUS COU-  
CANG (SLOW LORIS).//P08548

F-PLACE1008902

F-PLACE1008920

F-PLACE1008925//HYPOTHETICAL 41.2 KD PROTEIN IN GAPA-RND INTERGENIC REGION.//0.90:77:33//ES-  
CHERICHIA COLI.//P76242

30 F-PLACE1008934//HYPOTHETICAL PROTEIN IN ADHS 5'REGION (ORF3) (FRAGMENT).//0.14:77:45//GLU-  
CONOBACTER SUBOXYDANS.//O05543

F-PLACE1008941//ZINC FINGER PROTEIN 141.//1.1e-17:45:95//HOMO SAPIENS (HUMAN).//Q15928

F-PLACE1008947//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B).//4.1e-  
14:136:39//MUS MUSCULUS (MOUSE).//P27790

35 F-PLACE1009020//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.74:37:48//BOS TAURUS (BOVINE).//P20072

F-PLACE1009027//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.39:57:36//BALAENOP-  
TERA MUSCULUS (BLUE WHALE).//P41301

F-PLACE1009039

40 F-PLACE1009045//HYPOTHETICAL 9.5 KD PROTEIN IN SPEA-METK INTERGENIC REGION (F83).//0.48:32:  
43//ESCHERICHIA COLI.//P46879

F-PLACE1009048

F-PLACE1009050

45 F-PLACE1009060//HYPOTHETICAL 98.3 KD PROTEIN R10E12.1 IN CHROMOSOME III.//4.9e-23:244:31//  
CAENORHABDITIS ELEGANS.//P34552

F-PLACE1009090//50S RIBOSOMAL PROTEIN L35.//1.0:27:51//MYCOPLASMA GENITALIUM.//P47439

F-PLACE1009091

F-PLACE1009094//NEL-LIKE PROTEIN (FRAGMENT).//3.6e-15:180:30//HOMO SAPIENS (HUMAN).//Q92832

F-PLACE1009099//ZINC FINGER PROTEIN 27 (ZFP-27) (MKR4 PROTEIN) (FRAGMENT).//1.4e-94:228:71//  
MUS MUSCULUS (MOUSE).//P10077

50 F-PLACE1009110//HIRUDIN HV1 (BUFRUDIN).//1.0:49:34//HIRUDINARIA MANILLENSIS (BUFFALO LEECH).//  
P81492

F-PLACE1009111//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.4e-05:30:83//HOMO SAPIENS (HUMAN).//  
P39195

55 F-PLACE1009113//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.032:40:52//BOS TAURUS (BOVINE).//P20072

F-PLACE1009130//HYPOTHETICAL PROTEIN KIAA0032.//3.3e-37:214:38//HOMO SAPIENS (HUMAN).//  
Q15034

F-PLACE1009150//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.6e-32:56:76//HOMO SAPIENS (HUMAN).//

P39195  
 F-PLACE1009155!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.2e-17:101:57//HOMO SAPIENS (HUMAN).//P39194  
 5 F-PLACE1009158//HYPOTHETICAL PROTEIN HKRFX (J11).//0.0058:73:42//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P09711  
 F-PLACE1009166//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//0.0086:96:30//HOMO SAPIENS (HUMAN).//P49902  
 F-PLACE1009172//HYPOTHETICAL 8.7 KD PROTEIN IN GAPA-RND INTERGENIC REGION.//1.0:19:52//ESCHERICHIA COLI.//P76246  
 10 F-PLACE1009174!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.1e-17:47:82//HOMO SAPIENS (HUMAN).//P39194  
 F-PLACE1009183  
 F-PLACE1009186//HYPOTHETICAL 11.4 KD PROTEIN C13G6.04 IN CHROMOSOME I.//0.019:62:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09783  
 15 F-PLACE1009190//PALMITOYL-COA HYDROLASE (EC 3.1.2.2) (LONG-CHAIN FATTY-ACYL-COA HYDROLASE) (FRAGMENT).//0.027:53:28//RATTUS NORVEGICUS (RAT).//P80250  
 F-PLACE1009200!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.4e-28:84:71//HOMO SAPIENS (HUMAN).//P39194  
 F-PLACE1009230!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.8e-12:50:74//HOMO SAPIENS (HUMAN).//P39189  
 20 F-PLACE1009246//UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN (EC 1.10.2.2) (MITOCHONDRIAL HINGE PROTEIN) (CR7).//1.0:17:52//SOLANUM TUBEROSUM (POTATO).//P48504  
 F-PLACE1009298//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//6.6e-41:177:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P34110  
 25 F-PLACE1009308//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.00034:108:33//HOMO SAPIENS (HUMAN).//P26371  
 F-PLACE1009319//PRESYNAPTIC DENSITY PROTEIN 95 (PSD-95).//5.3e-16:84:50//HOMO SAPIENS (HUMAN).//P78352  
 F-PLACE1009328//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.9e-82:263:67//HOMO SAPIENS (HUMAN).//P08547  
 30 F-PLACE1009335//60S RIBOSOMAL PROTEIN L32.//0.95:71:36//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT).//P02433  
 F-PLACE1009338//TRANSCRIPTION FACTOR HES-5 (HAIRY AND ENHANCER OF SPLIT 5).//0.90:42:40//MUS MUSCULUS (MOUSE).//P70120  
 35 F-PLACE1009368//BASIC PROLINE-RICH PEPTIDE IB-1.//0.013:33:48//HOMO SAPIENS (HUMAN).//P04281  
 F-PLACE1009375//HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III.//0.0022:135:21//CAENORHABDITIS ELEGANS.//P34492  
 F-PLACE1009388!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.8e-22:73:65//HOMO SAPIENS (HUMAN).//P39195  
 40 F-PLACE1009398//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//8.1e-83:223:65//HOMO SAPIENS (HUMAN).//P51523  
 F-PLACE1009404//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR.//0.047:145:29//TRITICUM AESTIVUM (WHEAT).//P08489  
 45 F-PLACE1009410//TOXIN C13S1C1 PRECURSOR.//0.22:21:47//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P18329  
 F-PLACE1009434//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT K (EC 1.6.5.3) (FRAGMENT).//0.81:61:29//ANTHOCEROS FORMOSAE.//Q31791  
 F-PLACE1009443//SPICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//9.1e-05:93:32//MUS MUSCULUS (MOUSE).//Q62203  
 50 F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//6.4e-15:41:97//HOMO SAPIENS (HUMAN).//P42356  
 F-PLACE1009459//HYPOTHETICAL 42.3 KD PROTEIN C12G12.11C IN CHROMOSOME I.//0.0011:119:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09874  
 F-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//4.2e-34:101:75//RATTUS NORVEGICUS (RAT).//P54319  
 55 F-PLACE1009476//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.086:21:52//HOMO SAPIENS (HUMAN).//P30808  
 F-PLACE1009477



- F-PLACE1009493//HYPOTHETICAL 127.3 KD PROTEIN B0416.1 IN CHROMOSOME X.//1.4e-18:138:39//CAENORHABDITIS ELEGANS.//Q11069
- F-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FACTOR).//9.4e-80:155:35//HOMO SAPIENS (HUMAN).//Q99418
- 5 F-PLACE1009539//GTP-BINDING NUCLEAR PROTEIN RAN/TC4.//1.0:76:26//GIARDIA LAMBLIA (GIARDIA INTESTINALIS).//P38543
- F-PLACE1009542//ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00016:31:77//HOMO SAPIENS (HUMAN).//P39188
- 10 F-PLACE1009571//ATP SYNTHASE B CHAIN (EC 3.6.1.34) (SUBUNIT I).//0.88:116:29//STREPTOCOCCUS PNEUMONIAE.//Q59952
- F-PLACE1009581//50S RIBOSOMAL PROTEIN L32.//0.00023:37:51//RHODOBACTER CAPSULATUS (RHODOSPIRILLUM RUBRUM).//P30788
- F-PLACE1009595
- 15 F-PLACE1009596//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHROMOSOME III.//2.1e-36:116:49//CAENORHABDITIS ELEGANS.//Q17963
- F-PLACE1009607//ALU SUBFAMILY J WARNING ENTRY !!!!!/1.8e-43:73:69//HOMO SAPIENS (HUMAN).//P39188
- F-PLACE1009613
- 20 F-PLACE1009621//TRANSCRIPTION FACTOR BTF1 HOMOLOG 2.//0.91:29:44//HOMO SAPIENS (HUMAN).//Q13891
- F-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.3e-22:132:47//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25159
- F-PLACE1009637//HYPOTHETICAL 18.1 KD PROTEIN IN CFXA 3'REGION.//0.30:28:57//BACTEROIDES VULGATUS.//P30905
- 25 F-PLACE1009639//LIPASE MODULATOR PRECURSOR (LIPASE HELPER PROTEIN).//0.23:79:31//PSEUDOMONAS AERUGINOSA.//Q04591
- F-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (BRAIN PROTEIN H19) (MH19) (FRAGMENT).//3.9e-126:227:96//MUS MUSCULUS (MOUSE).//P28660
- F-PLACE1009665//IG KAPPA CHAIN V-I REGION (HAU).//0.52:89:35//HOMO SAPIENS (HUMAN).//P01600
- 30 F-PLACE1009670//CYCLOMALTODEXTRIN GLUCANOTRANSFERASE PRECURSOR (EC 2.4.1.19) (CYCLODEXTRIN-GLYCOSYLTRANSFERASE) (CGTASE).//0.16:114:29//PAENIBACILLUS MACERANS (BACILLUS MACERANS).//P31835
- F-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN CHROMOSOME I.//9.6e-19:156:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09876
- 35 F-PLACE1009721//MSF1 PROTEIN.//7.7e-23:176:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35200
- F-PLACE1009731//AIG1 PROTEIN.//1.1e-09:91:43//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P54120
- F-PLACE1009763//HYPOTHETICAL 48.9 KD PROTEIN C24H6.12C IN CHROMOSOME I.//8.3e-42:171:51//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09765
- 40 F-PLACE1009794//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.99:36:33//HORDEUM VULGARE (BARLEY).//P17991
- F-PLACE1009798//HYPOTHETICAL PROTEIN C22F3.14C IN CHROMOSOME I (FRAGMENT).//2.6e-34:191:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09779
- 45 F-PLACE1009845//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//2.2e-19:190:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38968
- F-PLACE1009861//CATHEPSIN B PRECURSOR (EC 3.4.22.1).//4.4e-20:171:33//BOS TAURUS (BOVINE).//P07688
- 50 F-PLACE1009879//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70).//0.99:30:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779
- F-PLACE1009886
- F-PLACE1009888//NONSTRUCTURAL POLYPROTEIN [CONTAINS: NONSTRUCTURAL PROTEIN NSP4] (FRAGMENT).//1.0:33:42//WESTERN EQUINE ENCEPHALITIS VIRUS.//P13896
- 55 F-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN C3F10.16C IN CHROMOSOME I.//3.1e-42:205:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10190
- F-PLACE1009921
- F-PLACE1009924//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.70:128:29//TRYPANOSOMA BRUCEI BRUCEI.//P24499

- F-PLACE1009925//ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34).//0.99:111:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P30902
- F-PLACE1009935//HYPOTHETICAL PROTEIN MJ0258.//0.063:75:32//METHANOCOCCUS JANNASCHII.//Q57706
- 5 F-PLACE1009947//NEUROGRANIN (NG) (P17) (B-50 IMMUNOREACTIVE C-KINASE SUBSTRATE) (BICKS) (FRAGMENT).//0.33:51:45//BOS TAURUS (BOVINE).//P35722
- F-PLACE1009971//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//0.022:84:27//MUS MUSCULUS (MOUSE).//P28575
- 10 F-PLACE1009992//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).//0.00011:35:51//HOMO SAPIENS (HUMAN).//P13497
- F-PLACE1009995//TROPOMYOSIN, SMOOTH MUSCLE/FIBROBLAST CTM1.//0.052:185:22//CIONA INTESTINALIS.//Q07068
- F-PLACE1009997//TRANSCRIPTION ELONGATION FACTOR S-II (RNA POLYMERASE II ELONGATION FACTOR DMS-II) (TFIIS).//0.68:98:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//P20232
- 15 F-PLACE1010023//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III.//6.6e-06:111:32//CAENORHABDITIS ELEGANS.//Q18262
- F-PLACE1010031//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//0.0024:72:33//AUTOGRAPH CALIFORNICA NUCLEAR POLYEDROSIS VIRUS (ACMPNV).//P41479
- F-PLACE1010053//HYPOTHETICAL PROTEIN HI0593.//0.83:24:45//HAEMOPHILUS INFLUENZAE.//P44022
- 20 F-PLACE1010069
- F-PLACE1010074//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5.//0.00027:192:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q92331
- F-PLACE1010076//HUNCHBACK PROTEIN (FRAGMENT).//0.80:39:30//SCIARA COPROPHILA (FUNGUS GNAT).//Q01790
- 25 F-PLACE1010083//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//2.7e-48:177:46//HOMO SAPIENS (HUMAN).//P98171
- F-PLACE1010089//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 13) (DEUBIQUITINATING ENZYME 11) (KIAA0055).//7.9e-07:55:43//HOMO SAPIENS (HUMAN).//P40818
- 30 F-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.0e-107:232:90//RATTUS NORVEGICUS (RAT).//Q62671
- F-PLACE1010102//DNA-DIRECTED RNA POLYMERASE SUBUNIT N (EC 2.7.7.6).//1.0:33:45//METHANOCOCCUS JANNASCHII.//Q57649
- F-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-47:200:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
- 35 F-PLACE1010108//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//1.2e-14:94:41//MUS MUSCULUS (MOUSE).//P11369
- F-PLACE1010134//HYPOTHETICAL 171.5 KD HELICASE IN NUT1-ARO2 INTERGENIC REGION.//4.0e-28:78:76//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53115
- F-PLACE1010148//GAR2 PROTEIN.//2.6e-05:180:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891
- 40 F-PLACE1010152//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E).//2.1e-59:227:54//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24574
- F-PLACE1010181//MALE SPECIFIC SPERM PROTEIN MST87F.//0.39:12:58//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175
- 45 F-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//1.4e-07:95:43//GALLUS GALLUS (CHICKEN).//P30352
- F-PLACE1010202//TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36).//0.094:109:29//RATTUS NORVEGICUS (RAT).//P47973
- 50 F-PLACE1010231//LANTIBIOTIC NISIN A PRECURSOR.//0.99:42:35//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).//P13068
- F-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//6.0e-71:201:62//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25722
- F-PLACE1010270
- 55 F-PLACE1010274//HYPOTHETICAL 16.2 KD PROTEIN C4F8.01 IN CHROMOSOME I.//4.4e-08:100:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14177
- F-PLACE1010293//ALU SUBFAMILY J WARNING ENTRY !!!!!/3.9e-26:94:64//HOMO SAPIENS (HUMAN).//P39188

- F-PLACE1010310//SYNAPSINS IA AND IB //5.7e-09:89:37//RATTUS NORVEGICUS (RAT)//P09951  
 F-PLACE1010321//IMMEDIATE-EARLY PROTEIN IE180.//0.033:145:31//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV)//P33479
- 5 F-PLACE1010324//MAST CELL DEGRANULATING PEPTIDE (MCDP) (MCD)//0.60:25:48//MEGABOMBUS PENNSYLVANICUS (AMERICAN COMMON BUMBLEBEE)//P04567  
 F-PLACE1010329//TOXIN S5C10.//1.0:39:33//DENDROASPIS JAMESONII KAIMOSAE (EASTERN JAMESON'S MAMBA)//P01419  
 F-PLACE1010341//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//0.0049:49:55//HOMO SAPIENS (HUMAN)//P39189
- 10 F-PLACE1010362//VARIANT-SURFACE-GLYCOPROTEIN PHOSPHOLIPASE C (EC 3.1.4.47) (VSG LIPASE) (GLYCOSYLPHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (GPI-PLC)//0.0034:89:30//TRYPANOSOMA CRUZI.//015886  
 F-PLACE1010364//NADH-UBIQUINONE OXIDOREDUCTASE B17 SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B17) (CI-B17)//1.0:40:35//SUS SCROFA (PIG)//Q29259
- 15 F-PLACE1010383  
 F-PLACE1010401//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140)//0.10:174:22//RATTUS NORVEGICUS (RAT)//P41777  
 F-PLACE1010481//HYPOTHETICAL 71.9 KD PROTEIN B0285.5 IN CHROMOSOME III.//1.5e-21:170:35//CAENORHABDITIS ELEGANS.//P46555
- 20 F-PLACE1010491//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION.//1.0:31:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40490  
 F-PLACE1010492//HYPOTHETICAL 42.3 KD PROTEIN C12G12.11C IN CHROMOSOME I.//0.77:97:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09874  
 F-PLACE1010522//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.74:45:37//HOMO SAPIENS (HUMAN)//P22531
- 25 F-PLACE1010529//DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS)[CONTAINS: GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE)]//0.70:58:39//VIGNA ACONITIFOLIA (MOTHBEAN)//P32296
- 30 F-PLACE1010547//HYPOTHETICAL 31.0 KD PROTEIN IN BUD9-RME1 INTERGENIC REGION.//0.17:68:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53227  
 F-PLACE1010562//CHLOROPLAST 50S RIBOSOMAL PROTEIN L33.//0.50:48:29//PORPHYRA PURPUREA.//P51255
- 35 F-PLACE1010579//HYPOTHETICAL PROTEIN HI1571.//0.29:37:43//HAEMOPHILUS INFLUENZAE.//P44260  
 F-PLACE1010580//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//3.3e-38:178:48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09747  
 F-PLACE1010599//PEROXISOMAL MEMBRANE PROTEIN PER10 (PEROXIN-14).//4.6e-17:192:31//PICHIA ANGUSTA (YEAST) (HANSENULA POLYMORPHA)//P78723
- 40 F-PLACE1010616//HYPOTHETICAL 9.2 KD PROTEIN IN RNPA 3'REGION.//0.44:32:37//PSEUDOMONAS PUTIDA.//P25753  
 F-PLACE1010622//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//5.0e-06:102:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32323  
 F-PLACE1010624//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.00036:134:32//HOMO SAPIENS (HUMAN)//P10162
- 45 F-PLACE1010628  
 F-PLACE1010629//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.7e-12:37:81//HOMO SAPIENS (HUMAN)//P39194  
 F-PLACE1010630  
 F-PLACE1010631//WNT-5B PROTEIN (FRAGMENT).//0.49:62:30//EUMECES SKILTONIANUS (WESTERN SKINK)//P28118
- 50 F-PLACE1010661//MATERNAL EXUPERANTIA 2 PROTEIN.//1.0:95:30//DROSOPHILA PSEUDOBOBSCURA (FRUIT FLY).//Q24617  
 F-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//3.2e-05:117:24//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q09332
- 55 F-PLACE1010702//ZINC FINGER PROTEIN 195.//1.4e-62:117:62//HOMO SAPIENS (HUMAN).//O14628  
 F-PLACE1010714  
 F-PLACE1010720//CHROMOSOME ASSEMBLY PROTEIN XCAP-C.//1.1e-64:176:76//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P50532

- F-PLACE1010739//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).//0.97:31:41//  
HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1).//P04612
- F-PLACE1010743//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//3.8e-05:253:30//MUS MUSCULUS  
(MOUSE).//P05143
- 5 F-PLACE1010761//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//1.5e-14:175:25//  
CAENORHABDITIS ELEGANS.//Q09217
- F-PLACE1010771//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP.//1.3e-120:216:89//MUS MUSCULUS  
(MOUSE).//Q02614
- 10 F-PLACE1010786//CENTROSOMIN (ARROW PROTEIN).//0.97:133:24//DROSOPHILA MELANOGASTER  
(FRUIT FLY).//P54623
- F-PLACE1010800//HYPOTHETICAL 31.7 KD PROTEIN IN TRAX-FINO INTERGENIC REGION (ORFC).//  
0.0060:111:31//ESCHERICHIA COLI.//Q99390
- F-PLACE1010802//UREASE ACCESSORY PROTEIN UREI.//0.82:44:29//BACILLUS SP. (STRAIN TB-90).//  
Q07415
- 15 F-PLACE1010811//CYTOCHROME C-551 (C551).//0.99:42:38//ECTOTHIORHODOSPIRA HALOCHLORIS.//  
P38587
- F-PLACE1010833//CALTRACTIN, ISOFORM 1 (CENTRIN).//2.8e-09:90:34//HOMO SAPIENS (HUMAN).//  
P41208
- F-PLACE1010856//MOLT-INHIBITING HORMONE (MIH).//1.0:32:37//PROCAMBARUS CLARKII (RED SWAMP  
20 CRAYFISH).//P55848
- F-PLACE1010857//IG ALPHA-1 CHAIN C REGION.//0.49:73:34//GORILLA GORILLA GORILLA (LOWLAND GO-  
RILLA).//P20758
- F-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.2e-56:173:58//HO-  
MO SAPIENS (HUMAN).//Q05481
- 25 F-PLACE1010877//HEAT SHOCK PROTEIN 82.//0.13:130:25//ZEA MAYS (MAIZE).//Q08277
- F-PLACE1010891//HYPOTHETICAL 8.2 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION.//0.95:51:27//  
BACILLUS SUBTILIS.//P54436
- F-PLACE1010896//SERINE/THREONINE-PROTEIN KINASE PTK1/STK1 (EC 2.7.1.).//0.98:71:30//SACCHA-  
ROMYCES CEREVISIAE (BAKER'S YEAST).//P36002
- 30 F-PLACE1010900//HYPOTHETICAL PROTEIN H10840.//1.0:42:30//HAEMOPHILUS INFLUENZAE.//P44897
- F-PLACE1010916//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIB3.//0.060:59:35//OVIS ARIES (SHEEP).//  
P02444
- F-PLACE1010917//E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN) (PEPLOMER PROTEIN).//  
0.71:141:24//BOVINE CORONAVIRUS (STRAIN L9).//P25191
- 35 F-PLACE1010925//HYPOTHETICAL 8.1 KD PROTEIN.//1.0:17:58//THERMOPROTEUS TENAX VIRUS 1  
(STRAIN KRA1) (TTV1).//P19285
- F-PLACE1010926//HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269.//0.011:51:45//HOMO SAPIENS (HU-  
MAN).//Q92558
- 40 F-PLACE1010942//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN  
EPS15).//3.1e-09:64:37//MUS MUSCULUS (MOUSE).//P42567
- F-PLACE1010944//GAP JUNCTION ALPHA-3 PROTEIN (CONNEXIN 44) (CX44).//0.17:71:38//BOS TAURUS  
(BOVINE).//P41987
- F-PLACE1010947
- 45 F-PLACE1010954//TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE.//0.011:144:26//HOMO SAPIENS  
(HUMAN).//P09493
- F-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//1.1 e-60:136:52//DROSOPHILA MELANOGASTER (FRUIT  
FLY).//P45890
- F-PLACE1010965
- 50 F-PLACE1011026//PERIOD CLOCK PROTEIN (FRAGMENT).//1.0:64:31//DROSOPHILA ANANASSAE (FRUIT  
FLY).//Q03293
- F-PLACE1011032//RIBONUCLEASE HI (EC 3.1.26.4) (RNASE HI) (RIBONUCLEASE H) (RNASE H).//1.0:32:37//  
SALMONELLA TYPHIMURIUM.//P23329
- F-PLACE1011041//HOMEBOX PROTEIN VAB-7.//0.36:65:30//CAENORHABDITIS ELEGANS.//Q93899
- F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1 (EC  
3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-154).//1.3e-22:58:93//RATTUS NORVEGI-  
CUS (RAT).//P10687
- 55 F-PLACE1011054//ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.6e-07:38:73//HOMO SAPIENS (HUMAN).//  
P39195

- F-PLACE1011056//HISTONE H1.//2.2e-10:109.41//PISUM SATIVUM (GARDEN PEA).//P08283  
F-PLACE1011057
- 5 F-PLACE1011090//HYPOTHETICAL 33.8 KD PROTEIN IN TWT1-FLO5 INTERGENIC REGION.//1.8e-07:133:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38892  
F-PLACE1011109//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//5.4e-25:63:88//RAT-TUS NORVEGICUS (RAT).//Q07803  
F-PLACE1011114//PUTATIVE ATP-DEPENDENT RNA HELICASE C1F7.02C.//8.4e-31:157.45//SCHIZOSAC-CHAROMYCES POMBE (FISSION YEAST).//Q09916  
10 F-PLACE1011133//SERUM AMYLOID P-COMPONENT PRECURSOR (SAP) (9.5S ALPHA-1-GLYCOPRO-TEIN).//0.92:58:31//HOMO SAPIENS (HUMAN).//P02743  
F-PLACE1011143//PROBABLE E5 PROTEIN.//0.24:42:35//HUMAN PAPILLOMAVIRUS TYPE31.//P17385  
F-PLACE1011160//EARLY NODULIN 55-2 PRECURSOR (N-55-2) (NODULIN-315).//0.88:98:27//GLYCINE MAX (SOYBEAN).//Q02917  
15 F-PLACE1011165//HISTIDINE-RICH PROTEIN.//0.013:13:76//PLASMODIUM FALCIPARUM (ISOLATE FCM17 / SENEGAL).//P14586  
F-PLACE1011185//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!.//1.4e-13:98:50//HOMO SAPIENS (HUMAN).//P39188  
F-PLACE1011203  
F-PLACE1011214//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:48:27//EQUUS ASINUS (DONKEY).//P92479  
20 F-PLACE1011219//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//1.9e-15:162:31//STREPTOMYCES ANTIBI-OTICUS.//Q03326  
F-PLACE1011221//ANTITHROMBIN-III HOMOLOG.//0.84:74:33//FOWLPOX VIRUS (ISOLATE HP-438[MU-NICH]).//P14369  
25 F-PLACE1011229//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTE-RASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUI-TOUS NUCLEAR PROTEIN HOMOLOG).//3.5e-86:218:68//HOMO SAPIENS (HUMAN).//Q13107  
F-PLACE1011263//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//3.0e-07:99:36//HOMO SAPIENS (HUMAN).//Q01485  
30 F-PLACE1011273  
F-PLACE1011291//PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENTS).//0.011:36:50//RATTUS NORVEGICUS (RAT).//P20468  
F-PLACE1011296//HOMEBOX PROTEIN DLX-6.//0.76:55:32//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q98877  
35 F-PLACE1011310//ATP SYNTHASE PROTEIN 9, MITOCHONDRIAL (EC 3.6.1.34) (LIPID-BINDING PROTEIN).//0.46:43:44//PETUNIA SP. (PETUNIA).//Q07060  
F-PLACE1011325//HYPOTHETICAL 222.8 KD PROTEIN C1F3.06C IN CHROMOSOME I.//0.00021:171:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10411  
F-PLACE1011332//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT101 PRECURSOR.//7.3e-27:113:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q05211  
40 F-PLACE1011340//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!.//2.6e-07:40:62//HOMO SAPIENS (HUMAN).//P39188  
F-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2).//2.2e-54:227:44//MUS MUSCULUS (MOUSE).//Q61703  
45 F-PLACE1011375//PROBABLE E5 PROTEIN.//0.93:28:57//HUMAN PAPILLOMAVIRUS TYPE 51.//P26553  
F-PLACE1011399//HISTONE H2B-IV.//0.19:129:27//VOLVOX CARTERI.//P16868  
F-PLACE1011419  
F-PLACE1011433//ZINC FINGER PROTEIN GLI3 (FRAGMENT).//3.4e-05:133:24//GALLUS GALLUS (CHICK-EN).//P55879  
50 F-PLACE1011452//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.9e-25:76:63//HOMO SAPIENS (HU-MAN).//P08547  
F-PLACE1011465//ECTODERMAL DYSPLASIA PROTEIN (EDA PROTEIN).//0.97:36:41//HOMO SAPIENS (HU-MAN).//Q92838  
F-PLACE1011472//METALLOTHIONEIN-1 (CUMT-1).//0.084:55:30//HOMARUS AMERICANUS (AMERICAN LOBSTER).//P29499  
55 F-PLACE1011477//CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1).//0.028:129:34//CLOSTRIDIUM THERMOCELLUM.//Q06852  
F-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//

- 2.9e-13;147:31//BRASSICA OLERACEA (CAULIFLOWER).//P52178  
 F-PLACE1011503//PUTATIVE FERREDOXIN-LIKE PROTEIN IN PURL-DPJ INTERGENIC REGION (086).//0.66:32:40//ESCHERICHIA COLI.//P52102  
 F-PLACE1011520
- 5 F-PLACE1011563//LORICRIN.//0.00023:112:39//HOMO SAPIENS (HUMAN).//P23490  
 F-PLACE1011567!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//9.2e-31:78:76//HOMO SAPIENS (HUMAN).//P39195  
 F-PLACE1011576//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.5e-32:45:86//HOMO SAPIENS (HUMAN).//Q05481
- 10 F-PLACE1011586//N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (OMEGA-CONOTOXIN-SENSITIVE N-TYPE, BRAIN CALCIUM CHANNEL ALPHA-1 SUBUNIT).//0.26:81:37//HOMO SAPIENS (HUMAN).//Q00975  
 F-PLACE1011635//IMMEDIATE-EARLY PROTEIN IE180.//0.00045:170:30//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER/BECKER) (PRV).//P11675  
 F-PLACE1011641
- 15 F-PLACE1011643//CUTICLE COLLAGEN 40.//1.0:128:32//CAENORHABDITIS ELEGANS.//P34804  
 F-PLACE1011646!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-15:44:63//HOMO SAPIENS (HUMAN).//P39188  
 F-PLACE1011649//HYPOTHETICAL PROTEIN F-215.//0.48:106:34//HUMAN ADENOVIRUS TYPE 2.//P03291  
 F-PLACE1011650
- 20 F-PLACE1011664//CROOKED NECK PROTEIN.//1.2e-79:201:68//DROSOPHILA MELANOGASTER (FRUIT FLY).//P17886  
 F-PLACE1011675//FERREDOXIN.//1.0:44:29//METHANOCOCCUS THERMOLITHOTROPHICUS.//P21305  
 F-PLACE1011682//HYPOTHETICAL 7.0 KD PROTEIN IN RPS26A-COX4 INTERGENIC REGION.//1.0:40:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53098
- 25 F-PLACE1011719//NEUROTOXIN TX2-6.//0.90:31:35//PHONEUTRIA NIGRIVENTER (BRAZILIAN ARMED SPIDER).//P29425  
 F-PLACE1011725//NUCLEOBINDIN PRECURSOR (NUCB1) (BONE 63 KD CALCIUM-BINDING PROTEIN).//0.0065:125:25//RATTUS NORVEGICUS (RAT).//Q63083  
 F-PLACE1011729//SRY-RELATED PROTEIN LG27 (FRAGMENT).//0.97:48:39//EUBLEPHARIS MACULARIUS.//P40654
- 30 F-PLACE1011749  
 F-PLACE1011762//D-BINDING PROTEIN (DBP) (ALBUMIN D BOX-BINDING PROTEIN).//0.028:91:39//MUS MUSCULUS (MOUSE).//Q60925  
 F-PLACE1011778
- 35 F-PLACE1011783//EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1).//0.97:48:43//MUS MUSCULUS (MOUSE).//P20863  
 F-PLACE1011858//COLLAGEN 1(X) CHAIN PRECURSOR.//0.0027:154:33//BOS TAURUS (BOVINE).//P23206  
 F-PLACE1011874//BACTERIOCHLOROPHYLL A PROTEIN (BCHL A PROTEIN) (BCP).//1.0:60:26//PROSTHECOCHLORIS AESTUARII.//P11741
- 40 F-PLACE1011875//HYPOTHETICAL 6.6 KD PROTEIN IN GP54-ALT INTERGENIC REGION.//0.99:34:35//ACETRIOPHAGE T4.//P39495  
 F-PLACE1011891//SMOOTHELIN.//0.018:122:31//HOMO SAPIENS (HUMAN).//P53814  
 F-PLACE1011896//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//6.3e-09:203:35//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437
- 45 F-PLACE1011922//CRYPTIDIN-RELATED PROTEIN 4C-2 PRECURSOR (CRS4C).//0.067:37:48//MUS MUSCULUS (MOUSE).//P50715  
 F-PLACE1011923//SERINE/THREONINE-PROTEIN KINASE SNK (EC 2.7.1.-) (SERUM INDUCIBLE KINASE).//1.5e-83:175:89//MUS MUSCULUS (MOUSE).//P53351  
 F-PLACE1011962//MATING-TYPE PHEROMONE BAP1(2) PRECURSOR.//0.50:46:41//SCHIZOPHYLLUM COMMUNE (BRACKET FUNGUS).//Q02593
- 50 F-PLACE1011964//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.6e-05:47:51//NYCTICEBUS COUCANG (SLOW LORIS).//P08548  
 F-PLACE1011982//APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN).//0.98:83:31//PLASMODIUM FRAGILE.//P22622
- 55 F-PLACE1011995  
 F-PLACE1012031//HYPOTHETICAL PROTEIN KIAA0254.//0.032:62:33//HOMO SAPIENS (HUMAN).//Q82543  
 F-PLACE20000033!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//5.4e-18:63:73//HOMO SAPIENS (HUMAN).//P39193

- F-PLACE2000006//ANNEXIN VII (SYNEXIN) (FRAGMENT)//0.14:20:50//BOS TAURUS (BOVINE)//P20072  
 F-PLACE2000007//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//0.0045:176:30//MUS MUSCULUS (MOUSE)//P05143  
 F-PLACE2000011//ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.6e-25:57:78//HOMO SAPIENS (HUMAN)//P39194  
 F-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III//0.00013:237:27//CAENORHABDITIS ELEGANS//Q09475  
 F-PLACE2000015//ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-33:60:80//HOMO SAPIENS (HUMAN)//P39193  
 F-PLACE2000017//FOLATE RECEPTOR BETA PRECURSOR (FR-BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP)//1.0:83:31//HOMO SAPIENS (HUMAN)//P14207  
 F-PLACE2000021//EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR CEK8)//0.99:103:26//GALLUS GALLUS (CHICKEN)//Q07496  
 F-PLACE2000030//MALE SPECIFIC SPERM PROTEIN MST84DA//0.69:29:44//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01642  
 F-PLACE2000033//PROBABLE OXIDOREDUCTASE (EC 1.-.-.)//1.1e-05:74:41//STREPTOMYCES ANTIBIOTICUS//Q03326  
 F-PLACE2000034//AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) (TRANSIENT AXONAL GLYCOPROTEIN 1)//6.7e-18:191:35//HOMO SAPIENS (HUMAN)//Q02246  
 F-PLACE2000039//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C)//4.7e-80:163:96//RATTUS NORVEGICUS (RAT)//P38650  
 F-PLACE2000047//ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/6.4e-06:63:49//HOMO SAPIENS (HUMAN)//P39191  
 F-PLACE2000050//ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.2e-22:74:64//HOMO SAPIENS (HUMAN)//P39192  
 F-PLACE2000061  
 F-PLACE2000062//GLUCOSE STARVATION-INDUCIBLE PROTEIN B (GENERAL STRESS PROTEIN B)//1.9e-06:108:37//BACILLUS SUBTILIS//P26907  
 F-PLACE2000072//ZINC FINGER PROTEIN 165//3.5e-34:175:49//HOMO SAPIENS (HUMAN)//P49910  
 F-PLACE2000097//RIBONUCLEASE PANCREATIC (EC 3.1.27.5) (RNASE 1) (RNASE A)//0.36:39:38//ONDATRA ZIBETHICUS (MUSKRAT)//P00681  
 F-PLACE2000100  
 F-PLACE2000103//TUBULIN ALPHA-4 CHAIN (FRAGMENTS)//0.18:32:37//ZEA MAYS (MAIZE)//P33626  
 F-PLACE2000111//CMRF35 ANTIGEN PRECURSOR//0.056:107:27//HOMO SAPIENS (HUMAN)//Q08708  
 F-PLACE2000115//DIAMINOPIMELATE EPIMERASE (EC 5.1.1.7) (DAP EPIMERASE) (FRAGMENT)//1.0:21:52//CLOSTRIDIUM PERFRINGENS//Q46185  
 F-PLACE2000124//ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.4e-37:108:68//HOMO SAPIENS (HUMAN)//P39194  
 F-PLACE2000132//PROBABLE MEMBRANE ANTIGEN GP85//0.09:133:29//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)//P03224  
 F-PLACE2000136//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 2 PRECURSOR (VIP-R-2) (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE III RECEPTOR) (PACAP TYPE III RECEPTOR) (PACAP-R-3)//0.83:65:32//MUS MUSCULUS (MOUSE)//P41588  
 F-PLACE2000140  
 F-PLACE2000164//TIPD PROTEIN//5.7e-12:190:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//O15736  
 F-PLACE2000170//BACTERIOCIN CARNOBACTERIOCIN BM1 PRECURSOR (CARNOBACTERIOCIN B1)//1.0:30:26//CARNOBACTERIUM PISCICOLA//P38579  
 F-PLACE2000172  
 F-PLACE2000176//HYPOTHETICAL PROTEIN AF0526//0.76:44:43//ARCHAEOGLOBUS FULGIDUS//O29724  
 F-PLACE2000187//EM-LIKE PROTEIN GEA6//0.84:42:35//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//Q02973  
 F-PLACE2000216  
 F-PLACE2000223//NEUROTOXIN III (LQ III)//0.99:38:34//LEIURUS QUINQUESTRIATUS QUINQUESTRIATUS (EGYPTIAN SCORPION)//P01487  
 F-PLACE2000235  
 F-PLACE2000246//RING CANAL PROTEIN (KELCH PROTEIN)//5.1e-37:121:42//DROSOPHILA MELANOGASTER (FRUIT FLY)

NOGASTER (FRUIT FLY).//Q04652  
 F-PLACE2000264/////ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/2.4e-05:77.42//HOMO SAPIENS (HUMAN).//P39191  
 F-PLACE2000274//DYNEIN BETA CHAIN, CILIARY.//5.3e-46:232.45//TRIPNEUSTES GRATILLA (HAWAIIAN SEA URCHIN).//P23098  
 F-PLACE2000302//TRICHOHYALIN.//1.5e-06:215.29//ORYCTOLAGUS CUNICULUS (RABBIT).//P37709  
 F-PLACE2000305/////ALU SUBFAMILY J WARNING ENTRY !!!!!/5.3e-06:33.66//HOMO SAPIENS (HUMAN).//P39188  
 F-PLACE2000317//TOXIN C13S1C1 PRECURSOR.//0.44:45.33//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P18329  
 F-PLACE2000335/////ALU SUBFAMILY SX WARNING ENTRY !!!!!/7.9e-08:35.71//HOMO SAPIENS (HUMAN).//P39195  
 F-PLACE2000341//SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER).//0.014:141.24//ORYCTOLAGUS CUNICULUS (RABBIT).//P11170  
 F-PLACE2000342//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//5.7e-09:96.38//AUTOGRAHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479  
 F-PLACE2000347//ZINC FINGER PROTEIN 177.//5.9e-05:49.53//HOMO SAPIENS (HUMAN).//Q13360  
 F-PLACE2000359/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.5e-10:69.52//HOMO SAPIENS (HUMAN).//P39194  
 F-PLACE2000366  
 F-PLACE2000371//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//1.5e-05:216.29//HOMO SAPIENS (HUMAN).//P54259  
 F-PLACE2000373//MAX BINDING PROTEIN MNT (ROX PROTEIN) (MYC ANTAGONIST MNT).//0.27:63.33//HOMO SAPIENS (HUMAN).//Q99583  
 F-PLACE2000379//HYPOTHETICAL GENE 1 PROTEIN.//0.72:120.31//EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).//P28978  
 F-PLACE2000394//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.95:40.42//HOMO SAPIENS (HUMAN).//P02811  
 F-PLACE2000398//RIBONUCLEASE PRECURSOR (EC 3.1.27.-).//0.88:88.31//AEROMONAS HYDROPHILA.//Q07465  
 F-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//7.6e-16:180.39//HOMO SAPIENS (HUMAN).//P14209  
 F-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE-TRNA LIGASE) (LEURS).//1.7e-94:243.64//CAENORHABDITIS ELEGANS.//Q09996  
 F-PLACE2000411//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PPT) (FRAGMENT).//1.2e-09:78.39//MUS MUSCULUS (MOUSE).//Q60676  
 F-PLACE2000419/////ALU SUBFAMILY J WARNING ENTRY !!!!!/2.6e-20:61.62//HOMO SAPIENS (HUMAN).//P39188  
 F-PLACE2000425//HYPOTHETICAL 11.9 KD PROTEIN IN MSB2-UGA1 INTERGENIC REGION.//0.98:75.32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53211  
 F-PLACE2000427//INSULIN PRECURSOR.//0.98:55.34//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).//P30407  
 F-PLACE2000433/////ALU SUBFAMILY J WARNING ENTRY !!!!!/7.5e-07:65.50//HOMO SAPIENS (HUMAN).//P39188  
 F-PLACE2000435  
 F-PLACE2000438//HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III.//4.7e-66:178.47//CAENORHABDITIS ELEGANS.//P34678  
 F-PLACE2000450/////ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.1e-23:88.62//HOMO SAPIENS (HUMAN).//P39195  
 F-PLACE2000455//TOXIN II (TOXIN II 10.9.2) (FRAGMENT).//0.093:18.44//CENTRUROIDES LIMPIDUS LIMPIDUS (MEXICAN SCORPION).//P45630  
 F-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//3.1e-23:165.40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P33450  
 F-PLACE2000465/////ALU SUBFAMILY J WARNING ENTRY !!!!!/3.6e-23:73.63//HOMO SAPIENS (HUMAN).//P39188  
 F-PLACE2000477/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.4e-37:90.78//HOMO SAPIENS (HUMAN).//P39194



- F-PLACE3000004//EYES ABSENT HOMOLOG 3.//1.1e-09:27:100//MUS MUSCULUS (MOUSE).//P97480  
F-PLACE3000009//PUTATIVE CUTICLE COLLAGEN C09G5.6.//0.0061:148:34//CAENORHABDITIS ELE-  
GANS.//Q09457
- 5 F-PLACE3000020//ADENYLATE CYCLASE, OLFACTIVE TYPE (EC 4.6.1.1) (TYPE III) (ATP PYROPHOS-  
PHATE-LYASE) (ADENYL CYCLASE).//8.8e-93:193:92//RATTUS NORVEGICUS (RAT).//P21932  
F-PLACE3000029//50S RIBOSOMAL PROTEIN L31E.//0.15:50:38//METHANOCOCCUS JANNASCHII.//P54009  
F-PLACE3000059//TCP1-CHAPERONIN COFACTOR A.//0.96:50:34//BOS TAURUS (BOVINE).//P48427  
F-PLACE3000070//HYPOHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION.//0.29:22:59//SACCHAROMYCES  
CEREVISIAE (BAKER'S YEAST).//P38898
- 10 F-PLACE3000103//LYSIS PROTEIN (E PROTEIN) (GPE).//0.99:53:32//BACTERIOPHAGE ALPHA-3.//P31280  
F-PLACE3000119//ALU SUBFAMILY SB WARNING ENTRY !!!!!/5.4e-41:87:78//HOMO SAPIENS (HUMAN).//  
P39189  
F-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC151/1.0e-07:269:22//SACCHAROMYCES  
CEREVISIAE (BAKER'S YEAST).//P22224
- 15 F-PLACE3000124//ALU SUBFAMILY J WARNING ENTRY !!!!!/1.2e-29:97:73//HOMO SAPIENS (HUMAN).//  
P39188  
F-PLACE3000136//PARS INTERCEREBRALIS MAJOR PEPTIDE D1 (PMP-D1).//0.77:26:42//LOCUSTA MIGRA-  
TORIA (MIGRATORY LOCUST).//P80059  
F-PLACE3000142//HYPOHETICAL 7.1 KD PROTEIN IN NAD2 3'REGION (ORF 63).//0.82:34:41//MARCHAN-  
TIA POLYMORPHA (LIVERWORT).//P38468
- 20 F-PLACE3000145//TENSIN.//3.5e-91:238:74//GALLUS GALLUS (CHICKEN).//Q04205  
F-PLACE3000147//ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.4e-30:61:65//HOMO SAPIENS (HUMAN).//  
P39194  
F-PLACE3000148//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE  
(EC 2.7.7.49); ENDONUCLEASE].//1.4e-18:226:34//GIBBON APE LEUKEMIA VIRUS.//P21414  
F-PLACE3000155//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.00014:107:33//ZEA MAYS  
(MAIZE).//P14918
- 25 F-PLACE3000156//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE  
(EC 2.7.7.49); ENDONUCLEASE].//2.7e-19:169:30//BABOON ENDOGENOUS VIRUS (STRAIN M7).//P10272  
F-PLACE3000157//PROBABLE SERINE/THREONINE-PROTEIN KINASE CY50.16 (EC 2.7.1.-).//0.0061:92:30//  
MYCOBACTERIUM TUBERCULOSIS.//Q11053  
F-PLACE3000158//ALU SUBFAMILY SB WARNING ENTRY !!!!!/5.7e-49:56:80//HOMO SAPIENS (HUMAN).//  
P39189  
F-PLACE3000160//DNA TRANSFORMATION PROTEIN TFOX (COMPETENCE ACTIVATOR) (PROTEIN SKY).//  
0.39:94:34//HAEMOPHILUS INFLUENZAE.//P43779
- 35 F-PLACE3000169//ALU SUBFAMILY SP WARNING ENTRY !!!!!/5.6e-28:99:59//HOMO SAPIENS (HUMAN).//  
P39193  
F-PLACE3000194//PROLINE-RICH PROTEIN LAS17.//0.91:80:36//SACCHAROMYCES CEREVISIAE (BAK-  
ER'S YEAST).//Q12446
- 40 F-PLACE3000197//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//  
0.24:119:32//GALLUS GALLUS (CHICKEN).//P16053  
F-PLACE3000199//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//  
0.76:87:37//NICOTIANA TABACUM (COMMON TOBACCO).//P13983  
F-PLACE3000207//ALU SUBFAMILY J WARNING ENTRY !!!!!/4.5e-09:32:78//HOMO SAPIENS (HUMAN).//  
P39188
- 45 F-PLACE3000208  
F-PLACE3000218//ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.2e-34:96:70//HOMO SAPIENS (HUMAN).//  
P39194  
F-PLACE3000220//OSTEOCALCIN (GAMMA-CARBOXYGLUTAMIC ACID-CONTAINING PROTEIN) (BONE  
GLA- PROTEIN) (BGP).//0.46:13:53//CANIS FAMILIARIS (DOG).//P81455  
F-PLACE3000221//ALU SUBFAMILY J WARNING ENTRY !!!!!/2.8e-24:178:45//HOMO SAPIENS (HUMAN).//  
P39188
- 50 F-PLACE3000226//30S RIBOSOMAL PROTEIN S18.//0.98:38:34//NEISSERIA GONORRHOEAE.//O07815  
F-PLACE3000230//METALLOTHIONEIN (MT).//0.97:25:48//OREOCHROMIS MOSSAMBICUS (MOZAMBIQUE  
TILAPIA) (TILAPIA MOSSAMBICA).//P52726
- 55 F-PLACE3000242//MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN).//8.0e-21:121:39//HOMO SA-  
PIENS (HUMAN).//P43361  
F-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//2.3e-125:264:87//MUS MUS-

CULUS (MOUSE).//P53995  
 F-PLACE3000254//RTOA PROTEIN (RATIO-A).//0.99:142:23//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P54681  
 5 F-PLACE3000271//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.2e-12:63:53//HOMO SAPIENS (HUMAN).//P39188  
 F-PLACE3000276//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN).//1.0:55:38//HOMO SAPIENS (HUMAN).//P27658  
 F-PLACE3000304//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.0028:31:54//HOMO SAPIENS (HUMAN).//P30808  
 10 F-PLACE3000310//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//0.98:82:34//RATTUS NORVEGICUS (RAT).//P54258  
 F-PLACE3000320  
 F-PLACE3000322//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1 PRECURSOR.//2.2e-22:61:52//ORYZA SATIVA (RICE).//P25074  
 15 F-PLACE3000331//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.32:15:53//HOMO SAPIENS (HUMAN).//P22532  
 F-PLACE3000339//CHORION PROTEIN S19.//0.34:89:37//DROSOPHILA VIRILIS (FRUIT FLY).//P24516  
 F-PLACE3000341//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRAGMENT).//1.0:47:38//COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).//P24968  
 20 F-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE SULU (EC 2.7.1.-).//3.9e-50:168:60//CAENORHABDITIS ELEGANS.//P46549  
 F-PLACE3000352//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.8e-29:76:71//HOMO SAPIENS (HUMAN).//P39194  
 F-PLACE3000353//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1).//3.0e-09:100:41//HOMO SAPIENS (HUMAN).//Q10472  
 25 F-PLACE3000362//HYPOTHETICAL PROTEIN TP0064.//1.0:75:26//TREPONEMA PALLIDUM.//O83103  
 F-PLACE3000363//METALLOTHIONEIN (MT).//0.067:42:33//ASTACUS FLUVIATILIS (BROAD-FINGERED CRAYFISH) (ASTACUS ASTACUS).//P55951  
 30 F-PLACE3000365//LYSIS PROTEIN (E PROTEIN) (GPE).//1.0:65:27//BACTERIOPHAGE PHI-K.//Q38040  
 F-PLACE3000373//RETROVIRUS-RELATED ENV POLYPROTEIN.//1.5e-18:90:47//HOMO SAPIENS (HUMAN).//P10267  
 F-PLACE3000388  
 F-PLACE3000399//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/6.3e-45:60:75//HOMO SAPIENS (HUMAN).//P39193  
 35 F-PLACE3000400  
 F-PLACE3000401//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.6e-09:46:73//HOMO SAPIENS (HUMAN).//P39188  
 F-PLACE3000402//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.036:43:44//HOMO SAPIENS (HUMAN).//P39188  
 40 F-PLACE3000405//POSTERIOR PITUITARY PEPTIDE.//0.70:25:40//BOS TAURUS (BOVINE).//P01154  
 F-PLACE3000406//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.3e-09:49:67//HOMO SAPIENS (HUMAN).//P39195  
 F-PLACE3000413//MALE SPECIFIC SPERM PROTEIN MST87F.//0.12:42:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175  
 45 F-PLACE3000416//CYCLIN I (MULTIPLE-BAND POLYPEPTIDE I).//0.67:236:21//BOS TAURUS (BOVINE).//P35662  
 F-PLACE3000425//PROLINE-RICH PEPTIDE P-B.//0.45:19:42//HOMO SAPIENS (HUMAN).//P02814  
 F-PLACE3000455//AMELOGENIN, CLASS I PRECURSOR.//0.0073:81:43//BOS TAURUS (BOVINE).//P02817  
 50 F-PLACE3000475//8.6 KD TRANSGLUTAMINASE SUBSTRATE.//1.0:53:32//TACHYPLEUS TRIDENTATUS (JAPANESE HORSESHOE CRAB).//P81281  
 F-PLACE3000477//MUSCARINIC TOXIN 7 (MT-7).//0.13:55:32//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P80970  
 F-PLACE4000009//MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) (FRAGMENT).//7.0e-19:180:27//HOMO SAPIENS (HUMAN).//P35749  
 55 F-PLACE4000014//X-LINKED HELICASE II (X-LINKED NUCLEAR PROTEIN) (XNP).//3.2e-15:193:30//HOMO SAPIENS (HUMAN).//P46100  
 F-PLACE4000034//BRIDE OF SEVENLESS PROTEIN PRECURSOR.//0.0024:97:29//DROSOPHILA MELA-

NOGASTER (FRUIT FLY).//P22815  
 F-PLACE4000049!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.8e-32:79:75//HOMO SAPIENS (HUMAN).//  
 P39194  
 F-PLACE4000052//ATP-BINDING CASSETTE TRANSPORTER 1.//2.2e-99:178:97//MUS MUSCULUS  
 (MOUSE).//P41233  
 5 F-PLACE4000063//IMMEDIATE-EARLY PROTEIN //0.0017:159:25//HERPESVIRUS SAIMIRI (STRAIN 11).//  
 Q01042  
 F-PLACE4000089  
 F-PLACE4000093  
 10 F-PLACE4000100!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.5e-14:68:60//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-PLACE4000106//1A PROTEIN[CONTAINS: HELICASE; METHYLTRANSFERASE].//1.0:46:41//BROAD BEAN  
 MOTTLE VIRUS //Q00020  
 F-PLACE4000128//HYPOTHETICAL PROTEIN E-115.//0.00020:101:30//HUMAN ADENOVIRUS TYPE 2.//  
 15 P03290  
 F-PLACE4000129//CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) (14.9 KD PANCORNULIN).//  
 0.15:57:31//HOMO SAPIENS (HUMAN).//P22528  
 F-PLACE4000131  
 F-PLACE4000147//COMPETENCE PHEROMONE PRECURSOR.//1.0:45:24//BACILLUS SUBTILIS.//P45453  
 20 F-PLACE4000156//ZINC FINGER PROTEIN 136.//2.1e-88:194:59//HOMO SAPIENS (HUMAN).//P52737  
 F-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//0.083:148:26//HOMO SAPIENS (HU-  
 MAN).//P52746  
 F-PLACE4000211//CALPHOTIN.//0.20:43:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q02910  
 F-PLACE4000222!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-05:20:85//HOMO SAPIENS (HUMAN).//  
 25 P39188  
 F-PLACE4000230//DIHYDROFOLATE REDUCTASE (EC 1.5.1.3) / THYMIDYLATE SYNTHASE (EC 2.1.1.45)  
 (DHFR-TS).//1.0:96:28//TRYPANOSOMA BRUCEI BRUCEI.//Q27783  
 F-PLACE4000233  
 F-PLACE4000247//METALLOTHIONEIN (MT).//1.0e-05:34:41//PLEURONECTES PLATESSA (PLAICE).//  
 30 P07216  
 F-PLACE4000250//VPU PROTEIN (ORF-X PROTEIN) (UPX PROTEIN).//0.99:33:42//CAPRINE ARTHRITIS EN-  
 CEPHALITIS VIRUS (CAEV).//P31834  
 F-PLACE4000252//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.42:24:45//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY).//Q01643  
 35 F-PLACE4000259//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-).//3.5e-09:189:32//SACCHAROMYCES  
 CEREVISIAE (BAKER'S YEAST).//P32639  
 F-PLACE4000261//PEREGRIN (BR140 PROTEIN).//5.0e-11:103:37//HOMO SAPIENS (HUMAN).//P55201  
 F-PLACE4000269//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.037:181:25//SACCHARO-  
 MYCES CEREVISIAE (BAKER'S YEAST).//P25386  
 40 F-PLACE4000270//COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21).//1.0:46:39//MUS MUSCULUS  
 (MOUSE).//P70375  
 F-PLACE4000300//60S RIBOSOMAL PROTEIN L32.//0.81:28:46//THERMUS AQUATICUS (SUBSP. THER-  
 MOPHILUS).//P80339  
 F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (RAPAMYCIN TARGET PROTEIN).//  
 45 1.6e-29:44:93//HOMO SAPIENS (HUMAN).//P42345  
 F-PLACE4000323  
 F-PLACE4000326//PARATHYMOSIN.//0.0018:54:48//HOMO SAPIENS (HUMAN).//P20962  
 F-PLACE4000344//EPIDERMAL GROWTH FACTOR (EGF) (FRAGMENT).//0.97:28:42//SUS SCROFA (PIG).//  
 Q00968  
 50 F-PLACE4000367//NEUROTOXIN 1 (TOXIN SHP-I) (SHNA) (NEUROTOXIN SHI).//1.0:33:36//STOICHAETIS  
 HELIANTHUS (CARRIBEAN SEA ANEMONE) (STICHODACTYLA HELIANTHUS).//P19651  
 F-PLACE4000369//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.071:42:42//SORGHUM  
 VULGARE (SORGHUM).//P24152  
 F-PLACE4000379!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-16:54:77//HOMO SAPIENS (HUMAN).//  
 55 P39193  
 F-PLACE4000387//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR.//0.25:21:52//HOR-  
 DEUM VULGARE (BARLEY), AND SECALE CEREALE (RYE).//P25877  
 F-PLACE4000392//FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE)

(FRAGMENT).//0.91:36:50//YERSINIA PSEUDOTUBERCULOSIS.//Q05338  
 F-PLACE4000401//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.4e-29:96:67//HOMO SAPIENS (HUMAN).//  
 P39194  
 F-PLACE4000411//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.3e-18:41:73//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-PLACE4000431//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-).//5.4e-21:237:33//SACCHAROMYCES  
 CEREVISIAE (BAKER'S YEAST).//P32639  
 F-PLACE4000445//HYPOTHETICAL 99.7 KD PROTEIN IN SDL1 5'REGION PRECURSOR.//0.00081:210:28//  
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40442  
 F-PLACE4000450//TRANSCRIPTION FACTOR HBP-1A (HISTONE-SPECIFIC TRANSCRIPTION FACTOR  
 HBP1).//0.020:87:33//TRITICUM AESTIVUM (WHEAT).//P23922  
 F-PLACE4000465//METALLOTHIONEIN-IL (MT-1L) (MT1X).//0.20:18:38//HOMO SAPIENS (HUMAN).//P80297  
 F-PLACE4000487//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.5e-19:73:52//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-PLACE4000489  
 F-PLACE4000494//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//0.17:130:30//MUS MUSCULUS  
 (MOUSE).//Q03173  
 F-PLACE4000521//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS REVERSE TRANSCRIPTASE  
 (EC 2.7.7.49); ENDONUCLEASE] (FRAGMENT).//3.0e-05:50:36//MUS MUSCULUS (MOUSE).//P10400  
 F-PLACE4000522//NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR.//1.8e-45:231:47//  
 RATTUS NORVEGICUS (RAT).//Q07008  
 F-PLACE4000548//CYTOCHROME C-551 (C551).//0.96:50:34//ECTOTHIORHODOSPIRA HALOPHILA.//  
 P00122  
 F-PLACE4000558//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF (EC 3.1.2.15) (UBIQUITIN  
 THIOLESTERASE FAF) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF) (DEUBIQUITINATING EN-  
 ZYME FAF) (FAT FACETS PROTEIN).//1.6e-28:223:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//P55824  
 F-PLACE000581//P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)  
 (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).//9.7e-11:166:281//HOMO  
 SAPIENS (HUMAN).//P16109  
 F-PLACE4000590//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE  
 (EC 2.7.7.49); ENDONUCLEASE].//1.6e-17:134:35//GIBBON APE LEUKEMIA VIRUS.//P21414  
 F-PLACE4000593//GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R).//1.0:54:29//RATTUS  
 NORVEGICUS (RAT).//P30969  
 F-PLACE4000612//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12;  
 CORE SHELL PROTEIN P30].//2.6e-14:221:32//MOLONEY MURINE SARCOMA VIRUS (STRAIN TS110).//  
 P32594  
 F-PLACE4000638//HYPOTHETICAL 9.3 KD PROTEIN IN NRDB-INAA INTERGENIC REGION.//0.65:37:40//ES-  
 CHERICHA COLI.//P37910  
 F-PLACE4000650//ZINC FINGER PROTEIN 16 (ZINC FINGER PROTEIN KOX9) (FRAGMENT).//1.0:33:33//HO-  
 MO SAPIENS (HUMAN).//P17020  
 F-PLACE4000654  
 F-PLACE4000670//HYPOTHETICAL 44.1 KD PROTEIN IN RPB5-CDC28 INTERGENIC REGION.//1.6e-07:161:  
 25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33313  
 F-SKNMC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//7.4e-15:223:  
 31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q06100  
 F-SKNMC1000013//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (CBF-2) (T-14-6).//0.0013:128:  
 35//GALLUS GALLUS (CHICKEN).//Q98937  
 F-SKNMC1000046//CUTICLE COLLAGEN 1.//0.0010:154:33//CAENORHABDITIS ELEGANS.//P08124  
 F-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-  
 TRAL PROTEINASE) (CANP) (M-TYPE).//3.2e-41:87:98//HOMO SAPIENS (HUMAN).//P17655  
 F-SKNMC1000091//NTAK PROTEIN (NEURAL- AND THYMUS- DERIVED ACTIVATOR FOR ERBB KINASES).//  
 0.0032:154:35//HOMO SAPIENS (HUMAN).//O14511  
 F-THYRO1000017//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXI-  
 DASE).//1.6e-23:124:37//CAENORHABDITIS ELEGANS.//Q20939  
 F-THYRO1000026//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.0e-13:54:66//HOMO SAPIENS (HUMAN).//  
 P39192  
 F-THYRO1000034//HYPOTHETICAL 10.4 KD PROTEIN.//0.16:44:34//HEPATITIS B VIRUS (SUBTYPE AYW).//  
 P03163

- F-THYRO1000035//CAMPATH-1 ANTIGEN PRECURSOR (CD52 ANTIGEN) (CDW52) (CAMBRIDGE PATHOL-  
OGY 1 ANTIGEN).//0.83:59:37//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MON-  
KEY).//P32763
- 5 F-THYRO1000040//60S RIBOSOMAL PROTEIN L37 (FRAGMENT).//0.25:23:39//BOS TAURUS (BOVINE).//  
P79244
- F-THYRO1000070//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//2.3e-11:133:36//ORYGIA PSEUDOTSUGA-  
TA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341
- 10 F-THYRO1000072//C-PROTEIN, SKELETAL MUSCLE SLOW-ISOFORM.//1.5e-14:205:29//HOMO SAPIENS  
(HUMAN).//Q00872
- F-THYRO1000085
- F-THYRO1000092//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.063:59:33//HOMO SA-  
PIENS (HUMAN).//P49901
- 15 F-THYRO1000107
- F-THYRO1000111//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.0e-58:110:67//NYCTICEBUS COU-  
CANG (SLOW LORIS).//P08548
- F-THYRO1000121//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//2.6e-06:134:35//MUS  
MUSCULUS (MOUSE).//Q62203
- F-THYRO1000124//TENECIN 3 PRECURSOR.//0.047:76:35//TENEbrio MOLITOR (YELLOW MEALWORM).//  
Q27270
- 20 F-THYRO1000129//FBROSIN (FRAGMENT).//0.35:43:34//MUS MUSCULUS (MOUSE).//Q60791
- F-THYRO1000132//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!.//8.7e-14:104:42//HOMO SAPIENS (HUMAN).//  
P39188
- F-THYRO1000156
- 25 F-THYRO1000163//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!.//3.7e-20:71:71//HOMO SAPIENS (HUMAN).//  
P39189
- F-THYRO1000173//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN  
AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN  
ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//6.7e-88:216:76//MUS MUSCULUS (MOUSE).//P35585
- 30 F-THYRO1000186//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!.//2.9e-24:72:77//HOMO SAPIENS (HUMAN).//  
P39192
- F-THYRO1000187
- F-THYRO1000190//PROTEIN TRANSPORT PROTEIN SEC61 BETA 2 SUBUNIT.//0.060:50:42//SACCHARO-  
MYCES CEREVISIAE (BAKER'S YEAST).//P52871
- 35 F-THYRO1000197
- F-THYRO1000199//HYPOTHETICAL 49.8 KD PROTEIN D2007.5 IN CHROMOSOME III.//2.0e-06:88:35//  
CAENORHABDITIS ELEGANS.//34379
- F-THYRO1000206
- 40 F-THYRO1000221
- F-THYRO1000241//HYPOTHETICAL 11.8 KD PROTEIN IN HE65-PK2 INTERGENIC REGION.//1.0:51:35//  
AUTOGRAPH CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41661
- F-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//7.4e-37:137:36//HOMO SA-  
PIENS (HUMAN).//P51523
- 45 F-THYRO1000253//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.11:21:52//HO-  
MO SAPIENS (HUMAN).//P30808
- F-THYRO1000270//WDNM1 PROTEIN PRECURSOR.//0.40:52:32//MUS MUSCULUS (MOUSE).//Q62477
- F-THYRO1000279//BETA CRYSTALLIN A4.//0.97:64:26//BOS TAURUS (BOVINE).//P11842
- F-THYRO1000288//POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC  
ENDOPROTEASE 1) (PPSEP 1).//3.4e-48:142:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//  
Q10071
- 50 F-THYRO1000320//ZINC FINGER PROTEIN 14 (ZFP-14) (KROX-9 PROTEIN) (FRAGMENT).//0.87:35:45//MUS  
MUSCULUS (MOUSE).//P10755
- F-THYRO1000327//HYPOTHETICAL 64.7 KD PROTEIN F26E4.11 IN CHROMOSOME I.//0.00010:75:26//  
CAENORHABDITIS ELEGANS.//P90859
- 55 F-THYRO1000343//CHROMOGRANIN A PRECURSOR (CGA) [CONTAINS: PANCREASTATIN; BETA-GRANIN;  
WE-14].//0.88:107:26//MUS MUSCULUS (MOUSE).//P26339
- F-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN.//4.6e-25:49:81//MUS MUSCULUS (MOUSE).//  
P17563
- F-THYRO1000368//LOCOMOTION-RELATED PROTEIN HIKARU GENKI PRECURSOR.//1.0:136:26//DRO-

SOPHILA MELANOASTER (FRUIT FLY).//Q09101

F-THYRO1000381//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10].//0.032:99:35//SIMIAN SARCOMA VIRUS.//P03330

F-THYRO1000387//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.90:46:30//HALICHOERUS GRYPUS (GRAY SEAL).//P38592

F-THYRO1000394//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.00019:48:37//HOMO SAPIENS (HUMAN).//P22531

F-THYRO1000395//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-33:186:38//DROSOHILA MELANOASTER (FRUIT FLY).//Q04652

F-THYRO1000401//50S RIBOSOMAL PROTEIN L7/L12 (FRAGMENT).//0.57:67:31//STAPHYLOCOCCUS AUREUS.//P48860

F-THYRO1000438//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:42:38//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//P15997

F-THYRO1000452//BACTERIOCIN CARNOBACTERIOCIN A PRECURSOR (PISCICOLIN 61).//0.31:34:44//CARNOBACTERIUM PISCICOLA.//P38578

F-THYRO1000471//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.1e-31:94:72//HOMO SAPIENS (HUMAN).//P39194

F-THYRO1000484//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.9e-08:30:86//HOMO SAPIENS (HUMAN).//P39195

F-THYRO1000488//EARLY NODULIN 55-2 PRECURSOR (N-55-2) (NODULIN-315).//0.93:98:27//GLYCINE MAX (SOYBEAN).//Q02917

F-THYRO1000501//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//2.4e-51:198:50//MUS MUSCULUS (MOUSE).//P15533

F-THYRO1000502//HUNCHBACK PROTEIN (FRAGMENT).//0.84:41:43//APIS MELLIFERA (HONEYBEE).//P31504

F-THYRO1000505//HYPOTHETICAL BHLF1 PROTEIN.//0.99:231:33//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-THYRO1000558//ANTITHROMBIN-III PRECURSOR (ATIII) (FRAGMENT).//0.47:58:37//GALLUS GALLUS (CHICKEN).//Q03352

F-THYRO1000569//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.00048:64:42//RATTUS NORVEGICUS (RAT).//P02454

F-THYRO1000570//HYPOTHETICAL 11.6 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION.//0.94:61:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39725

F-THYRO1000585//SPLICING FACTOR, ARGININE/SERINE-RICH 6 (PRE-MRNA SPLICING FACTOR SRP55).//0.050:104:36//HOMO SAPIENS (HUMAN).//Q13247

F-THYRO1000596//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP34.5).//0.99:37:40//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN MGH-10).//P37319

F-THYRO1000602//EAMZP30-47 PROTEIN (FRAGMENT).//0.88:61:34//EIMERIA ACERVULINA.//P21959

F-THYRO1000605//SUPPRESSOR PROTEIN SRP40.//0.0016:116:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583

F-THYRO1000625//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.4e-33:88:78//HOMO SAPIENS (HUMAN).//P39194

F-THYRO1000637//METALLOTHIONEIN A (MT A).//1.0:23:43//SPARUS AURATA (GILT HEAD SEA BREAM).//P52727

F-THYRO1000641//PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN.//0.99:26:46//CYANIDIUM CALDARIUM (GALDIERIA SULPHURARIA).//O19925

F-THYRO1000658//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.5e-49:116:69//HOMO SAPIENS (HUMAN).//P39189

F-THYRO1000662//DNA-DAMAGE-INDUCIBLE PROTEIN P.//3.7e-15:119:43//ESCHERICHIA COLI.//Q47155

F-THYRO1000666//KINESIN-LIKE PROTEIN KLP1.//1.0e-44:232:41//CHLAMYDOMONAS REINHARDTII.//P46870

F-THYRO1000676//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.1e-15:144:39//HOMO SAPIENS (HUMAN).//P39193

F-THYRO1000684//HYPOTHETICAL 73.5 KD PROTEIN IN SCS3-RPS2 INTERGENIC REGION.//0.00033:84:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53129

F-THYRO1000699//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/0.97:20:85//HOMO SAPIENS (HUMAN).//P39192

F-THYRO1000712//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.2e-10:69:59//HOMO SAPIENS (HUMAN).//

P39188  
 F-THYRO1000715//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H]//4.6e-10:204:32//HOMO SAPIENS (HUMAN).//P04280  
 F-THYRO1000734  
 5 F-THYRO1000748//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8e-46:130:70//HOMO SAPIENS (HUMAN).//O43295  
 F-THYRO1000756//ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC 2.4.99.-) (ST6GALNACII) (STY).//1.1e-06:95:31//RATTUS NORVEGICUS (RAT).//Q84686  
 10 F-THYRO1000777//CUTICLE COLLAGEN 2C (FRAGMENT).//0.0031:119:34//HAEMONCHUS CONTORTUS.//P16252  
 F-THYRO1000783//MYOSIN IC HEAVY CHAIN.//0.0014:121:37//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569  
 F-THYRO1000787//HUNCHBACK PROTEIN (FRAGMENT).//0.54:25:52//PHOLCUS PHALANGIOIDES.//Q02031  
 15 F-THYRO1000793//PRE-MRNA SPLICING FACTOR PRP9.//0.91:3 0:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P19736  
 F-THYRO1000796  
 F-THYRO1000805//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION.//0.081:31:38//HUMAN ADENOVIRUS TYPE 41.//P23691  
 20 F-THYRO1000815//ALU SUBFAMILY SX WARNING ENTRY !!!!!/6.0e-30:81:70//HOMO SAPIENS (HUMAN).//P39195  
 F-THYRO1000829//NEUROTOXIN III (BOM III).//0.022:32:34//BUTHUS OCCITANUS MARDOCHEI (MOROCCAN SCORPION).//P13488  
 F-THYRO1000843//HYPOTHETICAL 7.7 KD PROTEIN IN GENES 5-4 INTERGENIC REGION (ORF 109).//0.98:25:44//BACTERIOPHAGE P22.//P26750  
 25 F-THYRO1000852//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//7.3e-09:83:42//VOLVOX CARTERI.//P21997  
 F-THYRO1000855//ANTIFREEZE PEPTIDE 4 PRECURSOR.//1.0:54:35//PSEUDOPLEURONECTA AMERICANUS (WINTER FLOUNDER).//P02734  
 30 F-THYRO1000865//ALU SUBFAMILY J WARNING ENTRY!!!!/5.2e-17:66:57//HOMO SAPIENS (HUMAN).//P39188  
 F-THYRO1000895//ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.0e-12:58:62//HOMO SAPIENS (HUMAN).//P39189  
 F-THYRO1000916//ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.0e-32:101:69//HOMO SAPIENS (HUMAN).//P39189  
 35 F-THYRO1000926//NITROGEN FIXATION REGULATORY PROTEIN.//5.5e-05:108:27//KLEBSIELLA OXYTOCA.//P56267  
 F-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//3.9e-50:147:40//HOMO SAPIENS (HUMAN).//P32322  
 40 F-THYRO1000951//DIHYDROXYACETONE KINASE (EC 2.7.1.9) (GLYCERONE KINASE).//1.8e-31:136:56//CITROBACTER FREUNDII.//P45510  
 F-THYRO1000952//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.//2.4e-05:91:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170  
 F-THYRO1000974//MITOCHONDRIAL ATP-DEPENDENT RNA HELICASE SUV3 PRECURSOR.//1.0:35:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32580  
 45 F-THYRO1000975  
 F-THYRO1000983//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//1.3e-20:96:51//CAENORHABDITIS ELEGANS.//Q11076  
 F-THYRO1000984//GTP-BINDING ADP-RIBOSYLATION FACTOR HOMOLOG 1 PROTEIN.//0.011:76:34//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25160  
 50 F-THYRO1000988  
 F-THYRO1001003//HYPOTHETICAL 8.1 KD PROTEIN IN MSL-RPLQ INTERGENIC REGION.//0.97:60:31//ESCHERICHIA COLI.//P36675  
 F-THYRO1001031//ALU SUBFAMILY SX WARNING ENTRY !!!!!/9.5e-18:56:66//HOMO SAPIENS (HUMAN).//P39195  
 55 F-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//5.0e-13:126:35//HOMO SAPIENS (HUMAN).//P31948  
 F-THYRO1001062//ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.1e-35:97:79//HOMO SAPIENS (HUMAN).//

P39194  
F-THYRO1001093!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/6.4e-13:70:57//HOMO SAPIENS (HUMAN).//  
P39194  
5 F-THYRO1001100//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT).//4.2e-63:219:63//HOMO SAPIENS (HUMAN).//P98168  
F-THYRO1001120//SPICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.00068:160:31//HOMO SAPIENS (HUMAN).//Q15427  
F-THYRO1001121//VERY HYPOTHETICAL 20.6 KD PROTEIN C56F8.15 IN CHROMOSOME 1.//0.37:158:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10263  
10 F-THYRO1001133!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.3e-15:59:66//HOMO SAPIENS (HUMAN).//P39188  
F-THYRO1001134//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.00088:159:29//HOMO SAPIENS (HUMAN).//P10161  
F-THYRO1001142!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.0e-29:81:71//HOMO SAPIENS (HUMAN).//  
15 P39194  
F-THYRO1001173//CYTOCHROME C OXIDASE POLYPEPTIDE VIIS (EC 1.9.3.1).//0.88:51:35//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P20610  
F-THYRO1001177!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.0e-24:91:68//HOMO SAPIENS (HUMAN).//P39192  
20 F-THYRO1001189//MKR2 PROTEIN (ZINC FINGER PROTEIN 2).//7.3e-27:165:39//MUS MUSCULUS (MOUSE).//P08043  
F-THYRO1001204//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.67:42:42//HOMO SAPIENS (HUMAN).//P02811  
F-THYRO1001213!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.9e-16:61:68//HOMO SAPIENS (HUMAN).//  
25 P39194  
F-THYRO1001262!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-36:50:84//HOMO SAPIENS (HUMAN).//P39193  
F-THYRO1001271//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.62: 126:30//STREPTOMYCES FRADIAE.//P20186  
30 F-THYRO1001287//HYPOTHETICAL 91.2 KD PROTEIN IN RPS4B-SCH9 INTERGENIC REGION.//1.9e-26:208:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38888  
F-THYRO1001290//GIANT HEMOGLOBIN AIV CHAIN (FRAGMENT).//1.0:31:38//LAMELLIBRACHIA SP. (DEEP-SEA GIANT TUBE WORM).//P20413  
F-THYRO1001313//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5.//0.00042:105:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q92331  
35 F-THYRO1001320//COLLAGEN ALPHA 1(III) CHAIN.//0.27:57:38//BOS TAURUS (BOVINE).//P04258  
F-THYRO1001321!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.5e-20:74:64//HOMO SAPIENS (HUMAN).//P39188  
F-THYRO1001322//HYPOTHETICAL 7.2 KD PROTEIN.//0.66:49:30//VACCINIA VIRUS (STRAIN COPENHAGEN).//P21123  
40 F-THYRO1001347//TOXIN F-VIII PRECURSOR (TOXIN TA2) (TOXIN DAF8).//0.94:61:36//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P01404  
F-THYRO1001363!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.0025:23:73//HOMO SAPIENS (HUMAN).//P39188  
45 F-THYRO1001365//MERSACIDIN PRECURSOR.//0.35:38:42//BACILLUS SP. (STRAIN HIL-Y85/54728).//P43683  
F-THYRO1001374//PROTEIN VOLD.//1.6e-3: 140:31//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//O05729  
F-THYRO1001401!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/0.047:43:48//HOMO SAPIENS (HUMAN).//  
50 P39192  
F-THYRO1001403  
F-THYRO1001405//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.0068:26:42//HOMO SAPIENS (HUMAN).//P22531  
F-THYRO1001406//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.-.-).//3.1e-81:97:83//MUS MUSCULUS (MOUSE).//O70503  
55 F-THYRO1001411!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.9e-26:89:74//HOMO SAPIENS (HUMAN).//P39193  
F-THYRO1001426!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-09:55:61//HOMO SAPIENS (HUMAN).//



P39193  
 F-THYRO1001434//BETA-DEFENSIN 4 PRECURSOR (BNDB-4).//0.68.44:34//BOS TAURUS (BOVINE).//  
 P46162  
 F-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE  
 5 B) (NMHC-B).//3.8e-64:216:62//HOMO SAPIENS (HUMAN).//P35580  
 F-THYRO1001460/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.3e-29:88:75//HOMO SAPIENS (HUMAN).//  
 P39194  
 F-THYRO1001487//HOMEBOX PROTEIN HOX-B4 (HOX-2.6).//0.99:59:37//MUS MUSCULUS (MOUSE).//  
 10 P10284  
 F-THYRO1001534/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.4e-14:40:82//HOMO SAPIENS (HUMAN).//  
 P39194  
 F-THYRO1001537//HYPOTHETICAL 33.8 KD PROTEIN IN TWT1-FLO5 INTERGENIC REGION.//2.4e-07:142:  
 32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38892  
 F-THYRO1001541/////ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.98:26:61//HOMO SAPIENS (HUMAN).//  
 15 P39195  
 F-THYRO1001559//PROTEIN Q300.//2.6e-05:20:75//MUS MUSCULUS (MOUSE).//Q02722  
 F-THYRO1001570  
 F-THYRO1001573//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.033:71:36//MUS MUS-  
 CULUS (MOUSE).//P15265  
 20 F-THYRO1001584//SUPPRESSOR PROTEIN SRP40.//2.1e-05:188:27//SACCHAROMYCES CEREVISIAE  
 (BAKER'S YEAST).//P32583  
 F-THYRO1001595//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//6.1e-21:35:91//HO-  
 MO SAPIENS (HUMAN).//Q15404  
 F-THYRO1001602//TRK SYSTEM POTASSIUM UPTAKE PROTEIN TRKH.//1.0:57:42//HAEMOPHILUS INFLU-  
 25 ENZAE.//P44843  
 F-THYRO1001605//VENOM BASIC PROTEASE INHIBITORS IX AND VIIIb.//1.0:34:38//BUNGARUS FASCIA-  
 TUS (BANDED KRAIT).//P25660  
 F-THYRO1001617/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.0e-18:55:81//HOMO SAPIENS (HUMAN).//  
 P39194  
 30 F-THYRO1001637/////ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.00020:25:80//HOMO SAPIENS (HU-  
 MAN).//P39195  
 F-THYRO1001656//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.0091:54:42//MUS MUSCULUS  
 (MOUSE).//P05142  
 35 F-THYRO1001661//HYPOTHETICAL 21.1 KD PROTEIN IN SSR-SERA INTERGENIC REGION (O182).//0.033:  
 77:35//ESCHERICHIA COLI.//P09160  
 F-THYRO1001671//((2'-5')OLIGOADENYLATE SYNTHETASE 1 (EC 2.7.7.-) ((2'-5')OLIGO(A) SYNTHETASE 1)  
 (2-5A SYNTHETASE 1) (P46/P41) (E18/E16).//4.3e-34:207:34//HOMO SAPIENS (HUMAN).//P00973  
 F-THYRO1001673/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.9e-08:49:65//HOMO SAPIENS (HUMAN).//  
 P39194  
 40 F-THYRO1001703//HYPOTHETICAL 69.8 KD PROTEIN IN BDF1-SFP1 INTERGENIC REGION.//6.4e-16:134:  
 35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06053  
 F-THYRO1001706  
 F-THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).//2.7e-27:191:36//DROSOPHILA MELA-  
 NOGASTER (FRUIT FLY).//Q04652  
 45 F-THYRO1001738//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1) (PROTEIN KINASE  
 A INTERFERENCE PROTEIN).//0.0032:105:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36027  
 F-THYRO1001745  
 F-THYRO1001746//GENE 10 PROTEIN.//1.0:55:30//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15901  
 50 F-THYRO1001772/////ALU SUBFAMILY J WARNING ENTRY !!!!!/1.2e-05:41:63//HOMO SAPIENS (HUMAN).//  
 P39188  
 F-THYRO1001793//HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN CHROMOSOME III.//1.5e-26:161:42//  
 CAENORHABDITIS ELEGANS.//P41880  
 F-THYRO1001809//LATENCY-RELATED PROTEIN 2.//0.49:74:27//HERPES SIMPLEX VIRUS (TYPE 1 /  
 STRAIN F).//P17589  
 55 F-THYRO1001828//PROTEINASE INHIBITOR.//0.11:34:50//SOLANUM MELONGENA (EGGPLANT) (AUBER-  
 GINE).//P01078  
 F-THYRO1001854//ACYL-COA-BINDING PROTEIN HOMOLOG (ACBP) (DIAZEPAM BINDING INHIBITOR HO-  
 MOLOG) (DBI).//0.63:50:38//RANA RIDIBUNDA (LAUGHING FROG) (MARSH FROG).//P45883

- F-THYRO1001895!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.1e-09:72:47//HOMO SAPIENS (HUMAN).//P39188
- F-THYRO1001907//TRYPOMASTIGOTE DECAY-ACCELERATING FACTOR (T-DAF) (FRAGMENT).//0.79:36:44//TRYPANOSOMA CRUZI.//Q26327
- 5 F-VESEN1000122//HOMEOBOX PROTEIN HB9.//0.57:64:32//HOMO SAPIENS (HUMAN).//P50219
- F-Y79AA1000013//METALLOTHIONEIN B (MT-B).//0.034:35:48//SALMO SALAR (ATLANTIC SALMON).//P52720
- F-Y79AA1000033//CHOLECYSTOKININ.//0.97:49:30//PSEUDEMYN SCRIPTA (SLIDER TURTLE).//P80345
- 10 F-Y79AA1000037//DNA-BINDING PROTEIN BMI-1.//1.4e-23:80:60//HOMO SAPIENS (HUMAN).//P35226
- F-Y79AA1000059//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.0075:127:36//STREPTOMYCES FRADIAE.//P20186
- F-Y79AA1000065//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.022:135:29//HOMO SAPIENS (HUMAN).//P10162
- 15 F-Y79AA1000131//REGULATORY PROTEIN E2.//1.1e-05:175:26//HUMAN PAPILLOMAVIRUS TYPE 24.//P50770
- F-Y79AA1000181//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.4e-06:187:29//MUS MUSCULUS (MOUSE).//P05143
- F-Y79AA1000202//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//6.2e-09:47:53//OWENIA FUSIFORMIS.//P21260
- 20 F-Y79AA1000214//HISTONE H2A VARIANT.//1.7e-50:107:100//GALLUS GALLUS (CHICKEN).//P02272
- F-Y79AA1000230//GONADOLIBERIN I PRECURSOR (LHRH I) (LUTEINIZING HORMONE RELEASING HORMONE I) (GONADOTROPIN RELEASING HORMONE I) (GNRH I) (LULIBERIN I).//0.27:64:34//HOMO SAPIENS (HUMAN).//P01148
- 25 F-Y79AA1000231//HYPOTHETICAL 47.9 KD PROTEIN M021B04.12.//2.5e-72:277:53//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//O04658
- F-Y79AA1000258//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//2.8e-08:174:35//MUS MUSCULUS (MOUSE).//P05142
- F-Y79AA1000268//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.00020:176:33//RATTUS NORVEGICUS (RAT).//P13941
- 30 F-Y79AA1000313//HYPOTHETICAL 54.0 KD PROTEIN C32A3.1 IN CHROMOSOME III.//0.092:127:21//CAENORHABDITIS ELEGANS.//Q09260
- F-Y79AA1000328//SEL-10 PROTEIN.//5.3e-05:129:28//CAENORHABDITIS ELEGANS.//Q93794
- F-Y79AA1000342//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//1.0:73:30//OVIS ARIES (SHEEP).//P26372
- 35 F-Y79AA1000346//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.8e-95:205:83//BOS TAURUS (BOVINE).//P53620
- F-Y79AA1000349//ANTIFREEZE PEPTIDE 4 PRECURSOR.//0.036:37:54//PSEUDOPLEURONECTA AMERICANUS (WINTER FLOUNDER).//P02734
- 40 F-Y79AA1000355//HYPOTHETICAL 18.2 KD PROTEIN ZK632.13 IN CHROMOSOME III.//0.0031:106:28//CAENORHABDITIS ELEGANS.//Q10120
- F-Y79AA1000368//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.4e-16:208:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25343
- F-Y79AA1000405//LIGHT-HARVESTING PROTEIN B-800-850, ALPHA CHAIN C (ANTENNA PIGMENT PROTEIN, ALPHA CHAIN C) (LH II-C ALPHA).//0.98:50:30//RHODOSPIRILLUM RUBRUM.//P35103
- 45 F-Y79AA1000410!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.9e-20:62:79//HOMO SAPIENS (HUMAN).//P39194
- F-Y79AA1000420//HYPOTHETICAL 27.7 KD PROTEIN IN UME3-HDA1 INTERGENIC REGION.//1.4e-06:86:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53970
- 50 F-Y79AA1000469//HYPOTHETICAL 48.4 KD PROTEIN F4B9.5 IN CHROMOSOME III.//2.8e-34:211:40//CAENORHABDITIS ELEGANS.//P34426
- F-Y79AA1000480//HYPOTHETICAL 63.2 KD PROTEIN C1F3.09 IN CHROMOSOME I.//3.9e-15:90:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10414
- F-Y79AA1000538!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.37:41:48//HOMO SAPIENS (HUMAN).//P39195
- 55 F-Y79AA1000539//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.8e-21:190:37//HOMO SAPIENS (HUMAN).//Q08170
- F-Y79AA1000540//SPERM PROTAMINE P1.//0.00045:66:45//DASYURUS VIVERRINUS (SOUTHEASTERN QUOLL), AND DASYURUS HALLUCATUS.//P42135

- F-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) //1.6e-79:186.87//MUS MUSCULUS (MOUSE) //P17427
- 5 F-Y79AA1000574//AKLAVINONE C-11 HYDROXYLASE (EC 1.-.-) (FRAGMENT) //0.010:35.60//STREPTOMYCES PEUCETIUS //P32009
- F-Y79AA1000589//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION //4.5e-27:197.36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P28320
- F-Y79AA1000627//ZINC FINGER PROTEIN 134 //1.6e-34:191.35//HOMO SAPIENS (HUMAN) //P52741
- 10 F-Y79AA1000705//HYPOTHETICAL 128.5 KD HELICASE IN AT5-1TPD3 INTERGENIC REGION //8.7e-36:250:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P31380
- F-Y79AA1000734//PEROXISOMAL MEMBRANE PROTEIN PMP30A (PMP31) (PEROXIN-11A) //0.00037:108:27//CANDIDA BOIDINII (YEAST) //Q00316
- F-Y79AA1000748//HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III //1.0e-23:210:34//CAENORHABDITIS ELEGANS //Q09316
- 15 F-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP) //1.4e-53:156.68//MUS MUSCULUS (MOUSE) //Q061990
- F-Y79AA1000774//HYPOTHETICAL 77.9 KD PROTEIN IN RRN10-MCM2 INTERGENIC REGION //1.2e-11:231:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P38205
- F-Y79AA1000782//CUTICLE COLLAGEN 2 //0.012:56:35//CAENORHABDITIS ELEGANS //P17656
- 20 F-Y79AA1000784//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR //1.3e-08:82:39//PLASMODIUM LOPHURAE //P04929
- F-Y79AA1000794//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS) //0.043:13:53//HOMO SAPIENS (HUMAN) //P30808
- F-Y79AA1000800//PRIA PROTEIN PRECURSOR //0.031:94:34//LENTINULA EDODES (SHIITAKE MUSHROOM) (LENTINUS EDODES) //Q01200
- 25 F-Y79AA1000802//HYPOTHETICAL 67.4 KD PROTEIN IN RPS3-PSD1 INTERGENIC REGION //0.26:186:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P53882
- F-Y79AA1000805//AMP DEAMINASE (EC 3.5.4.6) (MYOADENYLATE DEAMINASE) //0.99:78:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //P50998
- 30 F-Y79AA1000824//HYPOTHETICAL 81.7 KD PROTEIN IN MOL1-NAT2 INTERGENIC REGION //3.4e-44:111:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P48234
- F-Y79AA1000827//HYPOTHETICAL BHLF1 PROTEIN //0.0046:187:33//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4) //P03181
- F-Y79AA1000833//TUBULIN ALPHA-1 CHAIN //1.0e-75:239:66//CRICETULUS GRISEUS (CHINESE HAMSTER) //P05209
- 35 F-Y79AA1000850//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N) //0.0078:57:31//HOMO SAPIENS (HUMAN) //P22532
- F-Y79AA1000962//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE //8.5e-11:241:26//GALLUS GALLUS (CHICKEN) //P10587
- 40 F-Y79AA1000966//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6) //0.69:122:31//TRYPANOSOMA BRUCEI BRUCEI //P24499
- F-Y79AA1000968//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR) //3.3e-102:211:93//RATTUS NORVEGICUS (RAT) //P70541
- F-Y79AA1000969//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR //1.0:67:38//GALLUS GALLUS (CHICKEN) //P02457
- 45 F-Y79AA1000976//INVOLUCRIN //0.99:66:31//CEBUS ALBIFRONS (WHITE-FRONTED CAPUCHIN) //P24709
- F-Y79AA1000985//PERICENTRIN //1.1e-24:116:59//MUS MUSCULUS (MOUSE) //P48725
- F-Y79AA1001023//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION //0.37:79:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P38250
- 50 F-Y79AA1001041//SPERMATID-SPECIFIC PROTEIN T1 [CONTAINS: SPERM PROTAMINE SP1] //0.93:43:39//SEPIA OFFICINALIS (COMMON CUTTLEFISH) //P80001
- F-Y79AA1001048//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCD) //1.5e-51:211:52//BOS TAURUS (BOVINE) //P48818
- F-Y79AA1001061//ALU SUBFAMILY SQ WARNING ENTRY !!!! //3.8e-25:85:69//HOMO SAPIENS (HUMAN) //P39194
- 55 F-Y79AA1001068//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN] //0.0015:207:33//MUS MUSCULUS (MOUSE) //P28481
- F-Y79AA1001077//ADULT-SPECIFIC RIGID CUTICULAR PROTEIN 11.9 (ACP 11.9) //0.99:36:41//ARANEUS DI-

- ADEMATUS (SPIDER).//P80515  
 F-Y79AA1001078//HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III.//1.0e-06:197:23//  
 CAENORHABDITIS ELEGANS.//P34492  
 F-Y79AA1001105//HOMEBOX PROTEIN OTX2.//2.9e-62:163:79//MUS MUSCULUS (MOUSE).//P80206  
 5 F-Y79AA1001145!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!0.024:42:59//HOMO SAPIENS (HUMAN).//  
 P39195  
 F-Y79AA1001167//HYPOTHETICAL 7.1 KD PROTEIN IN IAP2-VLF1 INTERGENIC REGION.//0.96:20:50//  
 AUTOGRAHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMPNV).//P41471  
 10 F-Y79AA1001177//HYPOTHETICAL BHLF1 PROTEIN.//3.9e-05:135:34//EPSTEIN-BARR VIRUS (STRAIN  
 B95-8) (HUMAN HERPESVIRUS 4).//P03181  
 F-Y79AA1001185//PUTATIVE CUTICLE COLLAGEN C09G5.5.//0.00017:93:38//CAENORHABDITIS ELE-  
 GANS.//Q09456  
 F-Y79AA1001211  
 F-Y79AA1001216//TENSIN.//0.012:134:32//GALLUS GALLUS (CHICKEN).//Q04205  
 15 F-Y79AA1001228//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//0.088:75:34//HOMO SAPIENS (HUMAN).//  
 Q02817  
 F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HY-  
 DROXYSTEROID DEHYDROGENASE 1).//1.1e-40:139:51//RATTUS NORVEGICUS (RAT).//P51657  
 F-Y79AA1001236//HYPOTHETICAL 34.7 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION.//2.0e-22:108:53//  
 20 SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38238  
 F-Y79AA1001281  
 F-Y79AA1001299//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.0022:49:44//MUS MUSCULUS  
 (MOUSE).//P05143  
 F-Y79AA1001312//50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR.//0.98:117:25//ARABIDOP-  
 25 SIS THALIANA (MOUSE-EAR CRESS).//P92959  
 F-Y79AA1001323//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUA-  
 MOUS CELL MARKER) (SRP).//0.082:44:40//SUS SCROFA (PIG).//P35323  
 F-Y79AA1001384//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII).//0.99:47:40//MUS MUSCULUS  
 (MOUSE).//P33622  
 30 F-Y79AA1001391//HOMEBOX PROTEIN HOX-A13 (HOX-1J).//9.8e-58:157:62//HOMO SAPIENS (HUMAN).//  
 P31271  
 F-Y79AA1001394//TRICHOHYALIN.//4.7e-08:121:36//HOMO SAPIENS (HUMAN).//Q07283  
 F-Y79AA1001402//ETS-DOMAIN TRANSCRIPTION FACTOR ERF.//0.0087:81:33//MUS MUSCULUS  
 (MOUSE).//P70459  
 35 F-Y79AA1001493//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//4.5e-21:125:44//  
 CAENORHABDITIS ELEGANS.//Q11076  
 F-Y79AA1001511//HYPOTHETICAL 86.6 KD PROTEIN IN PFK1-TDS4 INTERGENIC REGION.//2.3e-17:249:  
 31//SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53313  
 F-Y79AA1001533//DNA-DIRECTED RNA POLYMERASE I49 KD POLYPEPTIDE (EC 2.7.7.6) (A49).//0.0099:  
 40 155:23//SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q01080  
 F-Y79AA1001541  
 F-Y79AA1001548!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!1.1e-17:53:83//HOMO SAPIENS (HUMAN).//  
 P39192  
 F-Y79AA1001555//MAJOR SURFACE ANTIGEN.//0.046:62:29//HEPATITIS B VIRUS.//P31873  
 45 F-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL-  
 ACTIVATING ENZYME).//8.6e-11:144:31//ESCHERICHIA COLI.//P27550  
 F-Y79AA1001585//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.012:64:40//MUS MUS-  
 CULUS (MOUSE).//P15265  
 F-Y79AA1001594//CORNIFIN BETA.//0.61:88:31//MUS MUSCULUS (MOUSE).//Q09116  
 50 F-Y79AA1001603//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135)  
 (TAFII-130) (TAFII130).//0.024:170:30//HOMO SAPIENS (HUMAN).//Q00268  
 F-Y79AA1001613//ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1).//4.5e-09:136:27//HOMO  
 SAPIENS (HUMAN).//P28698  
 F-Y79AA1001647//HYPOTHETICAL 23.1 KD PROTEIN CY277.20C.//0.093:94:26//MYCOBACTERIUM TUBER-  
 55 CULOSIS.//P71779  
 F-Y79AA1001665//HOMEBOX PROTEIN DLX-2 (HOMEBOX PROTEIN TES-1).//0.79:90:26//MUS MUSCU-  
 LUS (MOUSE).//P40764  
 F-Y79AA1001679//LAMBDA-CRYSTALLIN.//1.6e-95:224:81//ORYCTOLAGUS CUNICULUS (RABBIT).//P14755

- F-Y79AA1001692//GERM CELL-LESS PROTEIN //3.5e-08:78:38//DROSOPHILA MELANOGASTER (FRUIT FLY) //Q01820
- F-Y79AA1001696//INSULIN //1.0:33:27//ANGUILLA ROSTRATA (AMERICAN EEL) //P42633
- 5 F-Y79AA1001705//HYPOTHETICAL BHLF1 PROTEIN //0.0013:192:33//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4) //P03181
- F-Y79AA1001711//PARATHYMOSIN (ZINC-BINDING 11.5 KD PROTEIN) //0.032:38:34//RATTUS NORVEGICUS (RAT) //P04550
- F-Y79AA1001781
- 10 F-Y79AA1001805//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP) //0.0063:128:30//HOMO SAPIENS (HUMAN) //P50552
- F-Y79AA1001827//SPERM PROTAMINE P1 //0.015:45:40//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONDELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM) //P35305
- F-Y79AA1001846/////ALU SUBFAMILY J WARNING ENTRY!!!!//2.4e-09:42:73//HOMO SAPIENS (HUMAN) //P39188
- 15 F-Y79AA1001848//KRUEPPEL PROTEIN (FRAGMENT) //1.8e-10:63:44//PSYCHODA CINEREA //Q02035
- F-Y79AA1001866//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10) //0.00036:108:37//MUS MUSCULUS (MOUSE) //Q61967
- F-Y79AA1001874//CX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTIVATED GLYCOPROTEIN-1 RECEPTOR) (CD134 ANTIGEN) //3.2e-07:100:35//HOMO SAPIENS (HUMAN) //P43489
- 20 F-Y79AA1001875//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD) //0.020:25:64//HOMO SAPIENS (HUMAN) //P20931
- F-Y79AA1001923//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT) //0.016:83:36//HOMO SAPIENS (HUMAN) //P10162
- 25 F-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C //8.1e-13:94:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //Q42643
- F-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42) //9.8e-39:143:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS) //P42743
- 30 F-Y79AA1002083//DNA-BINDING P52/P190 COMPLEX, 100 KD SUBUNIT (FRAGMENTS) //0.036:53:45//HOMO SAPIENS (HUMAN) //P30808
- F-Y79AA1002089//HYPOTHETICAL 49.1 KD PROTEIN F02A9.4 IN CHROMOSOME III //0.12:171:22//CAENORHABDITIS ELEGANS //P34384
- F-Y79AA1002093//MAX PROTEIN //3.1e-07:111:29//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO) //P52161
- 35 F-Y79AA1002103//SHORT NEUROTOXIN C //0.040:21:47//AIPYSURUS LAEVIS (OLIVE SEA SNAKE) //P19958
- F-Y79AA1002115//HYPOTHETICAL PROTEIN MJ0827 //0.84:68:30//METHANOCOCCUS JANNASCHII //Q58237
- 40 F-Y79AA1002125//HYPOTHETICAL 24.7 KD PROTEIN IN POM152-REC114 INTERGENIC REGION //3.4e-29:197:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P40206
- F-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1) //1.9e-19:120:45//DROSOPHILA MELANOGASTER (FRUIT FLY) //Q24133
- F-Y79AA1002204//TBX6 PROTEIN (T-BOX PROTEIN 6) //0.0011:162:32//MUS MUSCULUS (MOUSE) //P70327
- 45 F-Y79AA1002208//ANKYRIN //2.9e-08:231:29//MUS MUSCULUS (MOUSE) //Q02357
- F-Y79AA1002209//TYROSYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (EC 6.1.1.1) (TYROSINE-TRNA LIGASE) (TYRRS) //3.7e-23:170:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P48527
- F-Y79AA1002210//CORNIFIN A (SMALL PROLINE-RICH PROTEIN IA) (SPR-IA) (SPRK) //0.0061:69:31//HOMO SAPIENS (HUMAN) //P35321
- 50 F-Y79AA1002211/////ALU SUBFAMILY SP WARNING ENTRY!!!!//9.2e-10:43:62//HOMO SAPIENS (HUMAN) //P39193
- F-Y79AA1002220
- F-Y79AA1002229//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME I //1.9e-21:147:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //Q10264
- 55 F-Y79AA1002234
- F-Y79AA1002246//MYOSIN IC HEAVY CHAIN //0.00066:131:34//ACANTHAMOEBA CASTELLANII (AMOEBA) //P10569

F-Y79AA1002258//HYPOTHETICAL 103.9 KD PROTEIN ZK370.3 IN CHROMOSOME III.//4.3e-45:164:48//CAENORHABDITIS ELEGANS.//Q02328

F-Y79AA1002298//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.0063:99:31//HOMO SAPIENS (HUMAN).//P10161

5 F-Y79AA1002307

F-Y79AA1002311//HYPOTHETICAL 105.3 KD PROTEIN C01G6.5 IN CHROMOSOME III.//0.75:198:24//CAENORHABDITIS ELEGANS.//P46012

F-Y79AA1002351//CUTICLE COLLAGEN 34.//0.74:128:35//CAENORHABDITIS ELEGANS.//P34687

10 F-Y79AA1002361//GLC7-INTERACTING PROTEIN 2.//0.050:71:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40036

F-Y79AA1002399//NEUROMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (PP46) (B-50) (PROTEIN F1) (CALMODULIN-BINDING PROTEIN P-57).//1.0:89:30//CARASSIUS AURATUS (GOLDFISH).//P17691

F-Y79AA1002407//HYPOTHETICAL 31.5 KD PROTEIN IN YGP1-YCK2 INTERGENIC REGION.//3.7e-16:232:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53899

15 F-Y79AA1002416//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).//6.7e-72:162:84//HOMO SAPIENS (HUMAN).//P17812

F-Y79AA1002431//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.81:34:41//HOMO SAPIENS (HUMAN).//P22531

20 F-Y79AA1002433//CELL DIVISION CONTROL PROTEIN 68.//0.00024:85:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32558

F-Y79AA1002472//ZINC FINGER PROTEIN 35 (ZFP-35).//2.3e-60:217:44//MUS MUSCULUS (MOUSE).//P15620

F-Y79AA1002482//ZINC FINGER PROTEIN 141.//2.0e-31:90:55//HOMO SAPIENS (HUMAN).//Q15928

25 F-Y79AA1002487//HYPOTHETICAL 67.1 KD TRP-ASP REPEATS CONTAINING PROTEIN C57A10.05C IN CHROMOSOME I.//0.18:41:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87053

## Homology Search Result Data 2.

**[0300]** The result of the homology search of the GenBank using the clone sequence of 5'-end except EST and STS.

**[0301]** Data include

the name of clone,  
definition of the top hit data,  
the P-value: the length of the compared sequence: identity (%), and  
the Accession No. of the top hit data, as in the order separated by //.

**[0302]** Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds.//3.4e-106:695:86//L16953

40 F-HEMBA1000012//Caenorhabditis-elegans cosmid C16C10, complete sequence.//1.5e-24:374:66//Z46787

F-HEMBA1000020//Homo sapiens beta 2 gene.//3.5e-112:529:90//X02344

F-HEMBA1000030//Rattus norvegicus G protein-coupled receptor kinase-associated ADP ribosylation factor GT-Pase-activating protein (GIT1) mRNA, complete cds.//5.6e-124:743:88//AF085693

F-HEMBA1000042//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-25:529:65//AC004581

45 F-HEMBA1000046//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 125i3, WORKING DRAFT SEQUENCE.//3.2e-11:330:63//AL033528

F-HEMBA1000050//Homo sapiens DNA sequence from PAC 172K10 on chromosome 6q24. Contains STS, GSS and chromosome 6 fragment, complete sequence.//0.32:407:59//AL022477

F-HEMBA1000076//Homo sapiens full-length insert cDNA clone ZB97G06.//6.2e-135:594:98//AF086182

50 F-HEMBA1000111//CIT-HSP-229I1M18.TF CIT-HSP Homo sapiens genomic clone 229I1M18 genomic survey sequence.//2.8e-16:132:79//AQ004134

F-HEMBA1000129//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//8.6e-98:230:93//AC003104

F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds.//2.1e-167:791:98//AB018340

55 F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 protein, partial cds.//2.2e-44:242:96//AB018331

F-HEMBA1000156//Rattus norvegicus scaffold attachment factor B mRNA, complete cds.//1.1e-10:409:60//AF056324

F-HEMBA1000158//Homo sapiens CAGH44 mRNA, partial cds.//1.6e-35:365:73//U80741

- F-HEMBA1000168//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 321D2, WORKING DRAFT SEQUENCE.//0.99:290:61//AL031033
- F-HEMBA1000180//rat u2 small nuclear rna gene and flanks.//3.7e-18:112:98//K00034
- F-HEMBA1000185
- 5 F-HEMBA1000193//Human FMR1 gene, 5' end.//0.0012:191:67//L19476
- F-HEMBA1000201//Human Ini1 mRNA, complete cds.//2.0e-73:440:92//U04847
- F-HEMBA1000213//Plasmodium falciparum MAL3P7, complete sequence.//0.90:332:59//AL034559
- F-HEMBA1000216//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//4.8e-117:585:83//AF060194
- 10 F-HEMBA1000227//H.sapiens CpG island DNA genomic Mse1 fragment, clone 179h6, reverse read cpq179h6.rt1a.//1.9e-14:95:98//Z64921
- F-HEMBA1000231//H.sapiens CpG island DNA genomic Mse1 fragment, clone 90a5, reverse read cpq90a5.rt1a.//5.1e-34:186:97//Z56144
- F-HEMBA1000243//Human DNA sequence from PAC 440021 on chromosome X contains ESTs and STS.//4.1e-67:291:82//Z84481
- 15 F-HEMBA1000244//M.musculus Ank-1 mRNA for erythroid ankyrin.//0.029:316:59//X69065
- F-HEMBA1000251//Homo sapiens PAC clone DJ0988L12 from 7q11.23-q21.1, complete sequence.//0.35:467:60//AC004454
- F-HEMBA1000264
- 20 F-HEMBA1000280//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//8.9e-20:218:78//AC004825
- F-HEMBA1000282//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//4.2e-08:134:77//AC004617
- F-HEMBA1000288//345L5.TPB CIT978SKA1 Homo sapiens genomic clone A-345L05, genomic survey sequence.//1.1e-06:152:73//B17459
- 25 F-HEMBA1000290//Human ornithine decarboxylase gene, complete cds.//3.2e-11:507:62//M33764
- F-HEMBA1000302//CIT-HSP-2169N13.TF CIT-HSP Homo sapiens genomic clone 2169N13, genomic survey sequence.//5.4e-06:86:88//B90730
- F-HEMBA1000303//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//7.9e-111:701:86//AF030131
- 30 F-HEMBA1000304//HS\_3006\_A1\_A09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=17 Row=A, genomic survey sequence.//5.2e-40:240:92//AQ118226
- F-HEMBA1000307//Mus musculus mRNA for CDV-1R protein.//7.9e-127:815:84//Y10495
- F-HEMBA1000327//HS\_3124\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence.//1.4e-11:87:96//AQ187492
- 35 F-HEMBA1000333
- F-HEMBA1000338//Homo sapiens chromosome X, PAC 671D9, complete sequence.//4.0e-66:271:84//AF031078
- F-HEMBA1000351//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.64:334:60//AC004848
- F-HEMBA1000355//Pseudorabies virus serine/threonine kinase (ULPK) gene, partial cds and alkaline nuclease (AN) gene, complete cds.//0.017:313:63//U25056
- 40 F-HEMBA1000356//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//0.87:198:61//L40178
- F-HEMBA1000357//HS\_3194\_A1\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=G, genomic survey sequence.//6.5e-90:436:98//AQ173748
- F-HEMBA1000366//HS\_3027\_B2\_G06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=12 Row=N, genomic survey sequence.//0.0074:192:64//AQ128843
- 45 F-HEMBA1000369//Human DNA sequence from clone 1039K5 on chromosome 22q13.2-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//4.2e-106:133:99//AL031587
- F-HEMBA1000376//Homo sapiens chromosome 19, BAC CIT-B-39315 (BC301323), complete sequence.//1.6e-22:659:63//AC006116
- 50 F-HEMBA1000387//Homo sapiens chromosome 12p13.3 clone RPC111-264F23, WORKING DRAFT SEQUENCE, 90 unordered pieces.//3.2e-06:136:75//AC006122
- F-HEMBA1000390//Homo sapiens BAC clone RG119C02 from 7p15, complete sequence.//3.5e-111:284:95//AC004520
- 55 F-HEMBA1000392//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 173D1, WORKING DRAFT SEQUENCE.//1.8e-39:332:80//AL031984
- F-HEMBA1000396//Human Xq13.3' end of PAC 92E23 containing the X inactivation transcript (XIST) gene, complete sequence.//9.5e-35:364:73//U80460

- F-HEMBA1000411//Human Xp22 contig of 3 PACS (R7-39D12, R7-134G1, R7-185L21) from the Roswell Park Cancer Institute, complete sequence.//8.1e-18:424:64//U96409
- F-HEMBA1000418//Drosophila melanogaster Oregon-R mitochondrial A+T region.//0.0026:564:59//U11584
- 5 F-HEMBA1000422//Human DNA from chromosome 19 specific cosmid R30292, genomic sequence, complete sequence.//9.2e-14:232:70//AC003112
- F-HEMBA1000428//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//3.8e-37:408:69//AC004554
- F-HEMBA1000434//Caenorhabditis elegans cosmid Y48E1B, complete sequence.//0.73:454:57//Z93393
- F-HEMBA1000442
- 10 F-HEMBA1000455//RPC11-30J5.TV RPC1-11 Homo sapiens genomic clone RPC1-11-30J5, genomic survey sequence.//6.3e-06:62:96//B85188
- F-HEMBA1000459//Mus musculus hemin-sensitive initiation factor 2 alpha kinase mRNA, complete cds.//6.8e-70:580:79//AF028808
- F-HEMBA1000460//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//2.8e-154:746:98//AC004839
- 15 F-HEMBA1000464//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//4.8e-25:397:72//AC006213
- F-HEMBA1000469//CIT-HSP-2167P21.TF CIT-HSP Homo sapiens genomic clone 2167P21, genomic survey sequence.//4.0e-83:406:99//B94160
- F-HEMBA1000488//Homo sapiens Chromosome 22q11.2 PAC Clone p\_m11 In BCRL2-GGT Region, complete sequence.//4.2e-53:312:93//AC004033
- 20 F-HEMBA1000490//Campylobacter jejuni groES, groEL genes.//0.59:451:62//Y13334
- F-HEMBA1000491//Murine sarcoma virus (Harvey-strain) H-ras transforming p21 gene.//8.6e-06:338:58//X00740
- F-HEMBA1000501//Homo sapiens chromosome 17, clone hRPK.264\_B\_14, complete sequence.//9.4e-41:591:69//AC005884
- 25 F-HEMBA1000504//Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os).//4.0e-07:57:100//D13666
- F-HEMBA1000505
- F-HEMBA1000508//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0135005; HTGS phase 1, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.035:329:61//AC004661
- 30 F-HEMBA1000518//Caenorhabditis elegans cosmid C17H12.//0.96:425:58//AF045642
- F-HEMBA1000519//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//1.6e-53:300:89//AC004616
- F-HEMBA1000520//Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.7e-10:117:86//AC006006
- F-HEMBA1000523
- 35 F-HEMBA1000531//Mus musculus Hsp70-related NST-1 (hsc.1) mRNA, complete cds.//3.9e-35:290:80//U08215
- F-HEMBA1000534//Homo sapiens chromosome 17, clone hRPK.177\_H\_5, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.7e-36:328:77//AC005973
- F-HEMBA1000540//Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2 (ESSAII project).//0.057:265:63//AL033545
- 40 F-HEMBA1000542//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//1.2e-110:572:88//D89340
- F-HEMBA1000545//Human DNA from cosmid L27h9, Huntington's Disease Region, chromosome 4p16.3 contains CpG island.//7.5e-130:780:89//Z49237
- F-HEMBA1000555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134019, WORKING DRAFT SEQUENCE.//3.2e-175:838:98//AL034555
- 45 F-HEMBA1000557//CIT-HSP-2369F15.TF CIT-HSP Homo sapiens genomic clone 2369F15, genomic survey sequence.//2.8e-32:315:78//AQ074611
- F-HEMBA1000561//Rattus norvegicus Olf-1/EBF associated Zn finger protein Roaz mRNA, alternatively spliced form, complete cds.//3.4e-69:665:72//U92564
- F-HEMBA1000563//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.59:261:61//AC005504
- 50 F-HEMBA1000568//HS\_3243\_B2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3243 Col=24 Row=B, genomic survey sequence.//3.1e-54:323:91//AQ219628
- F-HEMBA1000569//M.musculus mRNA for GPI-anchored protein.//1.4e-19:440:61//X89571
- F-HEMBA1000575//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0016:557:57//AC005506
- 55 F-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//1.7e-11:132:79//AF045573
- F-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.3e-43:228:97//AJ007509



- F-HEMBA1000592//Mus musculus clone OST7314, genomic survey sequence.//7.3e-07:68.94//AF046733  
F-HEMBA1000594//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//8.7e-71:553.79//Z83822
- 5 F-HEMBA1000604//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 237J2, WORKING DRAFT SEQUENCE.//2.9e-21:158.75//AL021394  
F-HEMBA1000608//Homo sapiens mRNA for KIAA0456 protein, partial cds.//1.1e-118:561.99//AB007925  
F-HEMBA1000622//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//2.2e-28:426.70//AC004382
- 10 F-HEMBA1000636//Human CpG island sequence, clone Q28B8.//1.0e-15:274.68//D85773  
F-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds.//6.7e-137:639.99//AB014590  
F-HEMBA1000655//, complete sequence.//5.1e-83:685.80//AC005815  
F-HEMBA1000657//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//1.1e-91:597.84//U35776
- 15 F-HEMBA1000662//Homo sapiens clone DJ0853H20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.019:695.57//AC004907  
F-HEMBA1000673//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING DRAFT SEQUENCE.//1.5e-48:325.85//Z86090  
F-HEMBA1000682//Homo sapiens (subclone 5\_g5 from P1 H25) DNA sequence.//7.7e-61:615.74//L43411  
F-HEMBA1000686
- 20 F-HEMBA1000702  
F-HEMBA1000705//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0037:569.57//AC005507  
F-HEMBA1000719//Streptomyces coelicolor cosmid 1C2.//2.0e-09:483.62//AL031124  
F-HEMBA1000722//Toxoplasma gondii chloroplast, complete genome.//0.00058:762.57//U87145
- 25 F-HEMBA1000726//H. sapiens HLA-DRB1\*15 gene.//9.8e-49:189.89//X88791  
F-HEMBA1000727//CIT-HSP-387P22.TRB CIT-HSP Homo sapiens genomic clone 387P22, genomic survey sequence.//0.0054:206.67//B60158  
F-HEMBA1000747  
F-HEMBA1000749//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.3e-05:124.75//AL024509  
F-HEMBA1000752//Human Chromosome X, complete sequence.//5.9e-48:502.75//AC004073  
F-HEMBA1000769//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.011:179.67//AC005043
- 35 F-HEMBA1000773//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y59A8, WORKING DRAFT SEQUENCE.//0.070:231.63//Z98870  
F-HEMBA1000774//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//6.2e-40:385.75//AC004953  
F-HEMBA1000791
- 40 F-HEMBA1000817//Myrmica pilosula HI87-135 mitochondrion cytochrome b gene, partial cds.//0.99:244.58//U15678  
F-HEMBA1000822//Human DNA sequence from PAC 179D3, between markers DXS6791 and DXS8038 on chromosome X contains S10 GTP-binding protein, ESTs and CpG island.//0.033:294.62//Z81370  
F-HEMBA1000827//Borrelia burgdorferi (section 50 of 70) of the complete genome.//9.7e-05:463.58//AE001164
- 45 F-HEMBA1000843//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//3.0e-153:732.98//AL022394
- 50 F-HEMBA1000851//Rattus norvegicus glucocorticoid modulatory element binding protein 2 mRNA, complete cds.//1.6e-31:386.72//AF059273  
F-HEMBA1000852//Homo sapiens Xp22 bins 3-5 PAC RPC41-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//8.5e-115:455.98//AC005295  
F-HEMBA1000867
- 55 F-HEMBA1000869//Human DNA sequence from cosmid J138017, between markers DXS6791 and DXS8038 on chromosome X contains EST CA repeat and an endogenous retroviral like element.//6.6e-41:424.75//Z72519  
F-HEMBA1000870//Gnaptodon pumilio cytochrome oxidase II gene, partial cds; and tRNA-Asp, tRNA-His, and tRNA-Lys genes, complete sequence, mitochondrial genes for mitochondrial products.//0.0049:211.66//AF034598

- F-HEMBA1000872//CIT-HSP-2355D20.TF CIT-HSP Homo sapiens genomic clone 2355D20, genomic survey sequence.//3.7e-33:180:98//AQ059583
- F-HEMBA1000876//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 473B4, WORKING DRAFT SEQUENCE.//5.6e-37:262:72//Z83826
- 5 F-HEMBA1000908//Triticum aestivum low-affinity cation transporter (LCT1) mRNA, complete cds.//1.0:304:59//AF015523
- F-HEMBA1000910//M.musculus necdin mRNA, complete cds.//6.1e-08:256:61//M80840
- F-HEMBA1000918//Tetrahymena thermophila micronuclear developmentally eliminated sequence region.//0.13:232:63//U88158
- 10 F-HEMBA1000919//Gallus domesticus filamin mRNA, complete cds.//1.0:213:65//U00147
- F-HEMBA1000934//CIT-HSP-2053H24.TR CIT-HSP Homo sapiens genomic clone 2053H24, genomic survey sequence.//5.5e-11:275:64//B69224
- F-HEMBA1000942//Homo sapiens clone DJ0754G14, WORKING DRAFT SEQUENCE, 15 unordered pieces.//9.7e-05:78:83//AC004878
- 15 F-HEMBA1000943//Homo sapiens chromosome 17, clone hRPK.640\_1\_15, complete sequence.//5.8e-140:661:99//AC005324
- F-HEMBA1000946
- F-HEMBA1000960//Homo sapiens clone DJ1111F22, WORKING DRAFT SEQUENCE, 12 unordered pieces.//8.3e-16:181:75//AC004967
- 20 F-HEMBA1000968//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 69M21, WORKING DRAFT SEQUENCE.//4.4e-117:398:86//AL031735
- F-HEMBA1000971//H.sapiens CpG island DNA genomic MseI fragment, clone 182f4, forward read cpG182f4 ft1a.//1.5e-20:126:96//Z57528
- F-HEMBA1000972//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 1/11.//0.34:642:59//AB020858
- 25 F-HEMBA1000974//Homo sapiens clone DA0091H08, complete sequence.//5.1e-183:865:98//AC004817
- F-HEMBA1000975//Orf virus homologue of retroviral pseudoprotease gene, complete cds.//0.00065:391:62//M30023
- F-HEMBA10009851//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence.//3.4e-05:243:65//Z93929
- 30 F-HEMBA1000986//Homo sapiens DNA from chromosome 19-cosmid R31491, genomic sequence.//6.6e-06:508:61//AD000813
- F-HEMBA1000991//Homo sapiens mRNA for Hrs, complete cds.//1.2e-22:193:84//D64064 F-HEMBA1001007
- 35 F-HEMBA1001008//Human DNA sequence from clone 391O22 on chromosome 6p21.2-21.31 Contains pseudogenes similar to ribosomal protein, ESTs, GSSs, complete sequence.//7.8e-46:532:73//AL031577
- F-HEMBA1001009//Human mRNA for IgM heavy chain complete sequence.//0.97:369:59//X17115
- F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds.//4.4e-139:661:98//AB007937
- F-HEMBA1001019//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//1.6e-16:521:64//AC006213
- 40 F-HEMBA1001020//Homo sapiens chromosome 17, clone hRPK.178\_C\_3, complete sequence.//3.8e-50:367:72//AC005702
- F-HEMBA1001022
- F-HEMBA1001024//Homo sapiens T-cell receptor alpha delta locus from bases 1 to 250529 (section 1 of 5) of the Complete Nucleotide Sequence.//5.0e-23:378:69//AE000658
- 45 F-HEMBA1001026//Homo sapiens DNA sequence from PAC 435D1 on chromosome Xq25. Contains ESTs and STS.//7.6e-19:867:60//Z86064
- F-HEMBA1001043//HS\_2219\_B1\_A10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=19 Row=B, genomic survey sequence.//3.0e-15:124:88//AQ301521
- 50 F-HEMBA1001051//Human Chromosome X clone bWDX342, complete sequence.//4.8e-79:308:84//AC004072
- F-HEMBA1001052//Homo sapiens chromosome 17, clone hRPK.146\_P\_2, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.53:384:61//AC005341
- F-HEMBA1001059//Human N-acetylglucosamine 6-sulphatase (GALNS) gene, exon 10.//2.8e-26:397:71//U06084
- F-HEMBA1001060//Homo sapiens chromosome 17, clone hRPK.855\_D\_21 complete sequence.//0.98:280:62//AC006079
- 55 F-HEMBA1001071//Human mRNA for pro alpha 1 (III) collagen C-terminal propeptide.//1.1e-31:181:96//X01742
- F-HEMBA1001077//nuclear protein TIF1 [mice, mRNA, 3951 nt].//3.6e-13:338:65//S78219
- F-HEMBA1001080//Streptomyces coelicolor cosmid 1A9.//0.00012:364:63//AL034446

- F-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290I21 containing fur, fes, and alpha mannosidase IIX genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//8.5e-134:476:96//AC004586
- F-HEMBA1001088//Sequence 1 from patent US 5552529.//2.2e-71:303:78//I25863
- 5 F-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence.//8.9e-119:609:96//AC005105
- F-HEMBA1001099
- F-HEMBA1001109//Homo sapiens BAC clone RG318M05 from 7q22-q31.1, complete sequence.//2.4e-58:347:87//AC005250
- F-HEMBA1001121//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 90G24, WORKING DRAFT SEQUENCE.//3.4e-21:226:65//AL008723
- 10 F-HEMBA1001122//Plasmodium falciparum chromosome 2, section 20 of 73 of the complete sequence.//9.2e-07:732:57//AE001383
- F-HEMBA1001123//Homo sapiens full-length insert cDNA clone ZD38E12.//1.1e-11:231:68//AF086247
- F-HEMBA1001133//Homo sapiens clone DJ0856O24, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.011:163:69//AC004909
- 15 F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 protein, complete cds.//6.9e-72:527:77//AB018341
- F-HEMBA1001140//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.3e-120:578:98//AC005077
- F-HEMBA1001172//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.010:520:59//AC005507
- 20 F-HEMBA1001174//R. norvegicus (Sprague Dawley) ARL5 mRNA for ARF-like protein 5.//1.0e-59:565:73//X78604
- F-HEMBA1001197//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0037:151:70//AC004815
- F-HEMBA1001208//Human BAC clone RG264L19 from 7p15-p21, complete sequence.//7.4e-35:195:81//AC002410
- 25 F-HEMBA1001213//Homo sapiens clone DJ0892G19, complete sequence.//1.9e-171:826:98//AC004917
- F-HEMBA1001226//Homo sapiens clone DJ0850101, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.00010:557:57//AC006009
- F-HEMBA1001235//Homo sapiens chromosome 17, clone hRPK.601\_N\_13, complete sequence.//0.0086:372:58//AC005389
- 30 F-HEMBA1001247//H. sapiens CpG island DNA genomic MseI fragment, clone 11b11, reverse read cpg11b11.r11a.//2.0e-24:154:93//Z64441
- F-HEMBA1001257//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.9e-88:659:81//AF047020
- F-HEMBA1001265//Human 18S ribosomal RNA.//1.0e-32:180:97//X03205
- 35 F-HEMBA1001281
- F-HEMBA1001286//B. taurus mRNA for RF-36-DNA-binding protein.//7.7e-26:236:81//X15543
- F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.//5.5e-28:530:64//AC004131
- F-HEMBA1001294//Yeast mitochondrial aapl gene for ATPase subunit 8.//2.8e-15:722:60//X00960
- 40 F-HEMBA1001299//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence.//4.2e-24:288:76//AL031003
- F-HEMBA1001302//cDNA encoding a human homologue of a mouse novel polypeptide derived from stromal cell.//7.2e-121:439:96//E12260
- F-HEMBA1001303//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.011:637:56//AC005505
- 45 F-HEMBA1001310//HS\_3252\_B2\_B12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=24 Row=D, genomic survey sequence.//1.2e-16:166:82//AQ217054
- F-HEMBA1001319//CIT-HSP-2034J6.TF CIT-HSP Homo sapiens genomic clone 2034J6, genomic survey sequence.//0.33:256:59//B79408
- 50 F-HEMBA1001323//Homo sapiens proto-oncogene (Wnt-5a) mRNA, complete cds.//7.8e-30:165:99//L20861
- F-HEMBA1001326//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs(BAC end sequences) and a CA repeat polymorphism, complete sequence.//5.4e-19:347:68//AL021368
- 55 F-HEMBA1001327//CIT-HSP-2354E10.TR CIT-HSP Homo sapiens genomic clone 2354E10, genomic survey sequence.//0.012:152:65//AQ075713
- F-HEMBA1001330//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-103, com-

plete sequence.//0.0037:254:62//AL010208

F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//1.1e-103:516:97//AF057358

F-HEMBA1001361//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//1.7e-150:706:99//AC006241

F-HEMBA1001375//Streptomyces coelicolor cosmid 1E6.//1.0:375:59//AL033505

F-HEMBA1001377//HS\_3020\_B1\_D12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3020 Col=23 Row=H, genomic survey sequence.//0.00022:63:77//AQ105297

F-HEMBA1001383//Plasmodium falciparum chromosome 2, section 68 of 73 of the complete sequence.//0.00035:317:60//AE001431

F-HEMBA1001387//HS\_3039\_B1\_D01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=1 Row=H, genomic survey sequence.//5.0e-90:437:98//AQ155035

F-HEMBA1001388//Homo sapiens clone RG189J21, WORKING DRAFT SEQUENCE, 15 unordered pieces.//4.2e-47:159:89//AC005073

F-HEMBA1001391//Human DNA sequence from clone 409010 on chromosome 20q12 Contains CA repeat, GSS, STS, complete sequence.//2.0e-06:495:60//AL031256

F-HEMBA1001398//H.sapiens CpG island DNA genomic MseI fragment, clone 70d11, forward read cpg70d11.ft1b.//0.018:46:97//Z62591

F-HEMBA1001405//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING DRAFT SEQUENCE.//2.3e-74:623:71//AL034380

F-HEMBA1001407//Mus musculus domesticus Torino (Sry) gene, complete cds.//0.36:363:57//U03645

F-HEMBA1001411//Homo sapiens genomic DNA, 21q region, clone: S39BG29, genomic survey sequence.//8.4e-12:516:60//AG001050

F-HEMBA1001413

F-HEMBA1001415//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 410I8, WORKING DRAFT SEQUENCE.//0.98:177:64//AL031732

F-HEMBA1001432//Homo sapiens clone DJ0893M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.0e-177:859:97//AC006148

F-HEMBA1001433//Homo sapiens clone DJ0892G19, complete sequence.//2.0e-35:376:84//AC004917

F-HEMBA1001435//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//1.2e-74:284:84//AC005670

F-HEMBA1001442//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-66, complete sequence.//0.056:194:63//AL010138

F-HEMBA1001446//Homo sapiens chromosome 4 clone B150J4 map 4q25, complete sequence.//0.96:328:61//AC004047

F-HEMBA1001450

F-HEMBA1001454//Human DNA sequence from clone 598A24 on chromosome Xp11.1-11.23 Contains zinc finger X-linked proteins ZXDA, ZXDB, ESTs and STS, complete sequence.//2.0e-47:468:73//AL031115

F-HEMBA1001455//CIT978SK-32J2.TV CIT978SK Homo sapiens genomic clone 32J2, genomic survey sequence.//1.5e-05:223:65//B78859

F-HEMBA1001463//cSRL-69d1-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-69d1, genomic survey sequence.//5.1e-66:564:77//B05652

F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cds.//1.9e-102:489:99//AB011144

F-HEMBA1001478//HS\_2228\_A2\_B03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=6 Row=C, genomic survey sequence.//4.5e-40:275:88//AQ032041

F-HEMBA1001497//Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains ESTs, STSs, GSSs, a putative CpG island and genomic marker D6S1553, complete sequence.//7.7e-47:311:85//AL031133

F-HEMBA1001510//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-IP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//2.0e-130:699:93//U89337

F-HEMBA1001515//Homo sapiens chromosome 19, cosmid F24866, complete sequence.//4.1e-114:711:85//AC005794

F-HEMBA1001517//Homo sapiens BAC clone RG459N13 from 7p15, complete sequence.//5.7e-162:769:98//AC004549

F-HEMBA1001522//Caenorhabditis elegans cosmid ZK328.//8.6e-17:498:61//U50193

F-HEMBA1001526//Human DNA sequence from cosmid 444G9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs and CpG islands.//0.31:120:69//Z98258

F-HEMBA1001533  
F-HEMBA1001557//Chionocetes opilio (clone COP41) DNA microsatellite repeat regions.//7.0e-25:303:72//L49136

5 F-HEMBA1001566//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethyl-aniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//7.2e-18:805:60//AL021026

10 F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2).//1.1e-64:338:95//AJ225044

F-HEMBA1001570//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.1e-148:698:99//AC004453

F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.2e-173:678:99//AJ012449

15 F-HEMBA1001581//Homo sapiens clone DJ1158B01, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.30:484:59//AC004980

F-HEMBA1001585  
F-HEMBA1001589//Human BAC clone RG317G18 from 7q31, complete sequence.//0.98:197:63//AC002432

F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds.//8.2e-109:855:78//D50918

20 F-HEMBA1001608//RPCI11-72E2.TJ RPCI11 Homo sapiens genomic clone R-72E2, genomic survey sequence.//3.8e-05:235:64//AQ267131

F-HEMBA1001620//Oryza sativa RINO1 mRNA for myo-inositol phosphate synthase, complete cds.//3.8e-40:719:64//AB012107

F-HEMBA1001635//HS\_3208\_A1\_D07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3208 Col=13 Row=G, genomic survey sequence.//1.4e-15:120:90//AQ176944

25 F-HEMBA1001636//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.15:221:64//AC004216

F-HEMBA1001640//HS\_3253\_B2\_D03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3253 Col=6 Row=H, genomic survey sequence.//9.1e-52:278:95//AQ216058

30 F-HEMBA1001647//H. sapiens gene for plectin.//0.00052:629:61//Z54367

F-HEMBA1001651//Salmo salar DNA for a cryptic repeat.//7.9e-08:270:64//AJ012206

F-HEMBA1001655//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//5.9e-164:802:97//AC005368

35 F-HEMBA1001658//M.musculus COL3A1 gene for collagen alpha-1.//2.4e-30:742:62//X52046

F-HEMBA1001661//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.2e-144:682:99//AC005740

F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//6.1e-152:725:98//AF072247

40 F-HEMBA1001675//RPCI11-54F8.TV RPCI11 Homo sapiens genomic clone R-54F8, genomic survey sequence.//5.3e-75:341:85//AQ082126

F-HEMBA1001678//Homo sapiens Xp22 PAC RPCI1-167A22 (from Roswell Park Cancer Center) complete sequence.//8.4e-54:551:74//AC002349

45 F-HEMBA1001681  
F-HEMBA1001702//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//0.94:676:54//AE001398

F-HEMBA1001709//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 702J19, WORKING DRAFT SEQUENCE.//0.74:659:58//AL033531

50 F-HEMBA1001711//Lysiphibius melandricola NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.//3.0e-07:413:60//AF069178

F-HEMBA1001712//Homo sapiens BAC clone RG041H04 from 7q21-q22, complete sequence.//0.091:315:61//AC004519

F-HEMBA1001714//Rattus norvegicus mitochondrial ATPase inhibitor gene, complete cds.//1.6e-28:218:75//U12250

55 F-HEMBA1001718//HS\_3056\_A2\_H08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3056 Col=16 Row=O, genomic survey sequence.//2.0e-79:383:99//AQ106367

F-HEMBA1001723//HS\_2188\_A2\_D02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=4 Row=G, genomic survey sequence.//3.8e-28:174:94//AQ116793

F-HEMBA1001731//HS\_3021\_A1\_A11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3021 Col=21 Row=A, genomic survey sequence.//2.5e-11:420:62//AQ154658

- F-HEMBA1001734//Homo sapiens chromosome Y, clone 264.M.20, complete sequence.//0.00060:392.60//AC004617
- F-HEMBA1001744//HS\_3194\_A1\_D05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=G, genomic survey sequence.//5.8e-29:163.97//AQ252295
- 5 F-HEMBA1001745//Homo sapiens chromosome 9q34, clone 280C11, complete sequence.//0.66:627:59//AC002102
- F-HEMBA1001746//HS\_2163\_B1\_F04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2163 Col=7 Row=L, genomic survey sequence.//1.4e-16:238.70//AQ085995
- 10 F-HEMBA1001761//Genomic sequence from Mouse 9, complete sequence.//3.5e-52:198.86//AC002109
- F-HEMBA1001781
- F-HEMBA1001784//Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.5e-13:296.65//AC002099
- F-HEMBA1001791//Homo sapiens DNA from chromosome 19-cosmids R31158, R31874, and R28125, genomic sequence, complete sequence.//0.18:534.59//AF038458
- 15 F-HEMBA1001800//CrT-HFP-2049N5.TF CIT-HSP Homo sapiens genomic clone 2049N5, genomic survey sequence.//2.2e-40:335.80//AQ009222
- F-HEMBA1001803//M.musculus (Ba1b/C) P/L01 mRNA.//1.7e-25:286.74//Z31360
- F-HEMBA1001804//Mouse Interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.9e-58:358.89//M21977
- 20 F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//7.8e-174:809.98//AB007969
- F-HEMBA1001809//Bovine herpesvirus 1 complete genome.//9.0e-09:639.57//AJ004801
- F-HEMBA1001815
- F-HEMBA1001819//HS\_3079\_B1\_E04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079 Col=7 Row=J, genomic survey sequence.//1.4e-79:396.97//AQ186616
- 25 F-HEMBA1001820//Homo sapiens BAC clone GS165.15 from 7p15, complete sequence.//0.00026:436.60//AC005013
- F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds.//1.2e-40:510.65//AF064243
- F-HEMBA1001824//Homo sapiens expanded SCA7 CAG repeat.//6.1e-20:344.68//AF020275
- F-HEMBA1001835//Homo sapiens BAC clone RG017K18 from 7q31, complete sequence.//0.00094:553.58//AC005161
- 30 F-HEMBA1001844//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SEQUENCE, 35 unordered pieces.//1.2e-22:316.70//AC005867
- F-HEMBA1001847//M.musculus Zfp-29 gene for zinc finger protein.//5.3e-27:397.69//X55126
- F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds.//8.8e-184:865.98//AB014517
- 35 F-HEMBA1001864//Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence.//0.38:337.62//AC005395
- F-HEMBA1001866//Caenorhabditis elegans cosmid F48E3.//1.4e-10:224.63//U28735
- F-HEMBA1001869//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//6.7e-98:288.91//AC005065
- 40 F-HEMBA1001888//Human Chromosome 11p15.5 PAC clone pDJ915f1 containing KvLQT1 gene, complete sequence.//4.9e-114:476.84//AC003693
- F-HEMBA1001896//Bos taurus pyruvate dehydrogenase phosphatase regulatory subunit precursor, mRNA, complete cds.//2.2e-137:839.86//AF026954
- 45 F-HEMBA1001910//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence.//0.90:221.63//AC003065
- F-HEMBA1001912//HS\_2237\_A1\_C10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=19 Row=E, genomic survey sequence.//9.7e-76:364.100//AQ033732
- F-HEMBA1001913//Leishmania major chromosome 3 clone L4625 strain Friedlin, WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.00063:219.65//AC005766
- 50 F-HEMBA1001915//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 5/10.//0.00011:366.63//AB020873
- F-HEMBA1001918//Pneumocystis carinii gene for major surface glycoprotein MSG105, exon 1-2, complete cds.//0.00024:562.58//D82031
- F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//2.1e-184:855.99//AF000145
- 55 F-HEMBA1001939//Human DNA sequence from clone 395P12 on chromosome 1q24-25, Contains the TXGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2)

- pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.1e-42:380:80//AL022310  
 F-HEMBA1001940//Homo sapiens clone DJ109316, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-175:861:97//AC005629
- 5 F-HEMBA1001942//Homo sapiens chromosome 12p13.3 clone RPC1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//0.097:107:71//AC006057  
 F-HEMBA1001945//Drosophila F family transposable element F12 3' region.//0.94:140:65//X01934  
 F-HEMBA1001950//H. sapiens CpG island DNA genomic MseI fragment, clone 15b5, forward read cpq15b5.ft1q.//1.4e-27:168:95//Z54728
- 10 F-HEMBA1001960//Locusta migratoria mRNA for nAChR alpha1 subunit.//0.010:108:71//AJ000390  
 F-HEMBA1001962//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//9.7e-05:494:60//AC005507  
 F-HEMBA1001964  
 F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs, complete sequence.//9.6e-122:373:99//AL031178
- 15 F-HEMBA1001979//HIS\_3067\_B1\_A06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3067 Col=11 Row=B, genomic survey sequence.//0.43:193:64//AQ143506  
 F-HEMBA1001987//Plasmodium falciparum MAL3P6, complete sequence.//1.0:428:56//Z98551  
 F-HEMBA1001991//HIS\_2237\_A2\_G09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=18 Row=M, genomic survey sequence.//4.3e-05:240:64//AQ067283
- 20 F-HEMBA1002003//protein phosphatase 2C isoform [rats, liver, mRNA, 1950 nt].//2.7e-33:364:74//S90449  
 F-HEMBA1002008//WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00032:214:68//AC005948  
 F-HEMBA1002018
- 25 F-HEMBA1002022//Human p37NB mRNA, complete cds.//0.014:58:96//U32907  
 F-HEMBA1002035//Mouse transcriptional control element.//7.8e-07:200:69//M17284  
 F-HEMBA1002039//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//0.31:497:58//AL031053  
 F-HEMBA1002049//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//4.5e-42:532:63//AC005216
- 30 F-HEMBA1002084//Homo sapiens chromosome 19 cosmid F15386, genomic sequence, complete sequence.//0.81:435:59//AF025422  
 F-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//7.2e-130:769:87//U92703
- 35 F-HEMBA1002100//Homo sapiens PAC clone DJ0991G20, complete sequence.//1.3e-47:124:96//AC004943  
 F-HEMBA1002102//Xenopus laevis mRNA for xSox7 protein, complete cds.//2.7e-13:132:71//DB3649  
 F-HEMBA1002113//F.rubripes GSS sequence, clone 063K10bB4, genomic survey sequence.//0.029:142:66//Z88840
- 40 F-HEMBA1002119//Human Chromosome 11 pac pDJ113a5, complete sequence.//1.3e-14:515:62//AC000378  
 F-HEMBA1002125//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds.//0.98:222:61//AF031815  
 F-HEMBA1002139//Caenorhabditis elegans cosmid F55C9, complete sequence.//0.0081:371:60//Z81549  
 F-HEMBA1002144//Saccharomyces cerevisiae mitochondrion transfer RNA-Met (tRNA-Met) gene, oxil gene, and ORF1.//4.9e-06:341:61//L36888
- 45 F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds.//0.00017:353:62//AB018263  
 F-HEMBA1002151  
 F-HEMBA1002153//CITBI-E1-2519120. TR CITBI-E1 Homo sapiens genomic clone 2519120, genomic survey sequence.//8.5e-61:334:94//AQ277613
- 50 F-HEMBA1002160//Homo sapiens clone DJ1189D06, complete sequence.//8.5e-44:385:77//AC005232  
 F-HEMBA1002161//Coturnix coturnix slow myosin heavy chain 2 (qmyhc2) mRNA, partial cds.//2.1e-59:571:74//AF006829
- 55 F-HEMBA1002162//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//5.3e-53:698:67//AC006210  
 F-HEMBA1002166//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//1.2e-50:319:78//AL008712  
 F-HEMBA1002177//Homo sapiens BAC clone RG293F11 from 7q21-7q22, complete sequence.//2.5e-18:150:88//AC000666
- F-HEMBA1002185//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00066:456:59//AC004825

- F-HEMBA1002189//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.3e-23:176:77//AC005015
- F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds.//1.0:382:59//AB014589
- F-HEMBA1002199//Homo sapiens chromosome 4 clone B55B24 map 4q25, complete sequence.//1.8e-20:368:66//AC005150
- F-HEMBA1002204//HS\_2055\_A1\_H09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=17 Row=O, genomic survey sequence.//1.2e-06:178:65//AQ235350
- F-HEMBA1002212//S. cerevisiae chromosome IV reading frame ORF YDL101c.//0.035:345:60//Z74149
- F-HEMBA1002215//M. musculus mRNA for testin.//4.6e-80:504:87//X78989
- F-HEMBA1002226//Homo sapiens Xp22 bins 87-93 PAC RPC11-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.7e-63:336:74//AC003035
- F-HEMBA1002229//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//2.6e-39:311:81//AC006044
- F-HEMBA1002237//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//1.6e-12:397:64//AC004861
- F-HEMBA1002241
- F-HEMBA1002253
- F-HEMBA1002257//Homo sapiens diacylglycerol kinase iota (DCKI) mRNA, complete cds.//3.5e-151:731:97//AF061936
- F-HEMBA1002265//Human DNA sequence from cosmid N28H9 on chromosome 22q11.2-qter contains ESTs, STS and endogenous retrovirus.//1.3e-09:313:62//Z71183
- F-HEMBA1002267
- F-HEMBA1002270//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//0.069:495:58//AC006210
- F-HEMBA1002321//Homo sapiens PAC clone DJ0991O23, complete sequence.//0.019:564:58//AC004944
- F-HEMBA1002328//CIT-HSP-2387N15.TF.1 CIT-HSP Homo sapiens genomic clone 2387N15, genomic survey sequence.//1.8e-71:346:99//AQ240836
- F-HEMBA1002337//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence.//0.84:547:57//AB020754
- F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds.//2.4e-185:872:98//AB018314
- F-HEMBA1002348//CIT-HSP-2372K24.TR CIT-HSP Homo sapiens genomic clone 2372K24, genomic survey sequence.//9.1e-33:230:75//AQ110676
- F-HEMBA1002349//Plasmodium falciparum histidine-rich protein II (HRP II) gene, complete cds.//9.4e-06:504:57//U69551
- F-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//7.3e-188:872:99//AF092563
- F-HEMBA1002381//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11.//2.1e-20:262:72//AB020868
- F-HEMBA1002389//D. discoideum spore coat 60 (sp60) gene, 5' flank.//0.010:95:73//M34546
- F-HEMBA1002417//Canis familiaris ZO-3 (zo-3) mRNA, complete cds.//6.2e-120:767:85//AF023617
- F-HEMBA1002419//HS-1047-A1-F01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=1 Row=k, genomic survey sequence.//7.6e-06:117:66//B38165
- F-HEMBA1002430//HS\_3137\_B2\_F10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3137 Col=20 Row=L, genomic survey sequence.//1.6e-56:367:88//AQ148697
- F-HEMBA1002439//Dictyostellium discoideum actin 8 gene, 3' UTR.//0.67:129:64//M25216
- F-HEMBA1002458//Mus musculus REX-3 mRNA, complete cds.//1.1e-30:274:72//AF051347
- F-HEMBA1002460//Homo sapiens clone DJ1137M13, complete sequence.//4.0e-173:822:98//AC005378
- F-HEMBA1002462//Sequence 41 from patent US 5708157.//9.8e-51:519:73//I80067
- F-HEMBA1002469//Human mRNA for KIAA0122 gene, partial cds.//4.0e-108:603:92//D50912
- F-HEMBA1002475//Streptomyces coelicolor cosmid 2H4.//0.0068:626:57//AL031514
- F-HEMBA1002477//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//1.5e-40:349:78//AC005034
- F-HEMBA1002486
- F-HEMBA1002495//HS\_3218\_B1\_A12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=23 Row=B, genomic survey sequence.//1.0:179:67//AQ181410
- F-HEMBA1002498//Homo sapiens full-length insert cDNA clone ZD76B01.//1.4e-129:619:98//AF086404
- F-HEMBA1002503//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.9e-24:306:68//AC004873



- F-HEMBA1002508//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//2.9e-76:464.83//AC004799
- F-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//2.8e-157:738.98//AJ011972
- 5 F-HEMBA1002515//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 407F11, WORKING DRAFT SEQUENCE.//2.6e-07:307.64//AL022329
- F-HEMBA1002538//HS\_2185\_B2\_B04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2185 Col=8 Row=D, genomic survey sequence.//4.7e-37:339.78//AQ298315
- 10 F-HEMBA1002542//HS\_3197\_B2\_B10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=20 Row=D, genomic survey sequence.//3.2e-70:372.95//AQ188792
- F-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds.//3.5e-137:655.98//AF016903
- F-HEMBA1002552//Human Hep27 protein mRNA, complete cds.//8.8e-07:173.68//U31875
- F-HEMBA1002555//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.2e-15:628.60//AC004670
- 15 F-HEMBA1002558//Human Xp22 BAC CT-28515 (from CalTech/Research Genetics), PAC RPC11-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//2.3e-41:353.76//AC002366
- F-HEMBA1002561//Homo sapiens chromosome 17, clone HRPC29G21, complete sequence.//1.1e-39:538.66//AC003687
- 20 F-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//1.3e-140:457.99//AF075587
- F-HEMBA1002583//CIT-HSP-2321D3.TR CIT-HSP Homo sapiens genomic clone 2321D3, genomic survey sequence.//5.1e-79:385.99//AQ038102
- F-HEMBA1002590//Homo sapiens chromosome 17, clone hRPK.167\_N\_20, complete sequence.//1.9e-35:430.70//AC005940
- 25 F-HEMBA1002592//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//4.4e-19:303.71//Z93403
- F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds.//4.4e-175:820.99//AB011169
- F-HEMBA1002621//Homo sapiens PAC clone DJ0650P09 from 7q21, complete sequence.//0.14:353.58//AC004413
- 30 F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//2.9e-187:632.97//AB018351
- F-HEMBA1002628//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.5e-05:792.58//AC004153
- F-HEMBA1002629//Streptomyces coelicolor cosmid 1A9.//8.4e-08:576.58//AL034446
- 35 F-HEMBA1002645//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 153G14, WORKING DRAFT SEQUENCE.//5.6e-47:222.86//AL031118
- F-HEMBA1002651//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//3.8e-182:859.99//AC004839
- F-HEMBA1002659//Z. mobilis alcohol dehydrogenase I (adhA) gene, complete cds.//0.97:144.66//M32100
- 40 F-HEMBA1002661//Homo sapiens PAC clone DJ0698G21 from 7p21-p22, complete sequence.//1.3e-116:774.84//AC004535
- F-HEMBA1002666
- F-HEMBA1002678//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1137F22, WORKING DRAFT SEQUENCE.//5.7e-156:750.98//AL034421
- 45 F-HEMBA1002679//nbxb0002cC12r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0002F23r, genomic survey sequence.//4.3e-09:517.58//AQ051621
- F-HEMBA1002688//Herpes simplex virus type 2 (strain HG52), complete genome.//8.3e-20:651.61//Z86099
- F-HEMBA1002696//Mus musculus proteasome regulator PA28 beta subunit gene, complete cds.//7.6e-62:306.81//AF060195
- 50 F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds.//1.9e-10:327.62//AB007924
- F-HEMBA1002712
- F-HEMBA1002716//HS\_3064\_A1\_C10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=19 Row=E, genomic survey sequence.//8.4e-97:491.96//AQ142980
- F-HEMBA1002728//Homo sapiens chromosome 5, BAC clone 205e20 (LBNI.H170), complete sequence.//6.1e-21:217.77//AC004782
- 55 F-HEMBA1002730//Human platelet glycoprotein IIIa (GP1IIa) gene, exon 1.//0.57:125.67//M57481
- F-HEMBA1002742//RPC11-39J10.TP RPC11-11 Homo sapiens genomic clone RPC11-11-39J10, genomic survey sequence.//1.1e-86:414.99//AQ029102

- F-HEMBA1002746//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//7.1e-70:303.82//AC003694
- F-HEMBA1002748//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 410I8, WORKING DRAFT SEQUENCE.//0.096:212.62//AL031732
- 5 F-HEMBA1002750//Homo sapiens chromosome 5, PAC clone 170m10 (LBNL H89), complete sequence.//6.7e-40:232.70//AC004622
- F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds.//9.0e-177:834.98//AB011126
- F-HEMBA1002770//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.3e-140:840.88//E12829
- 10 F-HEMBA1002777//F.rubripes GSS sequence, clone 189C06dB12, genomic survey sequence.//1.1e-28:263.77//AL007965
- F-HEMBA1002779//CIT-HSP-233311.TF CIT-HSP Homo sapiens genomic clone 233311, genomic survey sequence.//1.8e-32:180.98//AQ036891
- F-HEMBA1002780//Homo sapiens PAC clone DJ0244J05 from 5q31, complete sequence.//7.0e-06:199.67//AC004592
- 15 F-HEMBA1002794//H.sapiens mRNA for protein kinase C mu.//0.00015:244.67//X75766
- F-HEMBA1002801//Plasmodium falciparum MAL3P2, complete sequence.//0.0010:534.57//AL034558
- F-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.1e-167:820.97//AF071185
- F-HEMBA1002816//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.1e-113:254.90//AC005043
- 20 F-HEMBA1002818//Cricetulus griseus H411 precursor (H411) mRNA, complete cds.//1.2e-122:760.86//AF046870
- F-HEMBA1002826//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//0.0055:235.65//AL022153
- F-HEMBA1002833//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//1.4e-170:744.99//AC004707
- 25 F-HEMBA1002850//Ephedrus persicae NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.//1.3e-05:334.59//AF069186
- F-HEMBA1002863//CIT-HSP-2323A16.TF CIT-HSP Homo sapiens genomic clone 2323A16, genomic survey sequence.//2.9e-140:750.93//AQ028419
- 30 F-HEMBA1002876//HS\_2270\_B1\_H03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=5 Row=F, genomic survey sequence.//0.44:163.64//AQ164031
- F-HEMBA1002886
- F-HEMBA1002896//Homo sapiens chromosome 5, P1 clone 793C5 (LBNL H58), complete sequence.//0.00015:277.61//AC005195
- 35 F-HEMBA1002921
- F-HEMBA1002924//CIT-HSP-2171H4.TR CIT-HSP Homo sapiens genomic clone 2171H4, genomic survey sequence.//0.0016:175.66//B89715
- F-HEMBA1002934//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//1.2e-169:797.98//AL031681
- 40 F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds.//4.9e-173:803.99//AB011148
- F-HEMBA1002937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 702J19, WORKING DRAFT SEQUENCE.//1.2e-163:411.99//AL033531
- F-HEMBA1002939//RPC111-74O14.TJ RPC111 Homo sapiens genomic clone R-74O14, genomic survey sequence.//1.7e-41:215.99//AQ266676
- 45 F-HEMBA1002944//RPC111-55C2.TV RPC111 Homo sapiens genomic clone R-55C2, genomic survey sequence.//1.7e-37:375.74//AQ082240
- F-HEMBA1002951//Homo sapiens chromosome 19, cosmid F20887, complete sequence.//0.00074:683.58//AC005578
- F-HEMBA1002954//RPC111-79F7.TV RPC111 Homo sapiens genomic clone R-79F7, genomic survey sequence.//6.1e-24:250.78//AQ284146
- 50 F-HEMBA1002968//HS\_2262\_B2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2262 Col=8 Row=N, genomic survey sequence.//0.99:270.60//AQ217059
- F-HEMBA1002970//RPC111-5L24.TV RPC111 Homo sapiens genomic clone RPC11-5L24, genomic survey sequence.//1.4e-10:189.71//B49289
- 55 F-HEMBA1002971//CIT-HSP-2363L16.TF CIT-HSP Homo sapiens genomic clone 2363L16, genomic survey sequence.//4.3e-21:181.80//AQ080538
- F-HEMBA1002973//Rattus norvegicus Wistar 3',5'-cyclic AMP phosphodiesterase (PDE4-10) gene, exon 10.//2.5e-40:257.89//U01290

- F-HEMBA1002997//CIT-HSP-2387H15.TF.1 CIT-HSP Homo sapiens genomic clone 2387H15, genomic survey sequence.//9.5e-17:128.92//AQ240797
- F-HEMBA1002999//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//3.1e-62:713.73//U20286
- 5 F-HEMBA1003021//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.5e-50:331.85//AC005484
- F-HEMBA1003033//Drosophila melanogaster, chromosome 3L, region 62A10-62B5, P1 clones DS02777, DS03222, DS02345, and DS04808, complete sequence.//2.6e-20:357.66//AC005557
- 10 F-HEMBA1003034//Human DNA sequence from 4PTEL, Huntington's Disease Region, chromosome 4p16.3//4.5e-60:415.73//Z95704
- F-HEMBA1003035//Homo sapiens chromosome Y, clone 264.M.20, complete sequence.//2.3e-05:591.57//AC004617
- F-HEMBA1003037//RPC111-88F2.TJ RPC111 Homo sapiens genomic clone R-88F2, genomic survey sequence.//0.68:230.80//AQ286677
- 15 F-HEMBA1003041//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//8.1e-128:550.94//AC004983
- F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds.//1.0e-164:777.98//AF054182
- F-HEMBA1003064//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.5e-07:744.59//AC005505
- 20 F-HEMBA1003067//Rat dynorphin gene, exon 3.//1.0:140.63//M32783
- F-HEMBA1003071//Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.//1.5e-20:595.65//U72648
- F-HEMBA1003077//CIT-HSP-2366J21.TF CIT-HSP Homo sapiens genomic clone 2366J21, genomic survey sequence.//4.4e-33:176.99//AQ080257
- 25 F-HEMBA1003078//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//9.4e-43:478.70//Z99297
- F-HEMBA1003079//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//0.96:57.85//AC004673
- 30 F-HEMBA1003083//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//8.0e-74:359.81//AC004548
- F-HEMBA1003086//Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.//3.6e-11:734.58//AF001550
- 35 F-HEMBA1003096//Sequence 4 from patent US 5440017.//5.7e-56:594.71//I13750
- F-HEMBA1003098//Human DNA sequence from cosmid SRL11M20, chromosome region 11p13. Contains EST and STS.//1.9e-09:230.69//Z83308
- F-HEMBA1003117//Mouse TIS11 primary response gene, complete cds.//0.00054:480.60//M58564
- 40 F-HEMBA1003129//HS\_3139\_B2\_F05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3139 Col=10 Row=L, genomic survey sequence.//2.3e-100:510.97//AQ187635
- F-HEMBA1003133//Mouse BAC CttbCJ7 219m7, genomic sequence, complete sequence.//1.3e-78:370.90//AC005259
- F-HEMBA1003136
- F-HEMBA1003142//Homo sapiens full-length insert cDNA clone ZC39B06.//6.9e-121:563.100//AF086197
- 45 F-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//6.7e-183:850.99//AJ005670
- F-HEMBA1003166//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 ~complete genomic sequence, complete sequence.//3.8e-27:229.76//AC002302
- F-HEMBA1003175//Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, WORKING DRAFT SEQUENCE.//9.4e-09:837.58//AB000882
- 50 F-HEMBA1003179//Homo sapiens DNA sequence from Fosmid 27C3 on chromosome 22q11.2-qter. Contains two possibly alternatively spliced unknown genes, one with homology to a worm protein. Contains ESTs, complete sequence.//5.4e-115:174.98//AL022325
- F-HEMBA1003197//Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence.//1.1e-05:473.59//AC005824
- 55 F-HEMBA1003199//Rattus norvegicus Sprague-Dawley thyroid hormone receptor alpha gene, exon 1.//1.6e-05:367.61//U09302
- F-HEMBA1003202//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//9.0e-23:247.73//AC004003

F-HEMBA1003204//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 409J21, WORKING DRAFT SEQUENCE.//4.7e-26:141:83//Z83824

F-HEMBA1003212//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.//1.9e-31:158:86//AC002037

5 F-HEMBA1003220//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.4e-24:284:75//AC004150

F-HEMBA1003222//RPC111-47P17.TJ RPC111 Homo sapiens genomic clone R-47P17, genomic survey sequence.//8.7e-39:202:99//AQ202885

10 F-HEMBA1003229//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence.//0.86:227:62//AB019230

F-HEMBA1003235//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence.//8.6e-05:372:61//AE001373

F-HEMBA1003250//HS-1063-A1-H02-MR abl CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 796 Col=3 Row=O, genomic survey sequence.//0.00032:57:96//B46142

15 F-HEMBA1003257//H.sapiens mRNA for RDC-1 POU domain containing protein.//2.2e-08:531:59//X64624

F-HEMBA1003273//H.sapiens full-length cDNA for RDC-1 POU domain containing protein.//0.070:267:64//Z78949

F-HEMBA1003276//CIT-HSP-2301B4.TF CIT-HSP Homo sapiens genomic clone 2301B4, genomic survey sequence.//5.2e-08:295:63//AQ015073

20 F-HEMBA1003278//HS\_3075\_A1\_G09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=17 Row=M, genomic survey sequence.//0.98:399:58//AQ120599

F-HEMBA1003281//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//4.8e-101:277:97//AC005840

F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyltransferase mRNA, complete cds.//9.0e-145:539:97//AF038662

25 F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//5.0e-166:799:98//AB011109

F-HEMBA1003296//CITBI-E1-2507M8.TR CITBI-E1 Homo sapiens genomic clone 2507M8, genomic survey sequence.//1.9e-05:388:63//AQ262551

F-HEMBA1003304//Budworm mitochondrial partial transfer RNA-Met (tRNA-Met) gene, and partial 12S ribosomal RNA (12S rRNA) gene.//8.0e-05:388:62//L17343

30 F-HEMBA1003309//Crassostrea gigas clone CN20 microsatellite sequence.//0.0017:210:64//AF051177

F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds.//4.6e-188:865:99//AB001872

F-HEMBA1003322//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING DRAFT SEQUENCE.//2.4e-54:316:87//Z93015

35 F-HEMBA1003327//CIT-HSP-2024C24.TRB CIT-HSP Homo sapiens genomic clone 2024C24, genomic survey sequence.//8.4e-12:166:76//B67147

F-HEMBA1003328//HS\_2230\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2230 Col=16 Row=P, genomic survey sequence.//0.026:128:71//AQ153313

40 F-HEMBA1003330//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//4.0e-160:745:99//AF045555

F-HEMBA1003348//HS\_3194\_A1\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=M, genomic survey sequence.//5.0e-79:381:99//AQ173779

F-HEMBA1003369//H. vulgare GAA-satellite DNA.//0.12:89:71//Z50100

45 F-HEMBA1003370//Homo sapiens cosmid 123E15, complete sequence.//3.5e-32:199:80//AF024533

F-HEMBA1003373//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE.//0.019:117:71//AL034405

F-HEMBA1003376//Human clone HS4.66 Alu-Ya5 sequence.//4.2e-30:196:85//U67229

F-HEMBA1003380//Homo sapiens DNA sequence from clone 394P21 on chromosome 1p36.12-36.13. Contains the PAX7 gene, locus D1S2644, ESTs and STSs, complete sequence.//4.6e-22:206:81//AL021528

50 F-HEMBA1003384//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00094:72:90//AC006026

F-HEMBA1003395//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.00041:826:57//AL031744

F-HEMBA1003402//CIT-HSP-2339K16.TR CIT-HSP Homo sapiens genomic clone 2339K16, genomic survey sequence.//2.4e-05:265:64//AQ056234

55 F-HEMBA1003403//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//4.3e-135:780:90//AC004066

F-HEMBA1003408

- F-HEMBA1003417//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//1.9e-41:239:95//AL031321
- F-HEMBA1003418//Rattus norvegicus Wistar polymeric immunoglobulin receptor (PIGR) gene, 3'UTR and trinucleotide repeat microsatellites.//2.2e-06:247:64//U08273
- 5 F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds.//1.4e-149:697:99//AF051334
- F-HEMBA1003447//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//1.7e-77:461:90//AC004066
- F-HEMBA1003461//Rhodobacter sphaeroides FliH (fliH) gene, partial cds, F1li (fliI) and FliJ (fliJ) genes, complete cds.//8.6e-08:752:58//U31090
- 10 F-HEMBA1003463//Homo sapiens chromosome 17, clone HCIT305D20, complete sequence.//0.089:172:68//AC004098
- F-HEMBA1003480//Homo sapiens clone NH0523H20, complete sequence.//4.5e-150:562:97//AC005041
- F-HEMBA1003528//Streptomyces fradiae gene for trypsinogen precursor, complete cds.//4.7e-09:433:60//D16687
- F-HEMBA1003531//Homo sapiens PAC clone DJ1185I07 from 7q11.23-q21, complete sequence.//2.3e-48:297:90//AC004990
- 15 F-HEMBA1003538//Human complement C1r mRNA, complete cds.//4.3e-22:474:63//M14058
- F-HEMBA1003545//Rattus norvegicus (clone 1.6kb) islet-2 mRNA, complete cds.//3.5e-143:805:91//L35571
- F-HEMBA1003548
- F-HEMBA1003555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 447E6, WORKING DRAFT SEQUENCE.//3.4e-58:331:83//AL031724
- 20 F-HEMBA1003556//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence.//6.0e-99:703:84//AC005913
- F-HEMBA1003560//Bovine GTP-binding regulatory protein gamma-6 subunit mRNA, complete cds.//1.3e-99:587:89//J05071
- 25 F-HEMBA1003568//HS\_3149\_A1\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3149 Col=7 Row=E, genomic survey sequence.//4.1e-05:389:57//AQ166810
- F-HEMBA1003569//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//1.6e-102:669:85//AC005539
- F-HEMBA1003571//Dictyostelium discoideum RegA (regA) gene, complete cds.//0.00033:649:58//U80170
- 30 F-HEMBA1003579//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.00034:623:56//AL031744
- F-HEMBA1003581//Mouse mRNA for talin.//3.3e-41:181:86//X56123
- F-HEMBA1003591//Homo sapiens chromosome 16, BAC clone RPCI-11\_192K18, complete sequence.//4.4e-70:273:94//AC006075
- 35 F-HEMBA1003595//Plasmodium falciparum chromosome 2, section 32 of 73 of the complete sequence.//6.0e-17:768:58//AE001395
- F-HEMBA1003597//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//4.0e-09:777:56//AE001398
- F-HEMBA1003598//Homo sapiens PAC clone DJ0537P09 from 7p11.2-p12, complete sequence.//1.3e-146:692:98//AC005153
- 40 F-HEMBA1003615//HS\_2010\_A2\_A07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2010 Col=14 Row=A, genomic survey sequence.//1.1e-22:137:97//AQ226592
- F-HEMBA1003617//Homo sapiens HRIHFB2157 mRNA, partial cds.//2.4e-169:501:97//AB015344
- F-HEMBA1003621//Mus musculus PIAS3 mRNA, complete cds.//4.7e-37:165:92//AF034080
- 45 F-HEMBA1003622//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0024:514:58//AC005139
- F-HEMBA1003630//CIT-HSP-2168N15.TR CIT-HSP Homo sapiens genomic clone 2168N15, genomic survey sequence.//6.5e-15:358:63//B92984
- F-HEMBA1003637//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.0e-21:238:76//AC005077
- 50 F-HEMBA1003640//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 112K5, WORKING DRAFT SEQUENCE.//2.3e-15:371:63//Z85987
- F-HEMBA1003645//A.thaliana 81kb genomic sequence.//1.0:529:57//X98130
- F-HEMBA1003646
- 55 F-HEMBA1003656
- F-HEMBA1003662//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//1.6e-175:824:98//AC005746
- F-HEMBA1003667//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces.

es.//1.1e-24:190.87//AC004765

F-HEMBA1003679//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//1.7e-162:579:99//AC005065

F-HEMBA1003680//H. sapiens DNA sequence.//7.3e-22:172:87//Z22322

F-HEMBA1003684//H. sapiens mRNA for Miz-1 protein.//0.0054:146:70//Y09723

F-HEMBA1003690//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//2.9e-72:606:77//AF039691

F-HEMBA1003692

F-HEMBA1003711//Homo sapiens chromosome 17, clone HRP41C23, complete sequence.//0.55:450:60//AC003101

F-HEMBA1003714

F-HEMBA1003715//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//3.0e-16:316:68//AL023575

F-HEMBA1003720//Homo sapiens chromosome 4 clone B227H22 map 4q25, complete sequence.//1.3e-41:483:73//AC004056

F-HEMBA1003725//CIT-HSP-2351H9.TF CIT-HSP Homo sapiens genomic clone 2351H9, genomic survey sequence.//1.1e-112:532:99//AQ079348

F-HEMBA1003729//HS\_3043\_A1\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3043 Col=13 Row=I, genomic survey sequence.//1.6e-12:87:98//AQ129345

F-HEMBA1003733//Homo sapiens, clone hRPK 15\_A\_1, complete sequence.//4.7e-104:761:82//AC006213

F-HEMBA1003742//HS\_3027\_A2\_B02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=4 Row=C, genomic survey sequence.//3.4e-08:67:97//AQ154731

F-HEMBA1003758//CIT-HSP-2379D18.TR CIT-HSP Homo sapiens genomic clone 2379D18, genomic survey sequence.//2.9e-10:310:63//AQ113513

F-HEMBA1003760//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//6.4e-114:714:86//AF060194

F-HEMBA1003773//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.078:378:58//AC005139

F-HEMBA1003783//Human DNA sequence from PAC 509L4 on chromosome 6q22.1-6q22.33. Contains SSX3 like pseudogene, EST, STS.//9.0e-135:804:89//Z99496

F-HEMBA1003784//Caenorhabditis elegans cosmid C55B6.//0.054:463:58//U88181

F-HEMBA1003799//Homo sapiens Chromosome 22q11.2 Cosmid Clone 105a In DGCR Region, complete sequence.//1.9e-44:425:76//AC000070

F-HEMBA1003803//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//0.95:198:62//L40178

F-HEMBA1003804//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//1.2e-138:275:99//AC004596

F-HEMBA1003805//Mus musculus quaking type I (QKI) mRNA, complete cds.//6.6e-148:753:95//U44940

F-HEMBA1003807//HS-1068-B1-G06-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 278 Col=11 Row=N, genomic survey sequence.//6.7e-07:241:67//B47212

F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cds.//1.0e-83:586:87//AB014516

F-HEMBA1003836//S. cerevisiae chromosome IX cosmid 9150//5.1e-16:368:63//Z38125

F-HEMBA1003838//CIT-HSP-384J15.TR CIT-HSP Homo sapiens genomic clone 384J15, genomic survey sequence.//1.4e-45:180:90//B54810

F-HEMBA1003856//Homo sapiens chromosome 10 clone CIT9875K-1188B12 map 10p12.1, complete sequence.//0.0014:574:58//AC005875

F-HEMBA1003864//, complete sequence.//2.1e-91:234:95//AC005300

F-HEMBA1003866//Mus musculus semaphorin VIa mRNA, complete cds.//5.9e-81:853:71//AF030430

F-HEMBA1003879//H. sapiens CBP80 mRNA.//2.0e-08:87:95//X80030

F-HEMBA1003880//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//1.7e-180:853:98//AP000036

F-HEMBA1003885//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//4.5e-39:376:67//AC004079

F-HEMBA1003893//H. sapiens CpG island DNA genomic MseI fragment, clone 11b6, forward read cpq11b6.ft1a.//3.6e-32:173:99//Z59012

F-HEMBA1003902//RPCI11-26M20.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-26M20, genomic survey sequence.//8.2e-12:422:61//AC003455

F-HEMBA1003908//Plasmodium falciparum chromosome 2, section 38 of 73 of the complete sequence.//0.0063:488:58//AE001401

F-HEMBA1003926//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 310O13, WORKING

DRAFT SEQUENCE.//3.6e-27:278.76//AL031658

F-HEMBA1003937//Homo sapiens chromosome 3 subtelomeric region.//1.4e-55:315.81//AF109718

F-HEMBA1003939//HS\_1047-A1-G04-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=7 Row=M, genomic survey sequence.//6.1e-09:413:63//B38195

F-HEMBA1003942//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.42:205:65//AC005140

F-HEMBA1003950//M. capricolum DNA for CONTIG MC072.//0.029:458:58//Z33058

F-HEMBA1003953//HS\_2268\_A1\_B04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=7 Row=C, genomic survey sequence.//9.0e-07:239:64//AQ085098

F-HEMBA1003958//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence.//2.8e-57:424:74//AC004894

F-HEMBA1003959//RPC11-78E8.TV RPC111 Homo sapiens genomic clone R-78E8, genomic survey sequence.//4.3e-86:441:9611AQ285498

F-HEMBA1003976//HS\_3146\_A1\_H09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3146 Col=17 Row=O, genomic survey sequence.//6.3e-10:129:80//AQ141146

F-HEMBA1003978

F-HEMBA1003985//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105C5, WORKING DRAFT SEQUENCE.//1.0:258:60//Z98855

F-HEMBA1003987

F-HEMBA1003989//Streptomyces coelicolor cosmid 1A9.//0.40:238:61//AL034446

F-HEMBA1004000//Rattus norvegicus satellite sequence d0Mco2.//2.0e-07:116:70//U19354

F-HEMBA1004011//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.098:286:60//AC004710

F-HEMBA1004012//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//2.8e-185:896:97//AC005670

F-HEMBA1004015//Homo sapiens chromosome 17, clone hRPK.721\_K\_1, complete sequence.//6.3e-68:417:80//AC005411

F-HEMBA1004024//Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete sequence.//2.0e-47:4.18:77//AC005859

F-HEMBA1004038//Homo sapiens genomic DNA, chromosome 21q11.1, segment 23/28, WORKING DRAFT SEQUENCE.//1.6e-51:564:74//AP000052

F-HEMBA1004042//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//1.2e-05:636:55//AE001398

F-HEMBA1004045//Homo sapiens (subclone 1\_g7 from BAC H76) DNA sequence, complete sequence.//1.9e-31:373:76//AC002252

F-HEMBA1004048//Homo sapiens DNA for P35-related protein, exon 2.//0.039:234:63//D63393

F-HEMBA1004049//Homo sapiens Xp22 GS-52411 (Genome Systems Human BAC library), complete sequence.//4.8e-135:780:89//AC003106

F-HEMBA1004055//Human chromosome 3p21.1 gene sequence.//4.7e-09:457:58//L13435

F-HEMBA1004056//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 447C4, WORKING DRAFT SEQUENCE.//3.3e-25:246:77//AL021977

F-HEMBA1004074//CIT-HSP-2053J5.TF CIT-HSP Homo sapiens genomic clone 2053J5, genomic survey sequence.//7.8e-24:233:76//B68555

F-HEMBA1004086//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//4.5e-08:614:59//U49822

F-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//5.9e-121:502:85//AF091234

F-HEMBA1004111//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0481P14; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.0e-36:317:80//AC006160

F-HEMBA1004131//Mus musculus clone OST2067, genomic survey sequence.//8.7e-24:320:71//AF046393

F-HEMBA1004132//HS\_3226\_B1\_D10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3226 Col=19 Row=H, genomic survey sequence.//9.7e-13:232:71//AQ182017

F-HEMBA1004133

F-HEMBA1004138//HS\_3036\_B1\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=21 Row=N, genomic survey sequence.//0.0035:165:64//AQ294763

F-HEMBA1004143

F-HEMBA1004146

- F-HEMBA1004150//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//0.00011:618:60//Z96811
- F-HEMBA1004164//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//2.9e-30:454:68//AC005913
- 5 F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//4.5e-133:649:97//AF067855
- F-HEMBA1004199
- F-HEMBA1004200//HS\_2015\_A1\_B05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2015 Col=9 Row=C, genomic survey sequence.//8.5e-34:236:87//AQ247957
- 10 F-HEMBA1004202//Mus musculus chromosome 11, clone mCIT.268\_P\_23, complete sequence.//7.8e-59:216:83//AC004807
- F-HEMBA1004203//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//6.3e-98:173:98//AC005488
- F-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//3.2e-166:791:98//U50748
- 15 F-HEMBA1004225//Plasmodium falciparum chromosome 2, section 61 of 73 of the complete sequence.//6.5e-08:584:60//AE001424
- F-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//8.0e-115:713:86//AF095927
- F-HEMBA1004238
- 20 F-HEMBA1004241//CIC5B11.1 check: 4870 from: 1 to: 167234, complete sequence.//0.57:552:58//AC004708
- F-HEMBA1004246//Human DNA sequence from clone 422F24 on chromosome 6q24.1-25.2. Contains a novel gene similar to C. elegans C02C2.5. Contains ESTs, STSs and GSSs, complete sequence.//6.1e-21:254:77//AL031010
- F-HEMBA1004248//Rattus rattus insulin-induced growth-respons protein (CL-6) mRNA, complete cds.//1.7e-30:315:74//L13619
- 25 F-HEMBA1004264//Homo sapiens cosmid clone LUCA20 from 3p21.3, complete sequence.//4.4e-07:674:60//AC004693
- F-HEMBA1004267//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//3.1e-78:335:87//AC004707
- 30 F-HEMBA1004272//Homo sapiens 12p13.3 PAC RPC15-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.4e-176:856:97//AC005831
- F-HEMBA1004274//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-28:153:100//AQ136993
- F-HEMBA1004275//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 501A4, WORKING
- 35 DRAFT SEQUENCE.//5.2e-17:109:99//Z98051
- F-HEMBA1004276//CIT-HSP-2387K6.TF.1 CIT-HSP Homo sapiens genomic clone 2387K6, genomic survey sequence.//5.0e-07:63:98//AQ240477
- F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//2.1e-185:868:99//AF022795
- 40 F-HEMBA1004289//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence.//1.0:387:59//AB013395
- F-HEMBA1004295//Homo sapiens DNA, anonymous heat-stable fragment RP11-3A.//7.8e-06:92:89//AB012254
- F-HEMBA1004306//Homo sapiens clone DJ0811N16, complete sequence.//0.00037:413:59//AC004897
- F-HEMBA1004312//Rickettsia prowazekii strain Madrid E, complete genome; segment 2/4.//0.28:522:57//AJ235271
- 45 F-HEMBA1004321//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//7.1e-136:548:92//AC006130
- F-HEMBA1004323//Human DNA sequence from PAC 450C20 on chromosome X.//1.3e-32:320:65//Z84720
- F-HEMBA1004327//Homo sapiens mRNA for KIAA0522 protein, partial cds.//0.93:222:62//AB011094
- 50 F-HEMBA1004330//Homo sapiens clone DJ1196H06, WORKING DRAFT SEQUENCE, 4 unordered pieces.//7.0e-168:895:93//AC004995
- F-HEMBA1004334//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//4.6e-73:713:75//AC002980
- F-HEMBA1004335//Human DNA-sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 417M14, WORKING
- 55 DRAFT SEQUENCE.//1.3e-25:121:85//AL024498
- F-HEMBA1004341
- F-HEMBA1004353//\*\*ALU WARNING: Human Alu-Sc subfamily consensus sequence.//6.4e-38:278:85//U14571
- F-HEMBA1004354//Human clone C3 CHL1 protein (CHLR1) mRNA, alternatively spliced, complete cds.//4.1e-45:



190:92//U75968  
 F-HEMBA1004356  
 F-HEMBA1004366//P.falciparum complete gene map of plastid-like DNA (IR-A).//2.2e-07:736:57//X95275  
 F-HEMBA1004372//H. sapiens dystrophin gene intron 44.//1.0:129:62//X77644  
 5 F-HEMBA1004389//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//4.7e-42:237:94//M21977  
 F-HEMBA1004394//Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence.//5.2e-05:  
 519:59//AE001402  
 F-HEMBA1004396//Human BAC clone RG302F04 from 7q31, complete sequence.//4.0e-32:261:76//AC002463  
 F-HEMBA1004405//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING  
 10 DRAFT SEQUENCE, 9 unordered pieces.//1.4e-07:693:58//AC005507  
 F-HEMBA1004408//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//  
 1.2e-69:195:100//AC005037  
 F-HEMBA1004429//HS\_3193\_A1\_B06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3193 Col=11 Row=C, genomic survey sequence.//5.1e-67:386:91//AQ172942  
 15 F-HEMBA1004433//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//3.2e-27:242:82//  
 AC002554  
 F-HEMBA1004460//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//  
 1.7e-75:590:81//AC004846  
 F-HEMBA1004461//Human DNA sequence from clone 657J8 on chromosome Xq26.1-26.3 Contains GSS, com-  
 20 plete sequence.//0.045:215:66//AL034407  
 F-HEMBA1004479//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//5.2e-43:364:79//  
 AF060194  
 F-HEMBA1004482//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING  
 DRAFT SEQUENCE, 8 unordered pieces.//6.8e-17:791:59//AC005505  
 25 F-HEMBA1004499//Homo sapiens chromosome 17, clone hRPC.1073\_F\_15, complete sequence.//4.4e-125:251:  
 94//AC004686  
 F-HEMBA1004502//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING  
 DRAFT SEQUENCE, 3 unordered pieces.//0.012:635:57//AC004709  
 F-HEMBA1004506//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.8e-127:766:  
 30 88//AC004453  
 F-HEMBA1004507  
 F-HEMBA1004509//Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 (ESSAII project).//1.0e-13:244:  
 67//AL021712  
 F-HEMBA1004534//Human mRNA for actin-binding protein (filamin) (ABP-280).//1.6e-72:678:74//X53416  
 35 F-HEMBA1004538//Sequence 1 from patent US 5612190.//0.00015:416:59//I36871  
 F-HEMBA1004542//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.95:  
 202:64//AC005038  
 F-HEMBA1004554//Arabidopsis thaliana BAC T26D22.//0.45:624:56//AF058826  
 F-HEMBA1004560//Human mRNA for KIAA0281 gene, complete cds.//9.1e-10:173:70//D87457  
 40 F-HEMBA1004573//Human BAC clone RG114A06 from 7q31, complete sequence.//6.1e-23:134:73//AC002542  
 F-HEMBA1004577//Homo sapiens Chromosome 16 BAC clone CIT987SK-582J2, complete sequence.//1.6e-15:  
 190:77//AC004525  
 F-HEMBA1004586//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//  
 3.1e-31:388:76//AC004895  
 45 F-HEMBA1004598//RPC111-81O21.TJ RPC111 Homo sapiens genomic clone R-81O21, genomic survey se-  
 quence.//2.2e-90:458:90//AQ285136  
 F-HEMBA1004604//Mus musculus COP9 complex subunit 7a (COPSTa) mRNA, complete cds.//8.6e-105:699:  
 84//AF071316  
 F-HEMBA1004610//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//5.4e-20:267:  
 50 72//AC004983  
 F-HEMBA1004617//CIT-HSP-2319H15.TF CIT-HSP Homo sapiens genomic clone 2319H15, genomic survey se-  
 quence.//6.2e-26:147:99//AQ034944  
 F-HEMBA1004629//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING  
 DRAFT SEQUENCE, 3 unordered pieces.//5.6e-06:766:56//AC005504  
 55 F-HEMBA1004631//Human DNA sequence from PAC 388A4 on chromosome X. Contains ESTs, CELLULAR NU-  
 CLEIC ACID BINDING PROTEIN (CNBP) like gene and STSs.//4.7e-73:412:92//Z83843  
 F-HEMBA1004632//Canine herpesvirus DNA for gene homolog of HSV1 UL16, EH1V ORF 46, VZV ORF 44.//  
 0.92:181:61//X90418

F-HEMBA1004637//G. gallus mRNA for LRP/alpha-2-macroglobulin receptor.//7.8e-47:784.65//X74904  
 F-HEMBA1004638//Rattus norvegicus homeodomain protein Nkx6.1 (nkx6.1) mRNA, complete cds.//6.4e-06:458:61//AF004431  
 F-HEMBA1004666//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y47D3,  
 5 WORKING DRAFT SEQUENCE.//0.30:733:55//Z98865  
 F-HEMBA1004669//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel  
 genes, ESTs, GSSs and CpG islands, complete sequence.//7.5e-136:521:98//AL031432  
 F-HEMBA1004670//Homo sapiens Chromosome 22q12 Cosmid Clone p90g5, complete sequence.//0.43:365:  
 59//AC000045  
 10 F-HEMBA1004672  
 F-HEMBA1004693//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING  
 DRAFT SEQUENCE, 5 unordered pieces.//0.096:651:54//AC005308  
 F-HEMBA1004697//CIT-HSP-2326C13.TR CIT-HSP Homo sapiens genomic clone 2326C13, genomic survey se-  
 quence.//0.23:238:65//AQ040642  
 15 F-HEMBA1004705//Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore X library) and PAC  
 RPC11-93D11 (from Roswell Park Cancer Center) complete sequence.//2.1e-27:375:72//AC002357  
 F-HEMBA1004709//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) com-  
 plete sequence.//1.6e-36:191:91//AC006210  
 F-HEMBA1004711//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds.//1.1e-133:639:  
 20 99//AC005562  
 F-HEMBA1004725//RPC11-75013.TJ RPC111 Homo sapiens genomic clone R-75013, genomic survey se-  
 quence.//6.2e-32:169:100//AQ266512  
 F-HEMBA1004730//Human BAC clone RG035E18 from 7q31, complete sequence.//8.0e-68:732:72//AC004029  
 F-HEMBA1004733//CIT-HSP-2305M23.TF CIT-HSP Homo sapiens genomic clone 2305M23, genomic survey se-  
 25 quence.//4.9e-18:209:69//AQ017556  
 F-HEMBA1004734//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds.//1.8e-  
 13:451:62//AF028340  
 F-HEMBA1004736//Human DNA Sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine  
 threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinosis (X-linked,  
 30 juvenile) 1 (XLR51). Contains ESTs, an STS and GSSs, complete sequence.//5.0e-87:646:78//Z94056  
 F-HEMBA1004748//Human BAC clone RG204I16 from 7q31, complete sequence.//0.24:526:57//AC002461  
 F-HEMBA1004751//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//  
 1.4e-25:268:76//AC004913  
 F-HEMBA1004752//R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).//1.1e-07:503:  
 35 61//X83546  
 F-HEMBA1004753//Homo sapiens Chromosome 12 Cosmid Clone 6e5, complete sequence.//4.5e-38:314:81//  
 AC000028  
 F-HEMBA1004756//Homo sapiens, complete sequence.//1.4e-111:326:84//AC005854  
 F-HEMBA1004758//Sequence 29 from patent US 5534410.//3.9e-135:769:91//Z3472  
 40 F-HEMBA1004763//Homo sapiens apoptosis inhibitor survivin gene, complete cds.//3.6e-47:404:79//U75285  
 F-HEMBA1004768//Homo sapiens PAC clone DJ0979P20 from 7q33-q35, complete sequence.//6.7e-107:890:  
 78//AC004941  
 F-HEMBA1004770//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING  
 DRAFT SEQUENCE, 3 unordered pieces.//7.9e-09:806:59//AC004709  
 45 F-HEMBA1004771//G. muris ribosomal RNA operon DNA encoding 16S, 23S and 5.8S ribosomal RNA.//0.69:239:  
 61//X65063  
 F-HEMBA1004776  
 F-HEMBA1004778  
 F-HEMBA1004795//Drosophila melanogaster A-kinase anchor protein DAKAP550 mRNA, partial cds.//3.4e-46:  
 50 778:64//AF003622  
 F-HEMBA1004803//Homo sapiens chromosome Y, clone 264.M.20, complete sequence.//4.3e-82:580:82//  
 AC004617  
 F-HEMBA1004806//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//5.4e-07:642:59//  
 AC005083  
 55 F-HEMBA1004807//Human HIV1 tate element modulatory factor mRNA sequence from chromosome 3.//1.4e-46:  
 171:92//L01042  
 F-HEMBA1004816//Homo sapiens calpastatin (CAST) gene, exons 10-14.//3.5e-31:546:66//M86257  
 F-HEMBA1004820//C.botulinum progenitor toxin complex genes.//0.0014:343:62//X87972

- F-HEMBA1004847//Canine mRNA for 68kDa subunit of signal recognition particle (SRP68).//1.5e-85.512.88//X53744
- F-HEMBA1004850//Homo sapiens TGF-beta type I receptor (TGFB1) gene, exon 1.//0.0065:284.61//AF054590
- F-HEMBA1004863//Genomic sequence from Mouse 11, complete sequence.//0.92:250.59//AC000400
- 5 F-HEMBA1004864
- F-HEMBA1004865//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//3.6e-12.214.72//AL031120
- F-HEMBA1004880//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//1.1e-08:255.69//AC004020
- 10 F-HEMBA1004889//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds.//0.062:155.69//J32943
- F-HEMBA1004900//Plasmodium falciparum unidentified mRNA sequence.//0.00055:323.60//L12043
- F-HEMBA1004909//Homo sapiens chromosome 17, clone 289A8, complete sequence.//9.6e-16:166.80//AC003051
- 15 F-HEMBA1004918//Turritella communis mitochondrial 16S ribosomal RNA gene, partial.//0.81:146.65//M94003
- F-HEMBA1004923//Human DNA from overlapping chromosome 19-specific cosmid R32543, and F15613 containing ZNF gene family member, genomic sequence, complete sequence.//1.4e-36:338.78//AC003006
- F-HEMBA1004929//CIT-HSP-2373116.TR CIT-HSP Homo sapiens genomic clone 2373116, genomic survey sequence.//2.4e-86:443.96//AQ108676
- 20 F-HEMBA1004930//Homo sapiens PAC clone DJ0608H12 from 7q21, complete sequence.//4.6e-20:219.73//AC004109
- F-HEMBA1004933//HS-1003-A1-E10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 497 Col=19 Row=I, genomic survey sequence.//1.4e-28:216.85//B30726
- F-HEMBA1004934//Homo sapiens chromosome 21q22.3 PAC 267010, complete sequence.//0.53:222.61//AF042091
- 25 F-HEMBA1004944//Homo sapiens clone DJ0736H05, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.2e-58:509.78//AC005482
- F-HEMBA1004954//HS\_2033\_A2\_A08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=16 Row=A, genomic survey sequence.//3.7e-47:243.99//AQ229758
- 30 F-HEMBA1004956//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.048:421.58//X95276
- F-HEMBA1004960//Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 8.//0.89:333.58//Z97343
- F-HEMBA1004972
- F-HEMBA1004973//RPCI11-66P8.TK RPCI11 Homo sapiens genomic clone R-66P8, genomic survey sequence.//3.5e-22:245.77//AQ238471
- 35 F-HEMBA1004977//Homo sapiens full-length insert cDNA clone YZ83B08.//9.0e-11:84.98//AF086080
- F-HEMBA1004978//CIT-HSP-2354E10.TR CIT-HSP Homo sapiens genomic clone 2354E10, genomic survey sequence.//0.0021:152.66//AQ075713
- F-HEMBA1004980//HS\_3018\_A2\_E04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=8 Row=I, genomic survey sequence.//1.9e-77:392.97//AQ071873
- 40 F-HEMBA1004983//Albinaria corrugata isolate cor. Pm.1 1.16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence.//0.0030:276.61//AF031680
- F-HEMBA1004995//Homo sapiens chromosome 16, cosmid bridge clone 306E6 (LANL), complete sequence.//4.2e-138:840.99//AC005590
- 45 F-HEMBA1005008//Human mariner1 transposase gene, complete consensus sequence.//6.8e-20:160.88//U52077
- F-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//2.0e-144:668.99//AF041474
- F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds.//1.4e-146:693.98//AB014548
- F-HEMBA1005029//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSS, GSSs and genomic marker D6S464, complete sequence.//2.2e-115:668.90//AL009179
- 50 F-HEMBA1005035//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//4.6e-138:591.98//AC004596
- F-HEMBA1005039//CIT-HSP-2338L5.TR CIT-HSP Homo sapiens genomic clone 2338L5, genomic survey sequence.//3.7e-61:271.88//AQ055486
- 55 F-HEMBA1005047//Mus musculus mRNA for Rab24 protein.//3.8e-17:218.73//Z22819
- F-HEMBA1005050//Human Tis11d gene, complete cds.//0.079:251.63//U07802

- F-HEMBA1005062//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.018:560:56//AC004688
- F-HEMBA1005066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 774G10, WORKING DRAFT SEQUENCE.//3.4e-97:432:84//AL034410
- 5 F-HEMBA1005075//H.sapiens DNA 3' flanking simple sequence region clone wg2c3.//6.9e-07:176:68//X76589
- F-HEMBA1005079//CIT-HSP-2325M21.TRB CIT-HSP Homo sapiens genomic clone 2325M21, genomic survey sequence.//2.1e-48:274:93//AQ038720
- F-HEMBA1005083//HS\_2248\_B1\_D05\_MR CIT Approved Human Genomic Spermi Library D Homo sapiens genomic clone Plate=2248 Col=9 Row=H, genomic survey sequence.//3.4e-06:230:64//AQ129575
- 10 F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//1.3e-161:762:98//AF080561
- F-HEMBA1005113//L.esculentum microsatellite repeat DNA region.//0.0038:742:57//X90770
- F-HEMBA1005123//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//9.6e-83:479:78//AC004854
- 15 F-HEMBA1005133//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y131F4, WORKING DRAFT SEQUENCE.//3.9e-24:576:64//AL023808
- F-HEMBA1005149//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//4.7e-36:283:80//AC004542
- F-HEMBA1005152//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.//5.0e-10:332:64//AC004469
- 20 F-HEMBA1005159//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE.//4.0e-10:734:58//AP000023
- F-HEMBA1005185//H.sapiens CpG island DNA genomic MseI fragment. clone 91b2, forward read cp91b2.ft1a.//12.2e-14:93:100//Z63847
- 25 F-HEMBA1005201//Drosophila melanogaster cosmid 152A3.//4.7e-35:679:64//AL009194
- F-HEMBA1005223//Canine mRNA for 68kDa subunit of signal recognition particle (SRP68).//6.7e-138:778:90//X53744
- F-HEMBA1005206//Drosophila melanogaster Su(P) and anon-73B1 genes and partial o25 gene and Pros26 gene.//7.1e-12:376:62//AJ011320
- 30 F-HEMBA1005219//Homo sapiens mRNA for KIAA0445 protein, complete cds.//7.1e-05:411:60//AB007914
- F-HEMBA1005223//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//3.5e-06:212:66//AC004542
- F-HEMBA1005232//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.7e-07:625:57//AC005308
- 35 F-HEMBA1005241//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete sequence.//8.7e-45:567:72//AC005154
- F-HEMBA1005244//Homo sapiens chromosome X clone U177G4, U152H5, U168D5, 174A6, U172D6, and U186B3 from Xp22, complete sequence.//0.96:298:62//AC002365
- F-HEMBA1005251
- 40 F-HEMBA1005252//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complete sequence.//4.5e-160:392:99//AC005837
- F-HEMBA1005274//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//2.3e-05:496:60//AF069291
- F-HEMBA1005275//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs. complete sequence.//5.7e-05:220:64//AL033521
- 45 F-HEMBA1005293//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//2.4e-20:338:65//U97018
- F-HEMBA1005296
- F-HEMBA1005304//Human DNA sequence from clone 364I22 on chromosome Xq21.31-22.3. Contains an STS and GSSs, complete sequence.//1.6e-51:381:78//AL031012
- 50 F-HEMBA1005311
- F-HEMBA1005314//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.//0.94:226:63//AP000031
- F-HEMBA1005315//Homo sapiens BAC810, complete sequence.//9.5e-15:684:62//U85198
- 55 F-HEMBA1005318//Human DNA sequence from PAC 394F12 on chromosome X contains EST, STS, CpG island clone.//2.6e-05:472:59//Z83823
- F-HEMBA1005331//Homo sapiens chromosome 17, clone hRPK.214\_C\_8, complete sequence.//3.3e-90:300:90//AC005803

F-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial.//1.4e-151:740:97//AJ007581  
 F-HEMBA1005353//CIT-HSP-2310N10. TR CIT-HSP Homo sapiens genomic clone 2310N10, genomic survey sequence.//2.1e-86:438:97//AQ016145

5 F-HEMBA1005359//Human zinc finger protein ZNF137 mRNA, complete cds.//1.8e-98:500:88//U09414  
 F-HEMBA1005367//Mus musculus melastatin mRNA, complete cds.//8.3e-72:577:73//AF047714  
 F-HEMBA1005372//Human DNA sequence from PAC 293E14 contains ESTs, STS.//1.3e-07:274:66//Z82900  
 F-HEMBA1005374//Homo sapiens clone 277F10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.9e-48:611:69//AC004813

10 F-HEMBA1005382//HIS\_3063\_B2\_F11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3063 Col=22 Row=L, genomic survey sequence.//1.6e-27:154:98//AQ103204  
 F-HEMBA1005389//Plasmodium falciparum telomere nucleotide sequence.//4.0e-07:443:61//M23175  
 F-HEMBA1005394//CIT-HSP-2368B11. TR CIT-HSP Homo sapiens genomic clone 2368B11, genomic survey sequence.//7.6e-17:225:71//AQ076749

15 F-HEMBA1005403//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//4.5e-131:278:98//AL034379  
 F-HEMBA1005408//HIS\_3007\_B2\_G04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=8 Row=N, genomic survey sequence.//8.0e-06:218:66//AQ294366  
 F-HEMBA1005410//Human DNA sequence from cosmid cU120E2, on chromosome X contains Lowe oculocerebrorenal syndrome (OCRL) ESTs and STS.//1.5e-41:432:76//Z73496

20 F-HEMBA1005411  
 F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.//1.0e-169:537:99//AF041248  
 F-HEMBA1005426

25 F-HEMBA1005443//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//7.1e-37:260:76//AC006130  
 F-HEMBA1005447//CIT-HSP-2173N7. TR CIT-HSP Homo sapiens genomic clone 2173N7, genomic survey sequence.//5.0e-133:631:98//B93234  
 F-HEMBA1005468//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.//1.5e-118:868:83//AL022576

30 F-HEMBA1005469//Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence.//1.2e-179:838:99//AC005212  
 F-HEMBA1005472//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//3.4e-20:187:74//AL031985

35 F-HEMBA1005474//Homo sapiens genomic DNA, chromosome 21q11.1, segment 12/28, WORKING DRAFT SEQUENCE.//4.1e-22:445:65//AP000041  
 F-HEMBA1005475//CIT-HSP-2322D14. TR CIT-HSP Homo sapiens genomic clone 2322D14, genomic survey sequence.//6.7e-51:269:97//AQ026941

40 F-HEMBA1005497//HIS\_3097\_A2\_G05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3097 Col=10 Row=M, genomic survey sequence.//1.4e-66:345:96//AQ103810  
 F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from Tq11.23-q21, complete sequence.//5.4e-178:818:98//AC004957  
 F-HEMBA1005506//Mus musculus (clone 0EBF17) early B-cell factor (EBF) mRNA, complete cds.//2.6e-06:73:98//L12147

45 F-HEMBA1005508//Homo sapiens clone hRPK.1\_A\_1, complete sequence.//0.00012:455:60//AC006196  
 F-HEMBA1005511//Homo sapiens MHC class 1 region.//3.3e-43:421:77//AF055066  
 F-HEMBA1005513//Drosophila melanogaster males-absent on the first (mof) gene, complete cds.//2.3e-20:352:69//U71219

50 F-HEMBA1005517//Homo sapiens DNA for (CGG)<sub>n</sub> trinucleotide repeat region, isolate E7.//2.5e-08:431:62//AJ001216  
 F-HEMBA1005518//M.musculus mRNA for paladin gene.//8.2e-90:651:81//X99384  
 F-HEMBA1005520//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.8e-167:755:99//AC004913

55 F-HEMBA1005526//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//2.4e-42:475:73//AC006241  
 F-HEMBA1005528//Mus musculus mCAF1 protein mRNA, complete cds.//1.2e-94:512:92//U21855  
 F-HEMBA1005530  
 F-HEMBA1005548//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 970A17, WORKING

DRAFT SEQUENCE.//9.4e-87:422:99//AL034431

F-HEMBA1005552//Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence.//6.1e-41:486:68//AC004743

F-HEMBA1005558//Drosophila melanogaster DNA sequence (P1 DS00837 (D87)), complete sequence.//2.9e-19:306:68//AC004377

F-HEMBA1005568//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0093:345:60//AC004153

F-HEMBA1005570//Plasmodium falciparum chromosome 2, section 44 of 73 of the complete sequence.//4.2e-09:592:59//AE001407

F-HEMBA1005575//Homo sapiens mRNA for KIAA0463 protein, partial cds.//5.9e-127:610:98//AB007932

F-HEMBA1005577//HS-1004-A1-E11 -MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 498 Col=21 Row=I, genomic survey sequence.//0.00034:254:64//B30971

F-HEMBA1005581//Rattus norvegicus mRNA for MEGF5, complete cds.//4.0e-57:826:65//AB011531

F-HEMBA1005582//HS\_3242\_A1\_B07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=13 Row=C, genomic survey sequence.//1.1e-13:91:98//AQ211275

F-HEMBA1005583

F-HEMBA1005588//Homo sapiens PAC clone DJ1188N21 from 7q11.23-q21.1, complete sequence.//8.7e-31:283:75//AC006025

F-HEMBA1005593//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//8.3e-158:748:99//AC005746

F-HEMBA1005595//CIT-HSP-2309F14.TF CIT-HSP Homo sapiens genomic clone 2309F14, genomic survey sequence.//6.4e-30:194:91//AQ016527

F-HEMBA1005606//CIT-HSP-232616.TR CIT-HSP Homo sapiens genomic clone 232616, genomic survey sequence.//0.0014:132:70//AQ041484

F-HEMBA1005609//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.9e-33:249:65//AC005089

F-HEMBA1005616//Homo sapiens DNA sequence from PAC 43C13 on chromosome Xq21.1-Xq21.3. rab proteins geranylgeranyltransferase component A 1 (rab escort protein 1) (REP-1) (choroideraemia protein) (TCD protein).//6.5e-29:279:69//AL009175

F-HEMBA1005621//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 330012, WORKING DRAFT SEQUENCE.//6.4e-90:158:87//AL031731

F-HEMBA1005627//RPCI11-34P9 TJ RPCI-11 Homo sapiens genomic clone RPCI-11-34P9, genomic survey sequence.//0.014:168:67//AQ045110

F-HEMBA1005631//Homo sapiens PAC clone DJ1086D14, complete sequence.//1.0e-149:736:93//AC004460

F-HEMBA1005632

F-HEMBA1005634//Human DNA sequence from PAC 187N21 on chromosome 6p21.2-6p21.33. Contains ESTs.//6.6e-38:452:67//Z98036

F-HEMBA1005666

F-HEMBA1005670//Homo sapiens PAC clone DJ0665C04 from 7p14-p13, complete sequence.//5.1e-59:687:74//AC004850

F-HEMBA1005679//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.0e-47:357:85//AC005478

F-HEMBA1005680

F-HEMBA1005685//RPCI11-23D19.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-23D19, genomic survey sequence.//0.99:228:63//AQ013742

F-HEMBA1005699//Human ligand for eph-related receptor tyrosine kinases (EPLG8) mRNA, complete cds.//1.4e-72:406:92//U57001

F-HEMBA1005705//Human (D21S172) DNA segment containing (CA) repeat.//0.00040:190:66//X56513

F-HEMBA1005717//Plasmodium falciparum MAL3P1, complete sequence.//0.0099:260:63//Z97348

F-HEMBA1005732//Human mRNA for KIAA0003 gene, complete cds.//8.1e-19:151:88//D14697

F-HEMBA1005737//Homo sapiens PAC clone DJ1099C19 from 7q21-q22, complete sequence.//5.6e-15:157:79//AC005156

F-HEMBA1005746//RPCI11-63N8.TK RPCI11 Homo sapiens genomic clone R-63N8, genomic survey sequence.//1.3e-18:113:100//AQ238535

F-HEMBA1005755//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//3.6e-56:764:70//Z97181

F-HEMBA1005765//Human DNA sequence from PAC 288L1 on chromosome 22q12-qter contains ESTs and polymorphic CA repeat (D22S1152).//1.1e-30:275:77//Z82196

- F-HEMBA1005780//RPC111-74E19.TJ RPC111 Homo sapiens genomic clone R-74E19, genomic survey sequence.//0.0011:283:62//AQ268432
- F-HEMBA1005813//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//0.14:326:61//AC004079
- 5 F-HEMBA1005815//M.musculus mRNA for skeletal muscle-specific calpain.//6.3e-10:706:59//X92523
- F-HEMBA1005822//Mouse Bac 291G16, WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.87:417:56//AC003020
- F-HEMBA1005829//Homo sapiens Chromosome 22q11.2 Fosmid Clone f39e1 In DGCR Region, complete sequence.//8.8e-42:370:79//AC000094
- 10 F-HEMBA1005834//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-42:690:67//AL022577
- 15 F-HEMBA1005852//F.rubripes GSS sequence, clone 163A22aE9, genomic survey sequence.//4.3e-07:253:59//AL018749
- F-HEMBA1005853//CIT-HSP-2289L23.TR CIT-HSP Homo sapiens genomic clone-2289L23, genomic survey sequence.//2.2e-68:333:99//B98952
- F-HEMBA1005884//Homo sapiens chromosome 5, BAC clone 78c6 (LBNL H191), complete sequence.//1.9e-57:331:87//AC005351
- 20 F-HEMBA1005891//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//5.1e-182:864:98//AC004945
- F-HEMBA1005894//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//3.0e-44:340:80//AC004086
- F-HEMBA1005909//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethyl-aniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//8.3e-12:828:57//AL021026
- 25 F-HEMBA1005911//Human DNA sequence from clone 1158E12 on chromosome Xp11.23-11.4 Contains EST, STS, GSS, CpG island, complete sequence.//1.0e-44:328:77//AL031584
- 30 F-HEMBA1005921//Homo sapiens chromosome 17, clone hRPK 112\_H\_10, complete sequence.//1.3e-41:431:77//AC005666
- F-HEMBA1005931//Homo sapiens chromosome 12p13.3 clone RPC14-761J14, WORKING DRAFT SEQUENCE, 60 unordered pieces.//1.1e-29:394:70//AC006086
- 35 F-HEMBA1005934//Homo sapiens PAC clone DJ1140G11 from 14q24.3, complete sequence.//8.1e-06:115:80//AC004974
- F-HEMBA1005962//RPC111-17O15.TV RPC111 Homo sapiens genomic clone RPC11-17O15, genomic survey sequence.//9.5e-36:315:84//B82821
- 40 F-HEMBA1005963//HS\_3055\_A1\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=15 Row=I, genomic survey sequence.//9.3e-73:372:97//AQ147357
- F-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//1.3e-149:697:99//AF082516
- F-HEMBA1005991//Plasmodium falciparum chromosome 2, section 45 of 73 of the complete sequence.//6.3e-07:423:60//AE001408
- 45 F-HEMBA1005999//Homo sapiens chromosome 4 clone C0026P05 map 4P16, complete sequence.//3.8e-09:360:64//AC005599
- F-HEMBA1006002
- F-HEMBA1006005//Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds.//4.5e-83:495:90//AF036405
- F-HEMBA1006031
- 50 F-HEMBA1006035
- F-HEMBA1006036//Human (lambda) DNA for immunoglobulin light chain.//2.4e-59:652:74//D87009
- F-HEMBA1006042//Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, complete sequence.//2.1e-43:330:7011AC005386
- F-HEMBA1006067//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.11:433:59//AC004153
- 55 F-HEMBA1006081
- F-HEMBA1006090//, complete sequence.//4.5e-139:748:92//AC005500
- F-HEMBA1006091//Homo sapiens gene encoding telethonin, exons 1 to 2, partial.//0.0091:346:62//AJ011098

- F-HEMBA1006100//Homo sapiens chromosome 10 clone CIT987SK-1143A11 map 10q25, complete sequence.//2.8e-18:180:78//AC005880
- 5 F-HEMBA1006108//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte-Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.26:84:71//AL031177
- F-HEMBA1006121//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 691N24, WORKING DRAFT SEQUENCE.//5.2e-18:147:87//AL031672
- 10 F-HEMBA1006124//CIT-HSP-2355617.TF CIT-HSP Homo sapiens genomic clone 2355B17, genomic survey sequence.//0.044:225:61//AQ058966
- F-HEMBA1006130//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clone 386A20, genomic survey sequence.//8.8e-07:173:69//B55085
- 15 F-HEMBA1006138//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//7.5e-22:164:75//AL022162
- F-HEMBA1006142//, complete sequence.//7.9e-125:586:99//AC005500
- F-HEMBA1006155//H.sapiens CpG island DNA genomic MseI fragment, clone 119b6, forward read cpg119b6.ft1a.//1.0:0:85:72//Z64426
- 20 F-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//1.1e-185:852:99//AF048693
- F-HEMBA1006173//Striatum enriched phosphatase=protein-tyrosine-phosphatase [rat, striata, mRNA, 2815 nt].//8.4e-50:642:73//S49400
- F-HEMBA1006182//Homo sapiens Chromosome 15q26.1 PAC clone pDJ10519, complete sequence.//1.4e-22:194:74//AC005318
- 25 F-HEMBA1006198
- F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//2.6e-175:836:98//AF070557
- F-HEMBA1006248//Pinctada fucata mRNA for insoluble protein, complete cds.//8.2e-05:359:61//D86074
- F-HEMBA1006252//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 531H16, WORKING DRAFT SEQUENCE.//0.98:397:58//AL031664
- 30 F-HEMBA1006253
- F-HEMBA1006259//HS\_2231\_A1\_D10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=19 Row=G, genomic survey sequence.//1.2e-11:233:68//AQ152722
- F-HEMBA1006268//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//5.2e-27:156:85//AC004673
- 35 F-HEMBA1006272//Human endogenous retrovirus gag mRNA.//8.1e-115:847:80//X72791
- F-HEMBA1006278//Mus musculus poly(A) polymerase V1 mRNA, complete cds.//2.1e-57:665:70//U58134
- F-HEMBA1006283
- 40 F-HEMBA1006284//Streptomyces fradiae tyllactone synthase, starter module and modules 1-7, (tylC) gene, complete cds.//9.6e-06:623:60//U78289
- F-HEMBA1006291//HS\_2208\_A1\_C03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=5 Row=E, genomic survey sequence.//1.2e-13:105:92//AQ091804
- F-HEMBA1006293//Sequence 8 from patent US 5721351.//5.6e-77:580:75//I89415
- F-HEMBA1006309//Caenorhabditis elegans cosmid F01F1.//1.1e-21:420:63//U13070
- 45 F-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//6.8e-120:748:85//AF076183
- F-HEMBA1006328//Homo sapiens fragile X mental retardation protein (FMR-1) gene (6 alternative splices), complete cds.//1.5e-46:485:73//L29074
- F-HEMBA1006334//HS-1051-B2-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 773 Col=2 Row=L, genomic survey sequence.//0.0032:61:91//B40563
- 50 F-HEMBA1006344//HS-1009-A2-B02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 331 Col=4 Row=C, genomic survey sequence.//3.3e-09:218:66//B31420
- F-HEMBA1006347//Drosophila melanogaster males-absent on the first (mof) gene, complete cds.//1.6e-31:484:68//U71219
- 55 F-HEMBA1006349//HS-1054-A1-G06-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 776 Col=11 Row=M, genomic survey sequence.//5.4e-15:95:100//B41671
- F-HEMBA1006359//Human ZNF43 mRNA.//1.4e-115:823:81//X59244
- F-HEMBA1006364//Mouse mRNA for transforming growth factor-beta2.//2.7e-10:247:71//X57413



- F-HEMBA1006377//Mus musculus chromosome 7, clone 19K5, complete sequence.//3.0e-57:401:81//AC002327  
F-HEMBA1006380//CIT-HSP-2172K18.TF CIT-HSP Homo sapiens genomic clone 2172K18, genomic survey sequence.//1.3e-110:525:99//B92570
- 5 F-HEMBA1006381//HS-1045-B2-F10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 828 Col=20 Row=L, genomic survey sequence.//4.4e-05:163:70//B37813  
F-HEMBA1006398//Homo sapiens 12q24.2 BAC RPC11-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.8e-62:370:86//AC004806  
F-HEMBA1006416//Homo sapiens chromosome 5, P1 clone 104F1F10 (LBNL H88), complete sequence.//3.7e-15:157:78//AC005179
- 10 F-HEMBA1006419//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055, complete sequence.//1.2e-39:752:63//AL022165  
F-HEMBA1006421//Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes.//2.4e-41:438:76//AF107885  
F-HEMBA1006424//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//0.027:293:64//AL031781
- 20 F-HEMBA1006426//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 292E10, WORKING DRAFT SEQUENCE.//1.7e-50:310:80//Z93930  
F-HEMBA1006438//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.051:440:59//X04465  
F-HEMBA1006445//Felis catus ras p21 (H-ras) mRNA, partial cds.//1.0:238:59//U62088
- 25 F-HEMBA1006446//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P6, WORKING DRAFT SEQUENCE.//2.4e-05:702:58//AL031749  
F-HEMBA1006461//Homo sapiens chromosome 19, cosmid R30676, complete sequence.//8.6e-55:409:83//AC004560  
F-HEMBA1006467//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//1.0:293:59//AC006120
- 30 F-HEMBA1006471//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.4e-05:731:59//AC004709  
F-HEMBA1006474//CIT-HSP-2017H3.TF CIT-HSP Homo sapiens genomic clone 2017H3, genomic survey sequence.//5.2e-60:435:83//B54247
- 35 F-HEMBA1006483//Homo sapiens chromosome 5, BAC clone 8e5 (LBNL H167), complete sequence.//2.9e-48:286:84//AC004752  
F-HEMBA1006485//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence.//0.96:283:59//AC006031  
F-HEMBA1006486//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.8e-14:259:67//AL022577
- 40 F-HEMBA1006489//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 467K16, WORKING DRAFT SEQUENCE.//6.6e-11:595:61//AL031283  
F-HEMBA1006492//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//0.0e-122:337:100//AC005828
- 50 F-HEMBA1006494//Homo sapiens chromosome 7qtel0 BAC E3, complete sequence.//3.8e-23:459:68//AF093117  
F-HEMBA1006497//HS\_3023\_B2\_H03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=6 Row=P, genomic survey sequence.//2.3e-81:433:95//AQ093846  
F-HEMBA1006502//H. sapiens 7SL repeat (clones 2-19b).//1.6e-13:86:87//X62364  
F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds.//2.3e-139:470:98//AB014566  
F-HEMBA1006521//Human BAC clone RG167B05 from 7q21, complete sequence.//4.3e-27:406:71//AC003991  
F-HEMBA1006530//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//2.9e-27:408:65//AL031650
- 55 F-HEMBA1006535//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.028:599:60//AL034557  
F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds.//1.4e-171:654:98//AF093419

- F-HEMBA1006546//Human DNA sequence from cosmid 232L22, between markers DXS366 and DXS87 on chromosome X contains ESTs glycerol kinase pseudogene.//3.8e-104:811.80//Z73986
- F-HEMBA1006559//Mus musculus PRAJA1 (Praja1) mRNA, complete cds.//4.8e-99:386:82//U06944
- 5 F-HEMBA1006562//Human fructose-1,6-biphosphatase (FBP1) gene, exon 1.//0.012:322:60//U21925
- F-HEMBA1006566//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0026:580:58//AC005504
- F-HEMBA1006569//Ovis aries beta actin mRNA, complete cds.//6.3e-08:231:70//U39357
- F-HEMBA1006579//CIT-HSP-2380A22.TR CIT-HSP Homo sapiens genomic clone 2380A22, genomic survey sequence.//0.036:250:62//AQ197107
- 10 F-HEMBA1006583//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.//1.0:225:63//AL021841
- F-HEMBA1006595//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE.//3.6e-50:689:69//AL022156
- F-HEMBA1006597//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.9e-42:253:84//AC004166
- 15 F-HEMBA1006612//RPC111-88F20.TJ RPC111 Homo sapiens genomic clone R-88F20, genomic survey sequence.//1.1e-51:266:98//AQ286726
- F-HEMBA1006617//HS\_2193\_B2\_H07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=14 Row=P, genomic survey sequence.//1.1e-59:413:85//AQ299685
- 20 F-HEMBA1006624//Human DNA sequence from clone 406A7 on chromosome 6q23-24. Contains three pseudogenes similar to Elongation Factor 1-Alpha (EF-1-ALPHA, Statin S1), 60S Acidic Ribosomal Protein P1 and NADH-Ubiquinone Oxidoreductase 15 kDa subunit, and part of the Microtubule Associated Protein E-MAP-115 gene. Contains ESTs, STSs and GSSs, complete sequence.//1.4e-35:257:89//AL023284
- F-HEMBA1006631//Homo sapiens Chromosome 11q23 PAC clone pDJ356d6, complete sequence.//9.6e-112:800:83//AC002036
- 25 F-HEMBA1006635//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P2, WORKING DRAFT SEQUENCE.//0.15:393:58//AL031745
- F-HEMBA1006639//Petromyzon marinus polyadenylate binding protein (PABP) mRNA, complete cds.//9.6e-15:318:68//AF032896
- 30 F-HEMBA1006643//Homo sapiens clone DJ0902E20, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.58:254:65//AC006148
- F-HEMBA1006648//Mus musculus integrin binding protein kinase mRNA, complete cds.//1.5e-37:108:88//U94479
- F-HEMBA1006652//Homo sapiens chromosome 5, BAC clone 343g16 (LBNL H180), complete sequence.//1.3e-154:671:96//AC005601
- 35 F-HEMBA1006653
- F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//5.2e-110:254:93//AC005189
- F-HEMBA1006665//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//1.4e-14:177:76//AC004554
- 40 F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56.//5.5e-15:122:90//Y12065
- F-HEMBA1006676//Homo sapiens chromosome 19, fosmid 37502, complete sequence.//0.098:218:63//AC004755
- F-HEMBA1006682//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 668J24, WORKING DRAFT SEQUENCE.//1.4e-05:719:57//AL034346
- 45 F-HEMBA1006695//Homo sapiens clone DJ0935K16, complete sequence.//3.1e-22:151:78//AC006011
- F-HEMBA1006696//CITBI-E1-2522D16.TF CITBI-E1 Homo sapiens genomic clone 2522D16, genomic survey sequence.//5.6e-17:324:66//AQ280738
- F-HEMBA1006708
- F-HEMBA1006709
- 50 F-HEMBA1006717//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.3e-08:136:79//AC005537
- F-HEMBA1006737//Homo sapiens chromosome 17, clone hRPC.269\_G\_24, complete sequence.//5.8e-162:497:98//AC005828
- F-HEMBA1006744//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//7.4e-48:320:87//AC004796
- 55 F-HEMBA1006754//Human DNA sequence from PAC 82J11 and cosmid U134E6 on chromosome Xq22. Contains NIK like and Thyroxin-binding globulin precursor (T4-binding globulin, TBG) genes, ESTs and STSs.//4.1e-129:804:85//Z83850

- F-HEMBA1006758//Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.//2.2e-162:766:99//AC005752
- F-HEMBA1006767//Human Xq28 cosmid U247A3 from LLOXNC01 X chromosome library, complete sequence.//1.2e-19:326:69//U73465
- 5 F-HEMBA1006779//Human DNA sequence from clone 80119 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//1.4e-103:355:87//AL022727
- F-HEMBA1006780//CIT-HSP-2359P7.TR CIT-HSP Homo sapiens genomic clone 2359P7, genomic survey sequence.//0.072:147:68//AQ077208
- 10 F-HEMBA1006789//nbxb0037113r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0037113r, genomic survey sequence.//0.00011:288:63//AQ290474
- F-HEMBA1006795//CIT-HSP-2307E3.TF CIT-HSP Homo sapiens genomic clone 2307E3, genomic survey sequence.//5.1e-80:420:96//AQ020511
- F-HEMBA1006796//Human clone 23803 mRNA, partial cds.//4.5e-06:202:68//U79298
- 15 F-HEMBA1006807//Homo sapiens mRNA for SPOP.//1.2e-66:651:73//AJ000644
- F-HEMBA1006821//Homo sapiens chromosome 17, clone hRPC.62\_O\_9, complete sequence.//6.0e-116:541:99//AC004797
- F-HEMBA1006824//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//0.40:159:66//AC004262
- F-HEMBA1006832//Homo sapiens (subclone 3\_g8 from P1 H25) DNA sequence, complete sequence.//1.8e-24:323:71//AC002196
- 20 F-HEMBA1006849//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 4/10.//0.15:403:60//AB020872
- F-HEMBA1006865//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence.//0.20:472:57//AE001369
- 25 F-HEMBA1006877//Mus musculus clone OST9241, genomic survey sequence.//3.4e-79:641:76//AF046757
- F-HEMBA1006885//HS\_2208\_B2\_G06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=12 Row=N, genomic survey sequence.//4.9e-18:206:76//AQ089246
- F-HEMBA1006900//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//5.4e-07:298:65//AL031321
- 30 F-HEMBA1006914//S. pombe chromosome II cosmid c16H5.//0.00040:194:66//AL022104
- F-HEMBA1006921//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//1.1e-174:813:99//AC006027
- F-HEMBA1006926//Caenorhabditis elegans cosmid ZK185.//0.0075:183:65//AF036704
- 35 F-HEMBA1006929//P.falciparum complete gene map of plastid-like DNA (IR-A).//4.0e-06:739:57//X95275
- F-HEMBA1006936
- F-HEMBA1006938//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P4, WORKING DRAFT SEQUENCE.//1.1e-05:733:57//AL031747
- F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.//1.3e-90:437:98//AJ010841
- 40 F-HEMBA1006949//Human DNA sequence from PAC 363L9 on chromosome X. contains STS and polymorphic CA repeat.//0.67:217:62//Z82205
- F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.6e-143:740:94//AF004828
- F-HEMBA1006976//cDNA encoding alpha 2 to 3 sialyltransferase.//2.8e-101:338:89//E06058
- 45 F-HEMBA1006993//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//7.1e-31:536:66//AC003071
- F-HEMBA1006996//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//9.5e-07:285:60//Z82209
- F-HEMBA1007002//Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence.//0.99:388:58//AC002328
- 50 F-HEMBA1007017//Sequence 3 from Patent WO94 16067.//0.96:220:62//A39358
- F-HEMBA1007018//G.gallus mRNA for dynein light chain-A.//1.3e-124:838:83//X79088
- F-HEMBA1007045
- F-HEMBA1007051//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//0.17:343:60//Z99281
- F-HEMBA1007052//Homo sapiens FSHD-associated repeat DNA, proximal region.//4.3e-67:659:74//U85056
- 55 F-HEMBA1007062//Tubulin gene.//1.0:113:67//A18572
- F-HEMBA1007066//HS\_3116\_A2\_A03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3116 Col=6 Row=A, genomic survey sequence.//0.80:214:62//AQ140467
- F-HEMBA1007073//Homo sapiens 12q13 PAC RPC1-1-316M24 (Roswell Park Cancer Institute Human PAC library)

complete sequence.//9.3e-54:519:68//AC004242

F-HEMBA1007078//CIT-HSP-2318N6.TF CIT-HSP Homo sapiens genomic clone 2318N6, genomic survey sequence.//8.7e-80:387:98//AQ044076

F-HEMBA1007080

F-HEMBA1007085//Streptomyces coelicolor cosmid 7A1.//3.5e-06:496:59//AL034447

F-HEMBA1007087//Plasmodium falciparum MAL3P6, complete sequence.//7.4e-07:553:56//Z98551

F-HEMBA1007112//HS\_2171\_A1\_B01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=1 Row=C, genomic survey sequence.//1.0:172:61//AQ091865

F-HEMBA1007113//Human DNA sequence from clone 1044017 on chromosome Xp11.3-11.4 Contains GSS and STS, complete sequence.//0.54:502:56//AL023875

F-HEMBA1007121//Caenorhabditis elegans cosmid ZK430.//1.4e-08:265:64//U42833

F-HEMBA1007129//CITBI-E1-2504A5.TF CITBI-E1 Homo sapiens genomic clone 2504A5, genomic survey sequence.//0.97:267:62//AQ264035

F-HEMBA1007147//HS\_3208\_A2\_C04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3208 Col=8 Row=E, genomic survey sequence.//9.1e-90:466:95//AQ176696

F-HEMBA1007149//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//6.0e-138:524:98//AC005239

F-HEMBA1007151//CITBI-E1-2522H6.TF CITBI-E1 Homo sapiens genomic clone 2522H6, genomic survey sequence.//2.0e-20:157:87//AQ280780

F-HEMBA1007174//Homo sapiens epsilon 2a mRNA, complete cds.//2.0e-62:318:97//AF062085

F-HEMBA1007178//Homo sapiens chromosome 12p13.3 clone RPC11-372B4, WORKING DRAFT SEQUENCE, 129 ordered pieces.//1.6e-21:205:80//AC005911

F-HEMBA1007194//HS\_3124\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence.//1.3e-11:87:96//AQ187492

F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds.//1.7e-156:478:98//D86987

F-HEMBA1007205//Homo sapiens chromosome 17, clone HRPCC837J1, complete sequence.//0.024:342:63//AC004223

F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds.//5.0e-176:839:98//AB018340

F-HEMBA1007243//Chinese hamster hpert mRNA, complete cds.//4.3e-58:687:68//J00060

F-HEMBA1007251//Rabbit troponin T messenger fragment (aa 49 to 129).//0.084:177:62//V00899

F-HEMBA1007256//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 328E19, WORKING DRAFT SEQUENCE.//1.3e-75:490:88//AL022240

F-HEMBA1007267//HS\_3218\_A1\_F07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=13 Row=K, genomic survey sequence.//2.9e-62:393:87//AQ181128

F-HEMBA1007273//CIT-HSP-2171B10.TF CIT-HSP Homo sapiens genomic clone 2171B10, genomic survey sequence.//1.1e-63:314:99//B95401

F-HEMBA1007279//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.//3.1e-31:401:72//AC004638

F-HEMBA1007281//HS\_3115\_A1\_A11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3115 Col=21 Row=A, genomic survey sequence.//5.0e-70:372:96//AQ186691

F-HEMBA1007288//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence.//1.2e-152:727:98//AL031003

F-HEMBA1007300//Canis familiaris PDE5 mRNA for 3',5'-Cyclic GMP Phosphodiesterase, complete cds.//2.1e-21:542:63//AB008467

F-HEMBA1007301//COL1A1=type I collagen pro alpha 1(I) chain propeptide (3' region) [human, fetal cells 86-237, 86-146, 88-251, mRNA Partial Mutant, 855 nt].//1.7e-08:388:61//S64596

F-HEMBA1007319//Genomic sequence from Mouse 9, complete sequence.//6.0e-84:390:75//AC000399

F-HEMBA1007320

F-HEMBA1007322//Homo sapiens BAC clone RG118E13 from 7p15-p21, complete sequence.//0.091:260:64//AC004485

F-HEMBA1007327//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.12:472:59//AC005140

F-HEMBA1007341//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//1.5e-18:408:64//AC006120

F-HEMBA1007342//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//8.7e-25:500:62//AC005377

F-HEMBA1007347//Homo sapiens chromosome 5, BAC clone 7g12 (LBNI H126), complete sequence.//0.75:269:61//AC005738

- F-HEM BB1000005//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//5.0e-05:441:60//AC004617
- F-HEM BB1000008//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//1.0e-44:417:77//AC004491
- 5 F-HEM BB1000018//HS\_2179\_B2\_E04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=8 Row=J, genomic survey sequence.//0.012:87:77//AQ023250
- F-HEM BB1000024//Human DNA sequence from PAC 106120 on chromosome 22q12-qter contains NADH pseudogene, ESTs, STS //8.1e-11:461:61//Z81369
- 10 F-HEM BB1000025//CIT-HSP-2348F3.TR CIT-HSP Homo sapiens genomic clone 2348F3, genomic survey sequence.//0.96:198:62//AQ062938
- F-HEM BB1000030//Homo sapiens DNA sequence from PAC 32F7 on chromosome X. Contains NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 3, ESTs.//0.00049:276:64//AL009173
- F-HEM BB1000036//H. sapiens chromosome 22 CpG island DNA genomic MseI fragment, clone 302e2, reverse read 302e2.r.//0.0057:66:81//Z79857
- 15 F-HEM BB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//1.9e-100:450:98//AF084928
- F-HEM BB1000039//HS\_2167\_B1\_F12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2167 Col=23 Row=L, genomic survey sequence.//0.022:108:69//AQ092404
- F-HEM BB1000044//Borrelia burgdorferi (section 50 of 70) of the complete genome.//1.0e-07:486:61//AE001164
- 20 F-HEM BB1000048//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.3e-05:585:58//AC005507
- F-HEM BB1000050//Homo sapiens DNA sequence from clone 501N12 on chromosome 6p22.1-22.3 Contains a gene almost identical to four genes of unknown function, a pseudogene, three (pseudo?) genes similar to genes of unknown function, an unknown gene similar to a rat EST, a PX19 LIKE pseudogene and another unknown gene.
- 25 Contains ESTs, STSs and GSSs, complete sequence.//5.8e-38:549:67//AL022170
- F-HEM BB1000054//Homo sapiens Xp22 PAC RPC11-167A22 (from Roswell Park Cancer Center) complete sequence.//7.0e-98:328:83//AC002349
- F-HEM BB1000055//Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, cosmid clone: TY2F10, WORKING DRAFT SEQUENCE.//3.7e-05:600:58//AB000880
- 30 F-HEM BB1000059//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//1.3e-48:472:78//AC005096
- F-HEM BB1000083
- F-HEM BB1000089//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.0036:679:56//AL031744
- 35 F-HEM BB1000099//Homo sapiens chromosome 18 BAC RPC11-128D14 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.1e-15:312:68//AC005909
- F-HEM BB1000103//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.0e-37:316:74//AC006210
- 40 F-HEM BB1000113//Homo sapiens chromosome 21q22.3 cosmid Q11M15, complete sequence.//3.1e-25:259:76//AF045450
- F-HEM BB1000119//Homo sapiens ASMTL gene.//1.2e-137:654:98//Y15521
- F-HEM BB1000136//Mycobacterium tuberculosis H37Rv complete genome; segment 127/162.//0.59:217:66//Z74697
- 45 F-HEM BB1000141//Homo sapiens DNA from chromosome 19q13.1 cosmid f14121 containing ATP4A and GADPH-2 genes, genomic sequence.//8.4e-31:113:88//AD000090
- F-HEM BB1000144//Human BAC clone RG114A06 from 7q31, complete sequence.//4.4e-58:339:87//AC002542
- F-HEM BB1000173//Homo sapiens 12q24 BAC RPC11-162P23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//9.4e-160:562:93//AC002996
- 50 F-HEM BB1000175
- F-HEM BB1000198//HS\_3071\_A2\_A10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=20 Row=A, genomic survey sequence.//0.99:261:61//AQ137388
- F-HEM BB1000215//Homo sapiens chromosome 17, clone hRPK481\_C\_4, complete sequence.//6.7e-17:138:86//AC005839
- 55 F-HEM BB1000217//Arabidopsis thaliana ubiquitin activating enzyme (UBA1) gene, complete cds.//0.00083:287:60//U80808
- F-HEM BB1000218//Caenorhabditis elegans cosmid C52A11, complete sequence.//0.90:337:56//Z46792
- F-HEM BB1000226//Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island.//1.7e-90:175:92//Z69890

- F-HEMBB1000240//Human G-protein-coupled inwardly rectifying potassium channel (KCNJ3) gene, polymorphic repeat sequence.//0.16:171:62//U07918
- F-HEMBB1000244//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.8e-08:355:63//AC005522
- 5 F-HEMBB1000250//Homo sapiens protein associated with Myc mRNA, complete cds.//6.6e-155:735:98//AF075587
- F-HEMBB1000258//Human adenosine monophosphate deaminase 1 (AMPD1) gene, exons 1-16.//0.58:396:59//M98818
- 10 F-HEMBB1000264//Human clone C3 CHL1 protein (CHLR1) mRNA, alternatively spliced, complete cds.//4.4e-32:100:100//U75968
- F-HEMBB1000266//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence.//3.8e-16:176:78//AC004470
- F-HEMBB1000272//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence.//0.011:379:58//AE001369
- 15 F-HEMBB1000274//Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSAI project).//0.92:272:61//AL022580
- F-HEMBB1000284//Human Xp22 BAC CT-28515 (from CalTech/Research Genetics), PAC RPC11-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//0.00071:568:57//AC002366
- 20 F-HEMBB1000307//Human DNA sequence from PAC 29K1 on chromosome 6p21.3-22.2. Contains glutathione peroxidase-like, zinc finger, ESTs, mRNA, STS, tRNAs, olfactory receptor pseudogene.//3.0e-13:439:65//Z98745
- F-HEMBB1000312//Homo sapiens clone GS051M12, complete sequence.//0.031:252:65//AC005007
- F-HEMBB1000317//Fugu rubripes GSS sequence, clone 060J22aE10, genomic survey sequence.//0.00033:173:65//AL026242
- 25 F-HEMBB1000318//HS\_3244\_B2\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=20 Row=P, genomic survey sequence.//3.9e-85:438:95//AQ252951
- F-HEMBB1000335//Homo sapiens chromosome 18, clone hRPK.24\_A\_23, complete sequence.//0.63:285:61//AC005968
- F-HEMBB1000336
- 30 F-HEMBB1000337//Homo sapiens chromosome 4 clone B208G5 map 4q25, complete sequence.//0.0014:309:64//AC004051
- F-HEMBB1000338//HS\_3108\_A2\_F07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=14 Row=K, genomic survey sequence.//3.8e-09:331:63//AQ140356
- F-HEMBB1000339//Homo sapiens 12q24 PAC RPC11-46F2 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.2e-52:295:77//AC002351
- 35 F-HEMBB1000341
- F-HEMBB1000343//Plasmodium falciparum MAL3P3, complete sequence.//0.00081:397:61//Z98547
- F-HEMBB1000354//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudo-gene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//9.1e-34:596:66//AL020989
- 40 F-HEMBB1000369//Genomic sequence from Human 17, complete sequence.//0.012:298:60//AC002090
- F-HEMBB1000374//Human Xp22 contig of 3 PACS (R7-39D12, R7-134G1, R7-185L21) from the Roswell Park Cancer Institute, complete sequence.//9.3e-69:294:89//U96409
- F-HEMBB1000376//Human DNA sequence from clone 751H9 on chromosome 6q13. Contains part of an unknown gene, ESTs, STSs and GSSs, complete sequence.//3.5e-54:352:88//AL034377
- 45 F-HEMBB1000391//Trichostema roseum internal transcribed spacer 1, 5.8S ribosomal RNA gene; and internal transcribed spacer 2, complete sequence.//0.011:168:67//U51982
- F-HEMBB1000399//Homo sapiens Rad17-like protein (RAD17) mRNA, complete cds.//2.6e-163:762:98//AF076838
- F-HEMBB1000402//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1, 2, and 3, complete sequence.//7.7e-15:466:63//AC002368
- 50 F-HEMBB1000404//Homo sapiens mRNA for myosin-IXA.//3.5e-65:324:98//AJ001714
- F-HEMBB1000420//244Kb Contig from Human Chromosome 11p15.5 spanning D11S1 through D11S25, complete sequence.//0.013:399:62//AC001228
- F-HEMBB1000434//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//6.1e-83:571:84//AC004263
- 55 F-HEMBB1000438//RPC11-21E14, TP RPC11-11 Homo sapiens genomic clone RPC11-21E14, genomic survey sequence.//0.0030:295:63//B83110
- F-HEMBB1000441//Homo sapiens Chromosome 22q12 Cosmid Clone l47g11, complete sequence.//2.5e-33:372:72//AC000035

- F-HEM BB1000449//Human DNA sequence from PAC 296K21 on chromosome X contains cytochrome c, delta-aminolevulinic synthase (erythroid); 5-aminolevulinic acid synthase.(EC 2.3.1.37). 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//1.3e-51:534:72//Z83821
- 5 F-HEM BB1000455//Saccharomyces cerevisiae mitochondrion origin of replication (oriF) and oli1 gene, complete cds.//0.016:522:58//L36899
- F-HEM BB1000472
- F-HEM BB1000480
- F-HEM BB1000487//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 128O3, WORKING DRAFT SEQUENCE.//0.00013:314:64//Z98742
- 10 F-HEM BB1000490//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//4.1e-110:529:98//AL034423
- F-HEM BB1000491//Plasmodium falciparum chromosome 2, section 25 of 73 of the complete sequence.//0.10:187:65//AE001388
- 15 F-HEM BB1000493//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNFZL1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.7e-06:637:58//AL022577
- F-HEM BB1000510//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence.//3.1e-96:737:81//AC005553
- 20 F-HEM BB1000518//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.00014:163:68//AC004676
- F-HEM BB1000523//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-105, complete sequence.//0.41:349:56//AL010212
- F-HEM BB1000530//H. sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus.//6.6e-37:138:96//Y11710
- 25 F-HEM BB1000550//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//3.9e-56:683:71//AB020860
- F-HEM BB1000554//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* WORKING DRAFT SEQUENCE.//2.2e-51:282:84//AJ011929
- 30 F-HEM BB1000556//Homo sapiens mRNA for KIAA0750 protein, complete cds.//6.1e-32:537:65//AB018293
- F-HEM BB1000564
- F-HEM BB1000573//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//8.2e-33:268:73//AC005077
- 35 F-HEM BB1000575//Human DNA sequence from clone 323M22 on chromosome 22q13.1-13.2. Contains the 5' part of the human ortholog of chicken P52 and mouse H74, and a novel gene coding for a protein similar to KIAA0173 and worm Tubulin Tyrosine Ligase. Contains ESTs, STSs, GSSs, genomic marker D22S418 and putative CpG islands, complete sequence.//5.8e-47:734:66//AL022476
- F-HEM BB1000586//H. sapiens highly polymorphic microsatellite DNA.//0.030:147:67//X79883
- 40 F-HEM BB1000589//Homo sapiens Chromosome 16 BAC clone CIT967SK-A-279B10, complete sequence.//6.3e-41:278:83//AC002300
- F-HEM BB1000591//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//1.1e-182:871:98//AC005184
- F-HEM BB1000592//Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #19.//0.012:185:64//AF009074
- 45 F-HEM BB1000593//Homo sapiens chromosome 7q22 sequence, complete sequence.//1.2e-131:353:93//AF053356
- F-HEM BB1000598//Homo sapiens 12p13.3 BAC RPC13-488H23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//9.1e-58:600:72//AC006207
- F-HEM BB1000623//cDNA encoding Coliulus manganese peroxidase.//0.89:284:62//E12284
- 50 F-HEM BB1000630//Mus musculus clone NSAT47 nonsatellite RNA sequence.//1.9e-15:129:87//U26231
- F-HEM BB1000631//Sequence 26 from patent US 5708157.//3.2e-27:180:88//B00057
- F-HEM BB1000632//Human mRNA for KIAA0351 gene, complete cds.//1.6e-48:811:65//AB002349
- F-HEM BB1000637//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.1e-58:649:73//AC005478
- 55 F-HEM BB1000638//HS\_3051\_A1\_G01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=M, genomic survey sequence.//0.0032:497:56//AQ155234
- F-HEM BB1000643//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.4e-50:791:68//AC005077

- F-HEM BB1000649//Homo sapiens Chromosome 16 BAC clone CIT987-SK502C10, complete sequence.//5.2e-64:775.69//AC003009
- F-HEM BB1000652//Homo sapiens chromosome 10 clone CRI-JC2048 map 10q22.1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.7e-52:334.89//AC006186
- 5 F-HEM BB1000665//Human DNA sequence from clone 452M16 on chromosome Xq21.1-21.33 Contains capping protein alpha subunit isoform 1 pseudogene, STS, GSS, and CA repeat, complete sequence.//0.0062:426.60//AL024493
- F-HEM BB1000671//Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG island.//9.6e-95:399.78//Z84488
- 10 F-HEM BB1000673//HS\_3039\_A2\_C08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=16 Row=E, genomic survey sequence.//3.8e-50:293.92//AQ155121
- F-HEM BB1000684//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 222C13, WORKING DRAFT SEQUENCE.//8.0e-65 :282.83//Z93241
- F-HEM BB1000693//Homo sapiens neuronan1 mRNA, complete cds.//1.6e-118:575.97//AF040723
- 15 F-HEM BB1000705//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//8.6e-07:251.61//AC005507
- F-HEM BB1000706//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 153G14, WORKING DRAFT SEQUENCE.//2.9e-20:434.64//AL031118
- F-HEM BB1000709//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 994L9, WORKING DRAFT SEQUENCE.//0.26:184.65//AL034554
- 20 F-HEM BB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//1.8e-129:692.93//U53475
- F-HEM BB1000726//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//2.7e-40:304:80//U91321
- F-HEM BB1000738//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence.//8.9e-35:582.63//AF011889
- 25 F-HEM BB1000749//Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE, 9 unordered pieces.//6.2e-46:262.89//AC005849
- F-HEM BB1000763//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE.//1.6e-99:316.98//AL034405
- 30 F-HEM BB1000770//Human DNA sequence from clone 801I9 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//0.044:325.60//AL022727
- F-HEM BB1000774
- F-HEM BB1000781//Sequence 3 from patent US 5753446.//1.2e-92:599.86//AR008277
- 35 F-HEM BB1000789//Homo sapiens mRNA for KIAA0677 protein, complete cds.//9.3e-64:672.71//AB014577
- F-HEM BB1000790//Homo sapiens 12q13.1 PAC RPC1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.4e-41:460.74//AC004801
- F-HEM BB1000794//HS\_3034\_B2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3034 Col=24 Row=H, genomic survey sequence.//1.8e-74:378.97//AQ117099
- 40 F-HEM BB1000807//H. sapiens CpG island DNA genomic Mse1 fragment, clone 39d7, reverse read cpg39d7.rt1a.//8.5e-14:95.97//Z58412
- F-HEM BB1000810//H. sapiens chromosome 22 CpG island DNA genomic Mse1 fragment, clone 303a8, complete read.//3.2e-05:138.71//Z79983
- F-HEM BB1000821//HS\_2168\_B1\_A12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=23 Row=B, genomic survey sequence.//0.85 :208.60//AQ086361
- 45 F-HEM BB1000822//Human BAC clone GS113H23 from 5p15.2, complete sequence.//3.0e-06:361.60//AC003015
- F-HEM BB1000826//Human BAC clone RG180F08 from 7q31, complete sequence.//1.1e-27:360.69//AC002431
- F-HEM BB1000827
- F-HEM BB1000831
- 50 F-HEM BB1000835//Human DNA sequence from clone 4514 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//0.00098:234.63//AL023581
- F-HEM BB1000840//Human Chromosome 11 Cosmid cSRL97a6, complete sequence.//4.5e-61:328.79//U73649
- F-HEM BB1000848//Homo sapiens DNA sequence from PAC 206D15 on chromosome 1q24. Contains a Reduced Folate Carrier protein (RFC) LIKE gene, a mitochondrial ATP Synthetase protein 8 (ATP8, MTATP8) LIKE pseudogene, an unknown gene and the last exon of the JEM1 gene coding for the Basic-Leucine Zipper nuclear factor JEM-1. Contains ESTs, an STS and a BAC end sequence (GSS), complete sequence.//9.7e-144:809.87//AL021068
- 55 F-HEM BB1000852//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING



DRAFT SEQUENCE, 9 unordered pieces.//0.12:492:58//AC004157  
 F-HEMBB1000870//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING  
 DRAFT SEQUENCE, 9 unordered pieces.//0.0024:212:67//AC004157  
 F-HEMBB1000876//Homo sapiens ELISC-1 mRNA, partial cds.//1.5e-32:200:94//AF085351  
 5 F-HEMBB1000883//HS\_3065\_B2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3065 Col=8 Row=F, genomic survey sequence.//0.0017:152:68//AQ137687  
 F-HEMBB1000887  
 F-HEMBB1000888//CIT-HSP-2329A10.TR CIT-HSP Homo sapiens genomic clone 2329A10, genomic survey sequence.//1.5e-31:172:98//AQ044369  
 10 F-HEMBB1000890  
 F-HEMBB1000893//Plasmodium falciparum MAL3P2, complete sequence.//9.5e-06:768:56//AL034558  
 F-HEMBB1000908//Homo sapiens clone DJ1119N05, complete sequence.//4.5e-21:199:82//AC004968  
 F-HEMBB1000910//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING  
 DRAFT SEQUENCE.//0.72:366:59//AL034557  
 15 F-HEMBB1000913//HS\_3078\_B1\_C02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=3 Row=F, genomic survey sequence.//9.9e-12:221:63//AQ144507  
 F-HEMBB1000915//Homo sapiens DNA for (CGG)<sub>n</sub> trinucleotide repeat region, isolate P4.//1.2e-49:252:99//AJ001215  
 F-HEMBB1000917//Homo sapiens chromosome 5, P1 clone 254f11 (LBNL H62), complete sequence.//2.3e-42:316:76//AC006077  
 20 F-HEMBB1000927//Human BDR-2 mRNA for hippocalcin, complete cds.//3.6e-30:528:65/D16593  
 F-HEMBB1000947//CpG0856B CplOWAGDNA1 Cryptosporidium parvum genomic, genomic survey sequence.//0.81:262:62//AQ254493  
 F-HEMBB1000959//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 346O6, WORKING  
 DRAFT SEQUENCE.//1.2e-43:454:75//Z84487  
 25 F-HEMBB1000973//Mus musculus schlafen2 (Sfn2) mRNA, complete cds.//8.3e-42:458:72//AF099973  
 F-HEMBB1000975//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence.//0.98:196:63//AB005234  
 F-HEMBB1000981  
 30 F-HEMBB1000985//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//2.9e-06:566:57//AC004476  
 F-HEMBB1000991//Human DNA sequence from PAC 238J17 on chromosome 6q22. Contains EST and STS.//0.099:391:57//Z98753  
 F-HEMBB1000996//Human DNA sequence from BAC 999D10 on chromosome 22q13.3. Contains two BAC end-sequences (GSSs).//6.2e-33:227:80//Z94802  
 35 F-HEMBB1001004  
 F-HEMBB1001008//Human Chromosome 16 BAC clone CIT987SK-A-951C11, complete sequence.//4.0e-13:164:79//AC002551  
 F-HEMBB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.//7.5e-13:229:69//AC002310  
 40 F-HEMBB1001014//Homo sapiens chromosome 16, BAC clone 375G12 (LANL), complete sequence.//0.32:474:58//AC005751  
 F-HEMBB1001020//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//2.6e-39:218:80//AF069291  
 45 F-HEMBB1001024//Homo sapiens BAC clone 393i22 from 8q21, complete sequence.//5.3e-05:656:59//AF070717  
 F-HEMBB1001037//CIT-HSP-2358K16.TF CIT-HSP Homo sapiens genomic clone 2358K16, genomic survey sequence.//6.6e-05:228:64//AQ080539  
 F-HEMBB1001047//Homo sapiens cosmid Qc14E2, Qc12H12, Qc11F9, Qc10G9, LA1733 and Qc17B8 from Xq28, complete sequence.//4.0e-27:385:71//U82671  
 50 F-HEMBB1001051//H. sapiens mRNA for FAN protein.//1.2e-27:160:98//X96586  
 F-HEMBB1001056//Homo sapiens clone DJ0953A04, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.3e-89:180:91//AC006014  
 F-HEMBB1001058//Homo sapiens 3p22-8 PAC RPC14-736H12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-41:468:74//AC006060  
 55 F-HEMBB1001060//Human Tigger1 transposable element, complete consensus sequence.//4.3e-122:785:86//U49973  
 F-HEMBB1001063//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 523G1, WORKING  
 DRAFT SEQUENCE.//7.1e-162:770:99//AL034375

- F-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//3.1e-146:736:95//AF034803
- F-HEM BB1001096//Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene, partial cds.//0.00088:690:57//AF008210
- 5 F-HEM BB1001102//Homo sapiens huntingtin interacting protein HYPH mRNA, partial cds.//2.1e-76:368:99//AF049612
- F-HEM BB1001105//CIT-HSP-2185N1.TR CIT-HSP Homo sapiens genomic clone 2185N1, genomic survey sequence.//1.0e-09:136:76//AQ002987
- 10 F-HEM BB1001112//Rattus rattus sec61 homologue mRNA, complete cds.//1.0e-108:909:76//M96630
- F-HEM BB1001114//Homo sapiens chromosome 17, clone hRPK.795\_F\_17, complete sequence.//17.0e-07:459:59//AC005284
- F-HEM BB1001117//HS\_2178\_B1\_E12\_MR CIT Approved-Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=23 Row=J, genomic survey sequence.//7.8e-50:331:86//AQ068244
- 15 F-HEM BB1001119//Human collagen type XII alpha-1 precursor (COL12A1) mRNA, complete cds.//1.6e-25:150:98//U73778
- F-HEM BB1001126
- F-HEM BB1001133//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//2.8e-24:228:80//AC004673
- F-HEM BB1001137
- 20 F-HEM BB1001142//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//1.0e-40:231:76//AC004617
- F-HEM BB1001151//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//2.9e-47:640:67//AF015264
- F-HEM BB1001153//CIT-HSP-2359K11.TR CIT-HSP Homo sapiens genomic clone 2359K11, genomic survey sequence.//0.76:136:67//AQ075724
- 25 F-HEM BB1001169//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//9.9e-63:259:79//AL008712
- F-HEM BB1001175//Human mRNA for ankyrin motif, complete cds.//2.2e-34:509:66//D78334
- F-HEM BB1001177//CIT-HSP-2321N17.TR CIT-HSP Homo sapiens genomic clone 2321N17, genomic survey sequence.//5.9e-27:320:75//AQ036473
- 30 F-HEM BB1001182//RPC111-30J5.TV RPC11-11-30J5, genomic survey sequence.//5.7e-06:62:96//B85188
- F-HEM BB1001199
- 35 F-HEM BB1001208//HS\_2026\_B1\_C07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=13 Row=F, genomic survey sequence.//0.00018:134:70//AQ229237
- F-HEM BB1001209//CITBI-E1-2521F23.TF CITBI-E1 Homo sapiens genomic clone 2521F23, genomic survey sequence.//1.4e-95:464:98//AQ278357
- F-HEM BB1001210//HS\_3102\_A2\_F09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3102 Col=18 Row=K, genomic survey sequence.//2.6e-90:446:98//AQ119196
- 40 F-HEM BB1001218//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796F18, WORKING DRAFT SEQUENCE.//1.0e-31:315:72//AL031291
- F-HEM BB1001221//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.7e-17:770:59//AC005504
- F-HEM BB1001234//H.sapiens CpG island DNA genomic MseI fragment, clone 39f9, forward read cp939f9.ft1e//4.0e-30:171:97//Z65435
- 45 F-HEM BB1001242//Homo sapiens mRNA for LAK-1, complete cds.//3.8e-30:458:67//AB005754
- F-HEM BB1001249//CIT-HSP-2375N19.TF CIT-HSP Homo sapiens genomic clone 2375N19, genomic survey sequence.//0.0076:250:63//AQ109087
- F-HEM BB1001253//Homo sapiens genomic DNA, chromosome 21q11.1, segment 3/28, WORKING DRAFT SEQUENCE.//0.0097:89:80//AP000032
- 50 F-HEM BB1001254//CIT-HSP-2320E5.TF CIT-HSP Homo sapiens genomic clone 2320E5, genomic survey sequence.//3.7e-54:284:97//AQ037173
- F-HEM BB1001267//Homo sapiens chromosome 17, clone hRPK.488\_L\_1, complete sequence.//3.5e-30:236:78//AC005303
- 55 F-HEM BB1001271//HS\_3011\_A1\_G02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3011 Col=3 Row=M, genomic survey sequence.//5.2e-07:364:62//AQ214217
- F-HEM BB1001282//CIT-HSP-2356J20.TF CIT-HSP Homo sapiens genomic clone 2356J20; genomic survey sequence.//1.8e-16:109:97//AQ060969

- F-HEM BB1001288//R. norvegicus mRNA for gephyrin.//3.4e-18:194:77//X66366  
 F-HEM BB1001289//Genomic sequence from Human 9q34, complete sequence.//4.8e-66:434:74//AC000387  
 F-HEM BB1001294//HS\_3039\_B1\_D01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=1 Row=H, genomic survey sequence.//2.0e-90:437:99//AQ155035
- 5 F-HEM BB1001302  
 F-HEM BB1001304//CIT-HSP-2053E15.TF CIT-HSP Homo sapiens genomic clone 2053E15, genomic survey sequence.//2.2e-07:370:61//B69144  
 F-HEM BB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//5.7e-116:663:85//U92703
- 10 F-HEM BB1001315//Homo sapiens chromosome 10 clone LA10NC01\_40\_G\_3 map 10q26.1-10q26.2, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.5e-33:328:77//AC006096  
 F-HEM BB1001317//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.4e-122:680:91//AC006210  
 F-HEM BB1001326//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.8e-09:518:60//AC004129
- 15 F-HEM BB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain: BALB/c.//3.7e-56:458:79//D63850  
 F-HEM BB1001335//HS\_3055\_A1\_H10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=19 Row=O, genomic survey sequence.//1.0:222:63//AQ147384
- 20 F-HEM BB1001337//Human PAC clone DJ0093103 from Xq23, complete sequence.//1.0e-74:319:85//AC003983  
 F-HEM BB1001339//Homo sapiens FSHD-associated repeat DNA, proximal region.//4.0e-135:856:87//U85056  
 F-HEM BB1001346//Human familial Alzheimer's disease (STM2) gene, complete cds.//3.3e-44:481:74//U50871  
 F-HEM BB1001348//Homo sapiens BAC clone NH0491B03 from 7p21-p15, complete sequence.//1.8e-17:210:73//AC006041
- 25 F-HEM BB1001356//Homo sapiens clone RG252P22, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:386:59//AC005079  
 F-HEM BB1001364//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//0.97:349:61//AC004662  
 F-HEM BB1001366//Homo sapiens chromosome 10 clone CIT987SK-1188I5 map 10p11.2-10p12.1, complete sequence.//5.5e-161:766:98//AC005876
- 30 F-HEM BB1001367//Homo sapiens chromosome 17, clone hRPC.906\_A\_24, complete sequence.//3.0e-55:510:76//AC004408  
 F-HEM BB1001369//Homo sapiens BAC clone RG163K11 from 7q31, complete sequence.//0.048:244:64//AC005192
- 35 F-HEM BB1001380//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//2.5e-26:257:78//AC006204  
 F-HEM BB1001384//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//5.1e-99:571:89//AF071314  
 F-HEM BB1001387//Leishmania tarentolae mitochondrial 12S ribosomal RNA gene.//7.1e-05:546:58//X02354
- 40 F-HEM BB1001394//Homo sapiens BAC clone GS421I03 from Xq25-q26, complete sequence.//4.0e-129:788:88//AC005023  
 F-HEM BB1001410//Homo sapiens wbscr1 (WBSR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//4.8e-11:632:59//AF045555  
 F-HEM BB1001424//Mus musculus Chromosome 4 BAC clone BacB6, complete sequence.//0.0012:435:59//AC003019
- 45 F-HEM BB1001426//Homo sapiens clone DJ0736H05, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.8e-17:360:64//AC005482  
 F-HEM BB1001429//leucine aminopeptidase [cattle, kidney, mRNA, 2056 nt].//4.1e-114:668:88//S56367  
 F-HEM BB1001436//Homo sapiens FUT2 gene, intron 1, complete sequence.//2.3e-37:438:74//AB000931
- 50 F-HEM BB1001443//Bos taurus pyruvate dehydrogenase phosphatase mRNA, complete cds.//9.1e-92:550:88//L18966  
 F-HEM BB1001449//Homo sapiens chromosome 5, PAC clone 228g9 (LBNL H142), complete sequence.//0.00024:385:62//AC004768  
 F-HEM BB1001454//Homo sapiens chromosome 19, cosmid R34169, complete sequence.//0.84:577:57//AC005790
- 55 F-HEM BB1001458//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//8.0e-40:377:78//AC000382  
 F-HEM BB1001463//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//0.011:482:

- 59//AF001549  
F-HEM BB1001464//Human chromosome 16p13 BAC clone CIT987SK-3H8 complete sequence.//0.019:263.61//U91320
- 5 F-HEM BB1001482//Rattus norvegicus Olf-1/EBF associated Zn finger protein Roaz mRNA, alternatively spliced form, complete cds.//1.0e-30:521.66//U92564  
F-HEM BB1001500//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.3e-31:479.71//AC004873  
F-HEM BB1001521//Homo sapiens clone RG269P13, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.7e-51:680.70//AC005080
- 10 F-HEM BB1001527  
F-HEM BB1001531//Homo sapiens Chromosome 22q11.2 Cosmid Clone 89h In DGCR Region, complete sequence.//1.3e-79:696.79//AC000089  
F-HEM BB1001535//O. aries DNA for polymorphic marker 'OVINRA01' (339 bp).//0.00034:217.62//X89268  
F-HEM BB1001536//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//0.54:266.60//AC004548
- 15 F-HEM BB1001537//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//4.6e-25:784.61//AC004262  
F-HEM BB1001555//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//6.9e-50:213.80//AC004605
- 20 F-HEM BB1001562//Homo sapiens clone NH0523H20, complete sequence.//0.46:269.60//AC005041  
F-HEM BB1001564//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmalpin, ESTs and GSSs, complete sequence.//1.7e-107:620.83//AL020989  
F-HEM BB1001565//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//2.4e-50:734.67//AC004003
- 25 F-HEM BB1001585//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//1.4e-166:816.97//AL031677  
F-HEM BB1001586  
F-HEM BB1001588//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.6e-21:419.65//AC005261
- 30 F-HEM BB1001603  
F-HEM BB1001618//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//4.5e-29:422.72//Z98289
- 35 F-HEM BB1001619//HS\_3079\_B1\_A04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079 Col=7 Row=B, genomic survey sequence.//0.0010:77.79//AQ123388  
F-HEM BB1001630//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-12:667.59//AC005089
- 40 F-HEM BB1001635//Plasmodium falciparum MAL3P7, complete sequence.//3.8e-05:475.57//AL034559  
F-HEM BB1001637//Homo sapiens DNA sequence from PAC 934G17 on chromosome 1p36.21. Contains the alternatively spliced CLCN6 gene for chloride channel proteins CLC-6A (KIAA0046) -B, -C and -D, the alternatively spliced NPFA gene coding for Atrial Natriuretic Factor ANF precursor (Atrial Natriuretic peptide ANP, Prepronatriuretin), the NPPB gene for Brain Natriuretic Protein BNP, and a pseudogene similar to SBF1 (and other Myotubularin-related protein genes). Contains ESTs, STSs and the genomic marker D1S2740, complete sequence.//9.2e-13:168.76//AL021155
- 45 F-HEM BB1001641//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence.//0.00097:721.58//AB006702  
F-HEM BB1001653//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//0.15:276.63//AC002038
- 50 F-HEM BB1001665//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.43:393.61//L14320  
F-HEM BB1001668//F16C15-T7 IGf Arabidopsis thaliana genomic clone F16C15, genomic survey sequence.//0.040:275.60//B12308
- 55 F-HEM BB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//7.2e-171:803.98//AB014546  
F-HEM BB1001684//Sequence 1 from patent US 5700927.//7.5e-124:883.81//B86429  
F-HEM BB1001685//CIT-HSP-2287O9.TF CIT-HSP Homo sapiens genomic clone 2287O9, genomic survey sequence.//2.3e-34:191.97//B99261  
F-HEM BB1001695//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding

- exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (*Drosophila*) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STss, GSSs, and a putative CpG island, complete sequence.//0.0091:334:63//AL0009178
- 5 F-HEMBB1001704//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STss, GSSs and genomic marker DXS8098, complete sequence.//1.2e-17:144:87//AL023575  
F-HEMBB1001706  
F-HEMBB1001707//Guinea pig CD19 mRNA, complete cds.//0.57:232:62//M62543  
F-HEMBB1001711//Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & amp; tRNA-Met genes.//1.1e-13:723:58//AJ223323
- 10 F-HEMBB1001735//Human PAC clone DJ0596009 from 7p15, complete sequence.//1.3e-36:427:73//AC003074  
F-HEMBB1001736//S. pombe chromosome II cosmid c4B4.//0.0085:479:57//AL023706  
F-HEMBB1001747//Homo sapiens PAC clone DJ1002N02 from 7p21-p22, complete sequence.//4.0e-112:532:84//AC005376
- 15 F-HEMBB1001749//Homo sapiens chromosome 17, clone hRPK.259\_G\_18, complete sequence.//1.3e-98:395:82//AC005829  
F-HEMBB1001753//S. maximus repeat region, 342bp.//4.2e-11:69:85//Z78099  
F-HEMBB1001756//Homo sapiens full-length insert cDNA clone ZD86A11.//0.0015:302:62//AF088064  
F-HEMBB1001760//P. falciparum complete gene map of plastid-like DNA (IR-A).//0.011:615:56//X95275
- 20 F-HEMBB1001762//CIT-HSP-2290J16.TF CIT-HSP Homo sapiens genomic clone 2290J16, genomic survey sequence.//0.84:208:64//AQ005184  
F-HEMBB1001785//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P3, WORKING DRAFT SEQUENCE.//0.0019:469:60//AL031746  
F-HEMBB1001797//Human heterogenous nuclear RNA W16W.//0.00012:83:86//X17272
- 25 F-HEMBB1001802//Plasmodium falciparum MAL3P7, complete sequence.//1.8e-11:538:60//AL034559  
F-HEMBB1001812//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B8, WORKING DRAFT SEQUENCE.//1.0e-56:304:84//Z98882  
F-HEMBB1001816//Homo sapiens chromosome 19, cosmid F24083, complete sequence.//3.6e-75:300:87//AC005204
- 30 F-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//2.3e-162:763:98//AF056209  
F-HEMBB1001834//CIT-HSP-2291012.TF CIT-HSP Homo sapiens genomic clone 2291012, genomic survey sequence.//7.6e-08:73:94//AQ004168  
F-HEMBB1001836//Homo sapiens 12q13.1 PAC RPC1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.7e-30:297:79//AC004801
- 35 F-HEMBB1001839//Human Chromosome X, complete sequence.//0.016:293:63//AC004073  
F-HEMBB1001850//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0027:812:58//AC005504  
F-HEMBB1001863//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.3e-43:520:72//AC004581
- 40 F-HEMBB1001867//Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.//1.7e-56:399:86//U07563  
F-HEMBB1001868//Rattus norvegicus clone 923 polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//6.1e-08:234:67//U01145
- 45 F-HEMBB1001869//Homo sapiens full-length insert cDNA clone YT86F01.//7.4e-87:432:97//AF085974  
F-HEMBB1001872  
F-HEMBB1001874//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.4e-14:631:61//AC005000  
F-HEMBB1001875//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//0.93:415:57//Z82209
- 50 F-HEMBB1001880//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//1.0e-18:729:60//Z93403  
F-HEMBB1001899//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-10, complete sequence.//0.0038:425:58//AL010216
- 55 F-HEMBB1001905//S. pombe chromosome III cosmid c330.//1.1e-23:520:62//AL031603  
F-HEMBB1001906  
F-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds.//3.7e-82:672:81//U47742

- F-HEM BB1001910//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0033:566:55//AC005505
- F-HEM BB1001911//Arabidopsis thaliana chromosome II BAC F26C24 genomic sequence, complete sequence.//1.0:581:58//AC004705
- 5 F-HEM BB1001915//Caenorhabditis elegans cosmid T05H10, complete sequence.//1.2e-16:283:67//Z47812
- F-HEM BB1001921//Homo sapiens chromosome 17, clone hCIT.123\_J\_14, complete sequence.//3.4e-07:803:58//AC003950
- F-HEM BB1001922//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence.//5.0e-06:756:56//AE001391
- 10 F-HEM BB1001925//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//3.1e-45:609:73//AL009181
- F-HEM BB1001930//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 10/11.//3.2e-158:745:99//AB020867
- F-HEM BB1001944//, complete sequence.//4.1e-60:638:73//AC005815
- 15 F-HEM BB1001945//HS\_3185\_B1\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=9 Row=N, genomic survey sequence.//1.0:280:58//AQ188882
- F-HEM BB1001947//Human mRNA for KIAA0392 gene, partial cds.//5.6e-20:333:66//AB002390
- F-HEM BB1001950//Human lipocortin (LIP) 2 gene, upstream region.//0.0094:180:63//M62899
- F-HEM BB1001952//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 101A4, WORKING DRAFT SEQUENCE.//5.4e-19:329:70//Z93341
- 20 F-HEM BB1001953//Homo sapiens chromosome 17, clone hRPK.795\_F\_17, complete sequence.//0.11:589:58//AC005284
- F-HEM BB1001957//Human DNA sequence from PAC 204E5 on chromosome 12. Contains exon similar to Wilms' Tumour-related protein QM-like P2X-like receptor, ATP ligand gated ion channel, ESTs, CpG island.//9.8e-25:446:67//Z98941
- 25 F-HEM BB1001962//Homo sapiens chromosome 16, BAC clone 462G18 (LANL), complete sequence.//2.8e-147:72:97//AC005736
- F-HEM BB1001967//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces.//3.2e-56:650:71//AC004963
- 30 F-HEM BB1001973//Homo sapiens chromosome 2p13.3-clone RPC111-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.//1.2e-42:327:84//AC005844
- F-HEM BB1001983//CIT-HSP-2315M4.TF CIT-HSP Homo sapiens genomic clone 2315M4, genomic survey sequence.//8.8e-35:198:96//AQ028071
- F-HEM BB1001988//D.polychoa microsatellite sequence (clone Dp 1C e12).//4.5e-07:337:62//X92189
- 35 F-HEM BB1001990//HS\_3234\_A1\_G08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3234 Col=15 Row=M, genomic survey sequence.//0.039:279:59//AQ204689
- F-HEM BB1001996//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191J18, WORKING DRAFT SEQUENCE.//0.18:392:58//AL024507
- F-HEM BB1001997//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.3e-43:446:71//AC005069
- 40 F-HEM BB1002002//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.077:444:58//AC004153
- F-HEM BB1002005//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 963K23, WORKING DRAFT SEQUENCE.//3.4e-16:173:78//AL031685
- 45 F-HEM BB1002009//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00033:790:56//AC005506
- F-HEM BB1002015//Homo sapiens genomic DNA, chromosome 21q11.1, segment 27/28, WORKING DRAFT SEQUENCE.//6.7e-05:126:76//AP000056
- F-HEM BB1002042//Oncorhynchus mykiss cytochrome P450 (CYP4V1) mRNA, partial cds.//6.4e-33:402:69//AF046012
- 50 F-HEM BB1002043
- F-HEM BB1002044//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//3.0e-167:809:97//AC005740
- F-HEM BB1002045
- 55 F-HEM BB1002049//Homo sapiens chromosome 17, clone hRPC.161\_P\_9, complete sequence.//0.87:177:65//AC006237
- F-HEM BB1002050//Streptomyces coelicolor cosmid D78.//8.5e-08:644:58//AL034355
- F-HEM BB1002068//Homo sapiens mRNA for KIAA0612 protein, partial cds.//2.5e-05:402:61//AB014512

F-HEMBB1002069  
 F-HEMBB1002092/\*\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B33108; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//7.8e-104:550:83//AC004064  
 F-HEMBB1002094//Homo sapiens genomic DNA, 21q region, clone: 125H6N2, genomic survey sequence.//2.9e-49:302:83//AG001476  
 5 F-HEMBB1002115//Homo sapiens chromosome 16, cosmid clone 378E2 (LANL), complete sequence.//0.00023:542.61//AC004035  
 F-HEMBB1002134//Human h-neuro-d4 protein mRNA, complete cds.//7.3e-43:533:70//U43843  
 10 F-HEMBB1002139//HS-1048-A2-B02-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 831 Col=4 Row=C, genomic survey sequence.//0.055:228:66//B38714  
 F-HEMBB1002142//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P5, WORKING DRAFT SEQUENCE.//0.0095:276:64//AL031748  
 F-HEMBB1002152//Human Chromosome X, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.055:520:57//AC002421  
 15 F-HEMBB1002189//Homo sapiens cosmid ICRF104I0935Q8 from Xq28, complete sequence.//2.6e-05:311.63//AF002998  
 F-HEMBB1002190//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//5.4e-05:647:59//AC005140  
 F-HEMBB1002193//Sequence 5 from patent US 5709858.//1.8e-34:179:100//I80846  
 20 F-HEMBB1002217//Homo sapiens mRNA for zinc finger protein 10.//1.2e-23:405:67//X52332  
 F-HEMBB1002218//HS\_2056\_B1\_C09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens clone Plate=2056 Col=17 Row=F, genomic survey sequence.//3.3e-45:245:97//AQ244711  
 F-HEMBB1002232//Human chromosome 11 72g7 cosmid, complete sequence.//1.9e-21:314:70//U73648  
 F-HEMBB1002247  
 25 F-HEMBB1002249//Homo sapiens DNA sequence from BAC 3418 on chromosome 6p21.3-22.1. Contains ZNF184 gene coding for Kruppel related Zinc Finger protein 184, a hnRNP core protein A1 (mouse Fli-2, rat helix destabilizing protein, mouse Topoisomerase-inhibitor suppressed gene TIS) LIKE pseudogene, a HB15 (CD83 antigen precursor) LIKE pseudogene, Ser-tRNA, Glu-tRNA and Met-tRNA (Met-tRNA-i gene 1) genes. Contains ESTs, STSs and GSSs, complete sequence.//4.1e-45:327:83//AL021918  
 30 F-HEMBB1002254//Human chromosome 16 BAC clone LANL cosmid-440E5, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.8e-40:315:82//AC002506  
 F-HEMBB1002255//Plasmodium falciparum MAL3P3, complete sequence.//0.0035:312:62//Z98547  
 F-HEMBB1002266//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.013:469:59//AC005504  
 35 F-HEMBB1002280//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-259H10, complete sequence.//5.3e-18:527.61//AC004682  
 F-HEMBB1002300//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//8.6e-139:818.88//U73642  
 F-HEMBB1002306//HS\_3109\_A2\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3109 Col=2 Row=O, genomic survey sequence.//1.3e-75:371:98//AQ148164  
 40 F-HEMBB1002327//HS\_3235\_B2\_G10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=20 Row=N, genomic survey sequence.//3.3e-83:418:97//AQ209752  
 F-HEMBB1002329//CITBI-E1.2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//3.3e-31:220:88//AQ263402  
 45 F-HEMBB1002340  
 F-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.//4.1e-154:724:98//AJ010841  
 F-HEMBB1002358//Human thymidylate kinase (CDC8) mRNA, complete cds.//3.3e-36:192:98//L16991  
 F-HEMBB1002359//Human Rev interacting protein Rip-1 mRNA, complete cds.//1.8e-13:96:96//U55766  
 F-HEMBB1002364//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 376D21, WORKING DRAFT SEQUENCE.//7.5e-24:202:71//Z98946  
 50 F-HEMBB1002371//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.9e-06:674:56//AC004153  
 F-HEMBB1002381//Homo sapiens chromosome 16, cosmid clone RT163 (LANL), complete sequence.//0.34:238:61//AC005222  
 55 F-HEMBB1002383  
 F-HEMBB1002387//CIT-HSP-2173E20.TR CIT-HSP Homo sapiens genomic clone 2173E20, genomic survey sequence.//5.2e-17:434:66//B91052  
 F-HEMBB1002409//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3

precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//1.2e-56:324:88//AL008712  
 F-HEM BB1002415//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 364i1, WORKING  
 DRAFT SEQUENCE.//8.9e-35:334:75//AL031319  
 F-HEM BB1002425//Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence.//1.0e-36:317:76//  
 5 U62317  
 F-HEM BB1002442//Rattus norvegicus lin-10 protein homolog (lin-10) mRNA, complete cds.//4.3e-88:296:92//  
 U92010  
 F-HEM BB1002453//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 86D1, WORKING  
 DRAFT SEQUENCE.//2.7e-43:419:78//AL034349  
 10 F-HEM BB1002457//Homo sapiens clone DJ0982E09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//  
 1.3e-27:542:68//AC005534  
 F-HEM BB1002458//HS\_3246\_A2\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3246 Col=10 Row=M, genomic survey sequence.//3.2e-51:257:99//AQ217993  
 F-HEM BB1002477//Human Grb2-associated binder-1 mRNA, complete cds.//1.9e-87:493:92//U43885  
 15 F-HEM BB1002489  
 F-HEM BB1002492//Arabidopsis thaliana BAC T15B16.//0.028:516:57//AF104919  
 F-HEM BB1002495//Homo sapiens chromosome 17, clone hRPK.421\_E\_14, complete sequence.//1.1e-16:297:  
 68//AC006141  
 F-HEM BB1002502//Homo sapiens clone DJ1163L11, complete sequence.//1.1e-91:675:82//AC005230  
 20 F-HEM BB1002509//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//2.7e-  
 11:648:60//AC004605  
 F-HEM BB1002510//HS\_3236\_B1\_H11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3236 Col=21 Row=P, genomic survey sequence.//1.2e-06:67:94//AQ205992  
 F-HEM BB1002520//Homo sapiens BAC clone NH0004N07 from Y, complete sequence.//1.2e-70:580:72//  
 25 AC006152  
 F-HEM BB1002522//Homo sapiens Xp22 bin 150 clone GSHB-223P11 (Genome Systems Human BAC library)  
 complete sequence.//5.6e-22:516:64//AC004553 F-HEM BB1002531  
 F-HEM BB1002534//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 668J24, WORKING  
 DRAFT SEQUENCE.//6.9e-62:265:87//AL034346  
 30 F-HEM BB1002545//Human BAC clone RG128M16 from 7q21-7q22, complete sequence.//2.7e-44:200:82//  
 AC000059  
 F-HEM BB1002550//Homo sapiens PAC clone DJ0910I17 from 7q11.21-q11.23, complete sequence.//0.02:161:  
 68//AC004927  
 F-HEM BB1002556//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//7.5e-43:306:77//  
 35 AC004861  
 F-HEM BB1002579  
 F-HEM BB1002582//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING  
 DRAFT SEQUENCE.//0.00018:431:61//AL033520  
 F-HEM BB1002590//Yeast (S.cerevisiae) mitochondrial apocytocrome b gene, 3' flank.//0.78:147:64//J01471  
 40 F-HEM BB1002596//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 9E21, WORKING  
 DRAFT SEQUENCE.//3.6e-50:692:69//AL008639  
 F-HEM BB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds.//9.1e-151:710:98//AF089749  
 F-HEM BB1002601//Human BAC clone RG020D02 from 7q22, complete sequence.//1.5e-07:416:60//AC002381  
 F-HEM BB1002603//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//0.40:341:60//AC002454  
 45 F-HEM BB1002607//Mus musculus homeobox containing nuclear transcriptional factor Hmx1 (Hmx1) gene, com-  
 plete cds.//0.0042:460:60//AF009614  
 F-HEM BB1002610//Homo sapiens Chromosome 12q24 PAC RPC13-462E2 (Roswell Park Cancer Institute Human  
 PAC library) complete sequence.//6.3e-23:559:63//AC003029  
 F-HEM BB1002613//Homo sapiens Chromosome 22q12 BAC Clone 566c1, complete sequence.//4.2e-17:441:63//  
 50 AC000025  
 F-HEM BB1002614//Plasmodium falciparum chromosome 2, section 54 of 73 of the complete sequence.//0.013:  
 324:56//AE001417  
 F-HEM BB1002617//Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.//2.1e-07:  
 441:60//AF001550  
 55 F-HEM BB1002623//C. hyalina microsatellite marker DNA (id ATCC4).//0.57:106:66//Z95304  
 F-HEM BB1002635//Human JNK3 alpha2 protein kinase (JNK3A2) mRNA, complete cds.//4.8e-22:127:100//  
 U34819  
 F-HEM BB1002664//HS\_2265\_A1\_H06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-



- nomic clone Plate=2265 Col=11 Row=O, genomic survey sequence.//0.54:115:67//AQ101557  
 F-HEMBB1002677//Homo sapiens (subclone 3\_d1 from P1 H25) DNA sequence, complete sequence.//2.2e-49:  
 784:68//L81774  
 F-HEMBB1002683//Homo sapiens type IV collagen 5a chain (COL4A5) gene, exon 23.//1.0:112:63//U04492  
 5 F-HEMBB1002684//HS-1050-A2-G06-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone  
 Plate=CT 772 Col=12 Row=M, genomic survey sequence.//4.4e-07:86:84//B39748  
 F-HEMBB1002686//HS-1023-B2-F10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone  
 Plate=CT 802 Col=20 Row=L, genomic survey sequence.//0.98:183:61//B34077  
 10 F-HEMBB1002692//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1108H3, WORKING  
 DRAFT SEQUENCE.//0.00039:408:60//AL033525  
 F-HEMBB1002697//Homo sapiens clone DJ1087M19, WORKING DRAFT SEQUENCE, 7 unordered pieces.//  
 7.3e-35:323:74//AC004955  
 F-HEMBB1002699//Mus musculus D6Mm5e protein (D6Mm5e) and DOK protein (Dok) genes, complete cds; and  
 LOR2 protein (Lor2) gene, partial cds.//0.031:325:62//AF084363  
 15 F-HEMBB1002702//HS-1025-A2-D01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic  
 clone Plate=CT 804 Col=2 Row=G, genomic survey sequence.//1.8e-25:158:95//B34720  
 F-HEMBB1002705//Homo sapiens DNA, chromosome 21q22.2, PAC clone 25P16 complete sequence, encoding  
 carbonyl reductase and carbonyl reductase 3 (complete cds).//1.7e-137:534:96//AB003151  
 F-HEMBB1002712//Human DNA sequence from cosmid cJ115G11, between markers DX56791 and DXS8038  
 20 on chromosome X contains ESTs and STS.//0.0019:612:58//Z71187  
 F-MAMMA1000009//Human chromosome 1 BAC 308G1 genomic sequence, WORKING DRAFT SEQUENCE, 3  
 unordered pieces.//6.1e-43:354:81//AC003117  
 F-MAMMA1000019  
 F-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FMO5).//2.0e-40:185:97//Z47553  
 25 F-MAMMA1000025//Homo sapiens PAC clone DJ0806A17 from 7p13-p14, complete sequence.//1.0:211:65//  
 AC005483  
 F-MAMMA1000043//Human angiotensin I-converting enzyme (ACE) gene, intron 12.//0.075:204:65//M73275  
 F-MAMMA1000045//Human DNA sequence from clone 142F18 on chromosome Xq26.3-27.2 Contains part of a  
 gene similar to melanoma-associated antigen, EST, GSS and an inverted repeat, complete sequence.//4.1e-122:  
 30 495:79//AL031073  
 F-MAMMA1000055//M.musculus mRNA for testin.//2.1e-35:559:66//X78989  
 F-MAMMA1000057//Homo sapiens chromosome 17, clone hRPK.259\_G\_18, complete sequence.//5.5e-121:703:  
 89//AC005829  
 F-MAMMA1000069//Homo sapiens minisatellite ceb1 repeat region.//0.00013:329:60//AF048727  
 35 F-MAMMA1000084//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains  
 ESTs STS and CpG island.//2.1e-53:445:79//Z93023  
 F-MAMMA1000085//Caenorhabditis elegans cosmid Y23H5A.//0.0017:164:64//AF077541  
 F-MAMMA1000092//Homo sapiens BAC clone GS465N13 from 7p15-p21, complete sequence.//1.2e-70:598:78//  
 AC004744  
 40 F-MAMMA1000103//Homo sapiens chromosome 17, clone hCIT.91\_J\_4, complete sequence.//1.1e-156:857:92//  
 AC003976  
 F-MAMMA1000117//HS\_3223\_B2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3223 Col=16 Row=H, genomic survey sequence.//5.4e-100:527:94//AQ221160  
 F-MAMMA1000129//ryanodine receptor.//0.055:492:59//A20359  
 45 F-MAMMA1000133  
 F-MAMMA1000134//HS\_3078\_B1\_C02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3078 Col=3 Row=F, genomic survey sequence.//2.1e-93:462:97//AQ144362  
 F-MAMMA1000139//Homo sapiens Xp22 PAC RPC1-5G11 (from Roswell Park Cancer Center) complete se-  
 quence.//3.3e-14:322:65//AC002369  
 50 F-MAMMA1000143//Homo sapiens mRNA for KIAA0695 protein, complete cds.//6.9e-25:148:97//AB014585  
 F-MAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2) mRNA, complete cds.//1.0e-29:  
 219:87//AF031924  
 F-MAMMA1000163  
 F-MAMMA1000171//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence.//6.3e-14:92:88//  
 AC005393  
 55 F-MAMMA1000173//Mus musculus SH3-containing protein SH3P7 mRNA, complete cds. similar to Human  
 Drebrin.//2.2e-114:698:87//U58894  
 F-MAMMA1000175//HS\_3050\_B1\_B03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

nomic clone Plate=3050 Col=5 Row=D, genomic survey sequence.//6.2e-73:357:99//AQ102678  
 F-MAMMA1000183//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING  
 DRAFT SEQUENCE.//4.6e-94:904:73//AL023808  
 F-MAMMA1000198//Z. diploperennis repetitive DNA (clone ZEAR 266).//0.18:152:70//X53610  
 5 F-MAMMA1000221//Human Chromosome 15q11-q13 PAC clone pDJ778a2, complete sequence.//0.017:99:75//  
 AC004583  
 F-MAMMA1000227//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 467K16, WORKING  
 DRAFT SEQUENCE.//0.36:312:62//AL031283  
 10 F-MAMMA1000241//HS\_3217\_B1\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3217 Col=3 Row=D, genomic survey sequence.//1.9e-94:456:98//AQ193401  
 F-MAMMA1000251//Homo sapiens NF2 gene.//0.00092:270:64//Y18000  
 F-MAMMA1000254//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
 DRAFT SEQUENCE, 14 unordered pieces.//0.0034:777:57//AC005140  
 F-MAMMA1000257//Homo sapiens DNA sequence from PAC 201D7 on chromosome 6p22.1-22.3. Contains EST  
 15 and STS.//0.00036:230:65//AL022717  
 F-MAMMA1000264//Homo sapiens (subclone 9\_f5 from P1 H17) DNA sequence, complete sequence.//1.5e-30:  
 499:68//L81612  
 F-MAMMA1000266//Bacillus lyncceum strain pMEL12 Bag320 satellite DNA.//0.28:218:64//AF034430  
 F-MAMMA1000270//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//1.4e-157:  
 788:96//AF001549  
 20 F-MAMMA1000277//Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.//0.70:320:61//  
 AL021897  
 F-MAMMA1000278//Sequence 23 from patent US 5708157.//9.3e-103:540:95//I80055  
 F-MAMMA1000279//Human DNA sequence from clone 769D20 on chromosome Xp21.1-21.3 Contains EST, STS,  
 25 GSS, complete sequence.//2.4e-49:262:77//AL031643  
 F-MAMMA1000284//cSRL-165E12-cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic  
 clone cSRL-165E12, genomic survey sequence.//1.1e-30:324:75//B03004  
 F-MAMMA1000287//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//2.7e-54:401:83//AC006213  
 F-MAMMA1000302//Drosophila melanogaster complete mitochondrial genome.//0.0051:307:61//U37541  
 30 F-MAMMA1000307//Homo sapiens chromosome 12p13.3 clone RPCI5-1154L15, WORKING DRAFT SE-  
 QUENCE, 67 unordered pieces.//0.15:449:59//AC006205  
 F-MAMMA1000309//cDNA coding human apolipoprotein E3.//0.00010:691:58//E00359  
 F-MAMMA1000312//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 798A17, WORKING  
 DRAFT SEQUENCE.//0.27:301:60//AL031274  
 35 F-MAMMA1000313  
 F-MAMMA1000331//Human Chromosome 16 BAC clone CIT987SK-A-735G6, complete sequence.//9.8e-06:151:  
 71//AC002400  
 F-MAMMA1000339  
 F-MAMMA1000340//HS\_2181\_B2\_F07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 40 nomic clone Plate=2181 Col=14 Row=L, genomic survey sequence.//4.3e-05:181:68//AQ024288  
 F-MAMMA1000348//Homo sapiens chromosome 17, clone HRPC843B9, complete sequence.//5.3e-30:575:66//  
 AC004139  
 F-MAMMA1000356//Homo sapiens clone RG038K21, WORKING DRAFT SEQUENCE, 3 unordered pieces.//  
 1.8e-52:264:76//AC005052  
 45 F-MAMMA1000360//Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence.//6.5e-91:569:88//  
 AC004879  
 F-MAMMA1000361//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribos-  
 omal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//1.4e-42:315:83//Z98950  
 F-MAMMA1000372//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING  
 50 DRAFT SEQUENCE.//2.9e-114:516:89//AL022345  
 F-MAMMA1000385//CITBI-E1-2517E13.TF CITBI-E1 Homo sapiens genomic clone 2517E13, genomic survey  
 sequence.//6.9e-26:377:71//AQ279944  
 F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds.//3.7e-148:710:  
 98//AB015132  
 55 F-MAMMA1000395  
 F-MAMMA1000402//Homo sapiens clone DJ0718N17, complete sequence.//4.0e-115:845:85//AC005999  
 F-MAMMA1000410//HS\_3245\_A1\_C02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3245 Col=3 Row=E, genomic survey sequence.//9.6e-42:350:80//AQ205768

- F-MAMMA1000413//HS\_3223\_B2\_F01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=2 Row=L, genomic survey sequence.//1.6e-48:318:89//AQ188456
- F-MAMMA1000414//HS\_2027\_B2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=8 Row=F, genomic survey sequence.//1.4e-46:286:92//AQ231369
- 5 F-MAMMA1000416//Drosophila melanogaster DNA sequence (P1s DS07528 (D169) and DS06665 (D220)), complete sequence.//9.4e-33:310:72//AC004640
- F-MAMMA1000421//Homo sapiens clone DJ1129D05, complete sequence.//3.3e-29:223:84//AC005630
- F-MAMMA1000422
- 10 F-MAMMA1000423//Drosophila yakuba mitochondrial DNA molecule.//2.2e-10:639:57//X03240
- F-MAMMA1000424//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.6e-47:556:68//AC003973
- F-MAMMA1000429//Mus musculus SDP8 mRNA, complete cds.//8.0e-99:545:92//AF062484
- F-MAMMA1000431//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.8e-41:289:79//AC005283
- 15 F-MAMMA1000444//Human DNA sequence from clone 71487 on chromosome 22q12.2-13.2 Contains CYTOCHROME C OXIDASE VIIB precursor like pseudogene and ESTs, complete sequence.//2.3e-34:291:80//Z9755
- F-MAMMA1000446
- F-MAMMA1000458//Mus musculus clone OST9003, genomic survey sequence.//5.0e-53:231:84//AF046620
- 20 F-MAMMA1000468//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 291J10, WORKING DRAFT SEQUENCE.//0.75:303:60//Z93017
- F-MAMMA1000472//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 414D7, WORKING DRAFT SEQUENCE.//4.0e-41:403:77//AL033543
- F-MAMMA1000478//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//9.5e-54:369:77//AC005081
- 25 F-MAMMA1000483//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//3.6e-34:332:77//AC004381
- F-MAMMA1000490//Homo sapiens 12q13.1 PAC RPC11-90J4 (Roswell Park Cancer Institute Human PAC library) complete sequence.//8.9e-128:822:87//AC003686
- F-MAMMA1000500//CIT-HSP-231905.TF CIT-HSP Homo sapiens genomic clone 2319O5, genomic survey sequence.//4.8e-29:175:94//AQ044812
- 30 F-MAMMA1000501//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//5.7e-45:334:82//AL022336
- F-MAMMA1000516//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATPSG1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.9e-43:529:69//Z92545
- 35 F-MAMMA1000522//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.//2.0e-14:380:63//AL022576
- 40 F-MAMMA1000524//Homo sapiens chromosome 10 clone CIT-HSP-1338F24 map 10p11.2-10p12.1, complete sequence.//1.4e-22:420:66//AC006101
- F-MAMMA1000559//Human HepG2 3' region cDNA, clone hmd3f08.//5.4e-29:168:97//D16922
- F-MAMMA1000565//RPC111-61K6.TJ RPC111 Homo sapiens genomic clone R-61K6, genomic survey sequence.//1.7e-120:561:100//AQ194238
- 45 F-MAMMA1000567//Human DNA sequence from PAC 179D3, between markers DXS6791 and DXS8038 on chromosome X contains S10 GTP-binding protein, ESTs and CpG island.//3.1e-43:387:80//Z81370
- F-MAMMA1000576//Homo sapiens BAC clone RC442F18 from 2, complete sequence.//1.2e-30:237:75//AC005104
- F-MAMMA1000583//RPC111-60M22.TJ RPC111 Homo sapiens genomic clone R-60M22, genomic survey sequence.//9.6e-102:487:99//AQ198091
- 50 F-MAMMA1000585//Homo sapiens clone UWGC:djs14 from 7p14-15, complete sequence.//5.2e-39:370:78//AC006195
- F-MAMMA1000594//Homo sapiens chromosome 19, cosmid R31646, complete sequence.//3.9e-43:328:83//AC005338
- 55 F-MAMMA1000597//Homo sapiens chromosome 17, clone hRPK.481\_C\_4, complete sequence.//1.5e-32:259:82//AC005839
- F-MAMMA1000605//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//2.4e-59:318:83//AL031297

- F-MAMMA1000612//HS\_2188\_A2\_D02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=4 Row=G, genomic survey sequence.//4.8e-30:171.96//AQ116793
- F-MAMMA1000616//HS\_3176\_A1\_E06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3176 Col=11 Row=I, genomic survey sequence.//4.7e-28:287.79//AQ300310
- 5 F-MAMMA1000621//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 273F20, WORKING DRAFT SEQUENCE.//0.015:478.58//AL034371
- F-MAMMA1000623
- F-MAMMA1000625//DNA encoding Hepatitis C virus antigen.//0.93:196.61//E06898
- F-MAMMA1000643//Homo sapiens nephrocytin (NPHP1) mRNA, partial cds.//0.95:365.59//AF023674
- 10 F-MAMMA1000684//HS\_3096\_B1\_C02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3096 Col=3 Row=F, genomic survey sequence.//2.7e-51:257.99//AQ145137
- F-MAMMA1000689//Homo sapiens chromosome 19, cosmid R26908, complete sequence.//2.0e-66:586.67//AC004785
- F-MAMMA1000670//HS\_2243\_B2\_A08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2243 Col=16 Row=B, genomic survey sequence.//8.7e-05:94.80//AQ153650
- F-MAMMA1000672//Mus musculus clone OST8270, genomic survey sequence.//3.9e-64:471.81//AF046705
- F-MAMMA1000684//Suid herpesvirus 1 Rsp40 mRNA, partial cds.//1.2e-07:186.67//U27489
- F-MAMMA1000696//Human oligodendrocyte myelin glycoprotein (OMG) exons 1-2; neurofibromatosis 1 (NF1) exons 28-49; ecotropic viral integration site 2B (EVI2B) exons 1-2; ecotropic viral integration site 2A (EVI2A) exons 1-2; adenylate kinase (AK3) exons 1-2.//3.0e-53:653.70//L05367
- 20 F-MAMMA1000707//CIT-HSP-2302019. TR CIT-HSP Homo sapiens genomic clone 2302019, genomic survey sequence.//1.8e-08:131.77//AQ017947
- F-MAMMA1000713//Rattus norvegicus clonol polymeric immunoglobulin receptor mRNA 3' untranslated region, GAA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//0.062:134.67//U00762
- 25 F-MAMMA1000714//Chicken hsp90 gene for 90 kDa-heat shock protein 5'-end.//1.0:266.61//X15028
- F-MAMMA1000718//CIT-HSP-2171B10. TF CIT-HSP Homo sapiens genomic clone 2171B10, genomic survey sequence.//3.6e-05:289.60//B95401
- F-MAMMA1000720//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//4.4e-184:842.98//AC005781
- 30 F-MAMMA1000723//Homo sapiens clone DJ0892G19, complete sequence.//8.8e-05:430.60//AC004917
- F-MAMMA1000731//Drosophila melanogaster DNA sequence (P1 DS07049 (D133)), complete sequence.//3.8e-55:796.66//AC004274
- F-MAMMA1000732//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//6.6e-77:555.74//AF064859
- 35 F-MAMMA1000733//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P6, WORKING DRAFT SEQUENCE.//0.98:479.58//AL031749
- F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//7.3e-168:802.98//AF100141
- F-MAMMA1000738//S. cerevisiae chromosome XIV reading frame ORF YNL132w.//8.6e-31:626.63//Z71408
- F-MAMMA1000744//Gorilla Alu-repetitive sequence in beta-globin gene cluster.//2.7e-54:410.82//X06123
- 40 F-MAMMA1000746//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-10F4, complete sequence.//3.7e-109:779.83//AC004158
- F-MAMMA1000752//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.2e-20:444.63//AC005075
- F-MAMMA1000760//Homo sapiens clone RG015P03, complete sequence.//1.5e-44:403.79//AC005048
- 45 F-MAMMA1000761//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.3e-22:159.81//AC004166
- F-MAMMA1000775//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//1.3e-51:789.68//AC005703
- F-MAMMA1000776//Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.//5.7e-40:238.78//Z95116
- 50 F-MAMMA1000778//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 153G14, WORKING DRAFT SEQUENCE.//7.6e-29:222.84//AL031118
- F-MAMMA1000782//Human 2,4-dienoyl-CoA reductase gene, exon 9.//0.90:137.62//U94987
- F-MAMMA1000791//\*\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECD region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//0.00058:163.71//AC003656
- 55 F-MAMMA1000802//Homo sapiens chromosome 19, cosmid R33729, complete sequence.//6.3e-151:714.99//